

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 15:19:10 ; Search time 23 Seconds
(without alignments)
3.723 Million cell updates/sec

Title: us-10-008-789-3
Perfect score: 1755
Sequence: 1 cgcgcggcggtcccaaaa.....aaaaaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1330 seqs, 24398 residues

Total number of hits satisfying chosen parameters: 2660

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1334 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24.2	1.4	29	1	HSA241944
C 2	22.4	1.3	24	1	AR261539
C 3	21.4	1.2	24	1	BD196419
C 4	21.4	1.2	25	1	BD056964
C 5	21.4	1.2	26	1	AR174581
C 6	21.4	1.2	26	1	BD248974
C 7	21.4	1.2	26	1	I79494
C 8	21.4	1.2	26	1	AR263648
C 9	21.4	1.2	26	1	AR374073
C 10	21.4	1.2	26	1	AX106717
C 11	21.4	1.2	27	1	AR241865
C 12	21.4	1.2	21	1	AX825131
C 13	21.4	1.2	21	1	AX825158
C 14	21.4	1.2	21	1	AX825164
C 15	21.4	1.2	24	1	AX817782
C 16	21.4	1.2	24	1	AX838369
C 17	21.4	1.2	25	1	I29929
C 18	21.4	1.2	25	1	AX338548
C 19	21.4	1.2	25	1	AX394507
C 20	21.4	1.2	25	1	AX394514
C 21	21.4	1.2	26	1	I79496
C 22	21.4	1.2	26	1	AX338547
C 23	21.4	1.2	26	1	BD192375
C 24	20.6	1.2	24	1	AX391871
C 25	20.6	1.2	26	1	BD237566
C 26	20.6	1.2	26	1	AR257336
C 27	20.6	1.2	26	1	AR263647
C 28	20.6	1.2	26	1	AX814950
C 29	20.6	1.2	26	1	BD062456
C 30	20.6	1.2	27	1	AX327980
C 31	20.6	1.2	27	1	AX513052
C 32	20.6	1.2	27	1	AX711956
C 33	20.4	1.2	22	1	AR164336

34	20.4	1.2	22	1	I31828	ACCESSION: I31828
35	20.4	1.2	22	1	I69425	ACCESSION: I69425
c 36	20.4	1.2	23	1	BD244857	ACCESSION: BD244857
37	20.4	1.2	24	1	AR010037	ACCESSION: AR010037
38	20.4	1.2	24	1	AR034772	ACCESSION: AR034772
39	20.4	1.2	24	1	AR068465	ACCESSION: AR068465
40	20.4	1.2	24	1	AR105984	ACCESSION: AR105984
41	20.4	1.2	24	1	AR107972	ACCESSION: AR107972
c 42	20.4	1.2	24	1	BD234330	ACCESSION: BD234330
43	20.4	1.2	24	1	I24762	ACCESSION: I24762
44	20.4	1.2	24	1	AR184443	ACCESSION: AR184443
45	20.4	1.2	24	1	AR202876	ACCESSION: AR202876
46	20.4	1.2	24	1	AR213697	ACCESSION: AR213697
47	20.4	1.2	24	1	AR232949	ACCESSION: AR232949
c 48	20.4	1.2	24	1	AR241846	ACCESSION: AR241846
49	20.4	1.2	24	1	AR340571	ACCESSION: AR340571
50	20.4	1.2	24	1	AR345020	ACCESSION: AR345020
51	20.4	1.2	24	1	AR431307	ACCESSION: AR431307
c 52	20.4	1.2	24	1	AR431310	ACCESSION: AR431310
c 53	20.4	1.2	24	1	AX104241	ACCESSION: AX104241
c 54	20.4	1.2	24	1	AX104769	ACCESSION: AX104769
55	20.4	1.2	24	1	AX104770	ACCESSION: AX104770
56	20.4	1.2	24	1	AX354553	ACCESSION: AX354553
c 57	20.4	1.2	24	1	AX355813	ACCESSION: AX355813
c 58	20.4	1.2	24	1	AX427163	ACCESSION: AX427163
59	20.4	1.2	24	1	AX428574	ACCESSION: AX428574
c 60	20.4	1.2	24	1	AX547294	ACCESSION: AX547294
c 61	20.4	1.2	24	1	AX547822	ACCESSION: AX547822
62	20.4	1.2	24	1	AX547823	ACCESSION: AX547823
c 63	20.4	1.2	24	1	AX684290	ACCESSION: AX684290
c 64	20.4	1.2	24	1	AX750585	ACCESSION: AX750585
c 65	20.4	1.2	24	1	AX829247	ACCESSION: AX829247
66	20.4	1.2	24	1	BD136714	ACCESSION: BD136714
c 67	20.4	1.2	25	1	AR105982	ACCESSION: AR105982
c 68	20.4	1.2	25	1	BD234336	ACCESSION: BD234336
c 69	20.4	1.2	25	1	I58009	ACCESSION: I58009
c 70	20.4	1.2	25	1	I96072	ACCESSION: I96072
c 71	20.4	1.2	25	1	AR288252	ACCESSION: AR288252
c 72	20.4	1.2	25	1	AX116188	ACCESSION: AX116188
73	20.4	1.2	25	1	BD187513	ACCESSION: BD187513
c 74	20.4	1.2	25	1	BD187514	ACCESSION: BD187514
c 75	20.4	1.2	25	1	BD204988	ACCESSION: BD204988
c 76	20.4	1.2	26	1	AR137712	ACCESSION: AR137712
c 77	20.4	1.2	26	1	AR174582	ACCESSION: AR174582
c 78	20.4	1.2	26	1	BD248975	ACCESSION: BD248975
c 79	20.4	1.2	26	1	I79495	ACCESSION: I79495
c 80	20.4	1.2	26	1	AR279358	ACCESSION: AR279358
c 81	20.4	1.2	26	1	AR374074	ACCESSION: AR374074
c 82	20.4	1.2	26	1	AR404597	ACCESSION: AR404597
c 83	20.4	1.2	26	1	AX427154	ACCESSION: AX427154
c 84	20.4	1.2	26	1	AX528804	ACCESSION: AX528804
c 85	20.4	1.2	26	1	BD007174	ACCESSION: BD007174
c 86	20.4	1.2	27	1	E04985	ACCESSION: E04985
c 87	20.4	1.2	27	1	AR214918	ACCESSION: AR214918
c 88	20.4	1.2	27	1	AX009609	ACCESSION: AX009609
c 89	20.4	1.2	27	1	AX104719	ACCESSION: AX104719
c 90	20.4	1.2	27	1	AX355814	ACCESSION: AX355814
c 91	20.4	1.2	27	1	AX492939	ACCESSION: AX492939
c 92	20.4	1.2	27	1	AX547772	ACCESSION: AX547772
c 93	20.4	1.2	27	1	BD175131	ACCESSION: BD175131
94	20.4	1.2	27	1	S6486283	ACCESSION: S64864
c 95	20.2	1.2	22	1	AX583623	ACCESSION: AX583623
c 96	20.1	1.1	20	1	AR064875	ACCESSION: AR064875
97	20.1	1.1	20	1	AR080000	ACCESSION: AR080000
98	20.1	1.1	20	1	AR085926	ACCESSION: AR085926
c 99	20.1	1.1	20	1	AR087520	ACCESSION: AR087520
100	20.1	1.1	20	1	AR093312	ACCESSION: AR093312
c 101	20.1	1.1	20	1	AR118970	ACCESSION: AR118970
102	20.1	1.1	20	1	AR121692	ACCESSION: AR121692
103	20.1	1.1	20	1	AR123335	ACCESSION: AR123335
c 104	20.1	1.1	20	1	AR141070	ACCESSION: AR141070
c 105	20.1	1.1	20	1	AR154115	ACCESSION: AR154115
106	20.1	1.1	20	1	AR164658	ACCESSION: AR164658

c 107	1.1	20	1	E12676	ACCESSION:E12676	c 180	19.4	1.1	21	1	AX825147	ACCESSION:AX825147
c 108	1.1	20	1	I36180	ACCESSION:I36180	c 181	19.4	1.1	21	1	AX825148	ACCESSION:AX825148
c 109	1.1	20	1	A1237738	ACCESSION:A1237738	c 182	19.4	1.1	21	1	AX825151	ACCESSION:AX825151
c 110	1.1	20	1	AR222466	ACCESSION:AR222466	c 183	19.4	1.1	21	1	AX825152	ACCESSION:AX825152
c 111	1.1	20	1	AR326083	ACCESSION:AR326083	c 184	19.4	1.1	21	1	AX825154	ACCESSION:AX825154
c 112	1.1	20	1	AR274394	ACCESSION:AR274394	c 185	19.4	1.1	21	1	AX825160	ACCESSION:AX825160
c 113	1.1	20	1	AR343047	ACCESSION:AR343047	c 186	19.4	1.1	21	1	AX825162	ACCESSION:AX825162
c 114	1.1	20	1	AR344936	ACCESSION:AR344936	c 187	19.4	1.1	24	1	E13209	ACCESSION:E13209
c 115	1.1	20	1	AR365970	ACCESSION:AR365970	c 188	19.4	1.1	24	1	AX708815	ACCESSION:AX708815
c 116	1.1	20	1	AR382312	ACCESSION:AR382312	c 189	19.4	1.1	25	1	AX708814	ACCESSION:AX708814
c 117	1.1	20	1	AR429653	ACCESSION:AR429653	c 190	19.2	1.1	24	1	AR074227	ACCESSION:AR074227
c 118	1.1	20	1	AX004876	ACCESSION:AX004876	c 191	19.2	1.1	24	1	AR074235	ACCESSION:AR074235
c 119	1.1	20	1	AX045779	ACCESSION:AX045779	c 192	19.2	1.1	24	1	AR074301	ACCESSION:AR074301
c 120	1.1	20	1	AX045787	ACCESSION:AX045787	c 193	19.2	1.1	24	1	AR074308	ACCESSION:AR074308
c 121	1.1	20	1	AX045790	ACCESSION:AX045790	c 194	19.2	1.1	24	1	AR094555	ACCESSION:AR094555
c 122	1.1	20	1	AX104034	ACCESSION:AX104034	c 195	19.2	1.1	24	1	I20473	ACCESSION:I20473
c 123	1.1	20	1	AX104364	ACCESSION:AX104364	c 196	19.2	1.1	24	1	AR307272	ACCESSION:AR307272
c 124	1.1	20	1	AX104368	ACCESSION:AX104368	c 197	19.2	1.1	24	1	AR307275	ACCESSION:AR307275
c 125	1.1	20	1	AX196224	ACCESSION:AX196224	c 198	19.2	1.1	24	1	AR307277	ACCESSION:AR307277
c 126	1.1	20	1	AX196239	ACCESSION:AX196239	c 199	19.2	1.1	24	1	AX032589	ACCESSION:AX032589
c 127	1.1	20	1	AX354974	ACCESSION:AX354974	c 200	19.2	1.1	24	1	AX032597	ACCESSION:AX032597
c 128	1.1	20	1	AX355810	ACCESSION:AX355810	c 201	19.2	1.1	24	1	AX032663	ACCESSION:AX032663
c 129	1.1	20	1	AX355811	ACCESSION:AX355811	c 202	19.2	1.1	24	1	AX032670	ACCESSION:AX032670
c 130	1.1	20	1	AX440125	ACCESSION:AX440125	c 203	19.2	1.1	25	1	AR074225	ACCESSION:AR074225
c 131	1.1	20	1	AX440140	ACCESSION:AX440140	c 204	19.2	1.1	25	1	AR074226	ACCESSION:AR074226
c 132	1.1	20	1	AX465311	ACCESSION:AX465311	c 205	19.2	1.1	25	1	BD244864	ACCESSION:BD244864
c 133	1.1	20	1	AX465326	ACCESSION:AX465326	c 206	19.2	1.1	25	1	AX032587	ACCESSION:AX032587
c 134	1.1	20	1	AX547087	ACCESSION:AX547087	c 207	19.2	1.1	25	1	AX032588	ACCESSION:AX032588
c 135	1.1	20	1	AX547417	ACCESSION:AX547417	c 208	19.2	1.1	25	1	AX042937	ACCESSION:AX042937
c 136	1.1	20	1	AX547421	ACCESSION:AX547421	c 209	19.2	1.1	25	1	AX043114	ACCESSION:AX043114
c 137	1.1	20	1	AX556139	ACCESSION:AX556139	c 210	19	1.1	19	1	A68209	ACCESSION:A68209
c 138	1.1	20	1	AX556139	ACCESSION:AX556139	c 211	19	1.1	19	1	AR048767	ACCESSION:AR048767
c 139	1.1	20	1	AX664307	ACCESSION:AX664307	c 212	19	1.1	19	1	AR111371	ACCESSION:AR111371
c 140	1.1	20	1	AX664308	ACCESSION:AX664308	c 213	19	1.1	19	1	AR111946	ACCESSION:AR111946
c 141	1.1	20	1	AX741040	ACCESSION:AX741040	c 214	19	1.1	19	1	AR111947	ACCESSION:AR111947
c 142	1.1	20	1	AX741052	ACCESSION:AX741052	c 215	19	1.1	19	1	AR111948	ACCESSION:AR111948
c 143	1.1	20	1	BD008523	ACCESSION:BD008523	c 216	19	1.1	19	1	AR111949	ACCESSION:AR111949
c 144	1.1	20	1	BD080522	ACCESSION:BD080522	c 217	19	1.1	19	1	AR111950	ACCESSION:AR111950
c 145	1.1	20	1	BD107450	ACCESSION:BD107450	c 218	19	1.1	19	1	AR111951	ACCESSION:AR111951
c 146	1.1	20	1	BD218101	ACCESSION:BD218101	c 219	19	1.1	19	1	AR111952	ACCESSION:AR111952
c 147	1.1	20	1	AR080294	ACCESSION:AR080294	c 220	19	1.1	19	1	AR111953	ACCESSION:AR111953
c 148	1.1	20	1	AR084521	ACCESSION:AR084521	c 221	19	1.1	19	1	AR111957	ACCESSION:AR111957
c 149	1.1	20	1	AR084524	ACCESSION:AR084524	c 222	19	1.1	19	1	AR111959	ACCESSION:AR111959
c 150	1.1	20	1	AR093143	ACCESSION:AR093143	c 223	19	1.1	19	1	AR111960	ACCESSION:AR111960
c 151	1.1	20	1	AR095412	ACCESSION:AR095412	c 224	19	1.1	19	1	AR111970	ACCESSION:AR111970
c 152	1.1	20	1	AR153849	ACCESSION:AR153849	c 225	19	1.1	19	1	AR124843	ACCESSION:AR124843
c 153	1.1	20	1	I36166	ACCESSION:I36166	c 226	19	1.1	19	1	AR124844	ACCESSION:AR124844
c 154	1.1	20	1	I65744	ACCESSION:I65744	c 227	19	1.1	19	1	AR124845	ACCESSION:AR124845
c 155	1.1	20	1	AR322245	ACCESSION:AR322245	c 228	19	1.1	19	1	AR124846	ACCESSION:AR124846
c 156	1.1	20	1	AX104720	ACCESSION:AX104720	c 229	19	1.1	19	1	AR124847	ACCESSION:AR124847
c 157	1.1	20	1	AX355812	ACCESSION:AX355812	c 230	19	1.1	19	1	AR124848	ACCESSION:AR124848
c 158	1.1	20	1	AX547773	ACCESSION:AX547773	c 231	19	1.1	19	1	AR124849	ACCESSION:AR124849
c 159	1.1	20	1	AX825132	ACCESSION:AX825132	c 232	19	1.1	19	1	AR124850	ACCESSION:AR124850
c 160	1.1	20	1	AX825133	ACCESSION:AX825133	c 233	19	1.1	19	1	AR124854	ACCESSION:AR124854
c 161	1.1	20	1	AX825134	ACCESSION:AX825134	c 234	19	1.1	19	1	AR124856	ACCESSION:AR124856
c 162	1.1	20	1	AX825155	ACCESSION:AX825155	c 235	19	1.1	19	1	AR124857	ACCESSION:AR124857
c 163	1.1	20	1	AX825156	ACCESSION:AX825156	c 236	19	1.1	19	1	AR124867	ACCESSION:AR124867
c 164	1.1	20	1	AX825157	ACCESSION:AX825157	c 237	19	1.1	19	1	AR135291	ACCESSION:AR135291
c 165	1.1	20	1	AX825163	ACCESSION:AX825163	c 238	19	1.1	19	1	AR135292	ACCESSION:AR135292
c 166	1.1	20	1	AX825165	ACCESSION:AX825165	c 239	19	1.1	19	1	AR135293	ACCESSION:AR135293
c 167	1.1	20	1	AX825166	ACCESSION:AX825166	c 240	19	1.1	19	1	AR135294	ACCESSION:AR135294
c 168	1.1	20	1	BD080832	ACCESSION:BD080832	c 241	19	1.1	19	1	AR135295	ACCESSION:AR135295
c 169	1.1	20	1	BD087491	ACCESSION:BD087491	c 242	19	1.1	19	1	AR135296	ACCESSION:AR135296
c 170	1.1	20	1	BD224108	ACCESSION:BD224108	c 243	19	1.1	19	1	AR135297	ACCESSION:AR135297
c 171	19.4	1.1	21	AX825103	ACCESSION:AX825103	c 244	19	1.1	19	1	AR135298	ACCESSION:AR135298
c 172	19.4	1.1	21	AX825110	ACCESSION:AX825110	c 245	19	1.1	19	1	AR135302	ACCESSION:AR135302
c 173	19.4	1.1	21	AX825115	ACCESSION:AX825115	c 246	19	1.1	19	1	AR135304	ACCESSION:AR135304
c 174	19.4	1.1	21	AX825116	ACCESSION:AX825116	c 247	19	1.1	19	1	AR135305	ACCESSION:AR135305
c 175	19.4	1.1	21	AX825119	ACCESSION:AX825119	c 248	19	1.1	19	1	AR135315	ACCESSION:AR135315
c 176	19.4	1.1	21	AX825123	ACCESSION:AX825123	c 249	19	1.1	19	1	AR141898	ACCESSION:AR141898
c 177	19.4	1.1	21	AX825126	ACCESSION:AX825126	c 250	19	1.1	19	1	AR153863	ACCESSION:AR153863
c 178	19.4	1.1	21	AX825127	ACCESSION:AX825127	c 251	19	1.1	19	1	AR164173	ACCESSION:AR164173
c 179	19.4	1.1	21	AX825142	ACCESSION:AX825142	c 252	19	1.1	19	1	BD274438	ACCESSION:BD274438

C 253	19	1.1	19	1	19	1	BD274439	ACCESSION: BD274439	C 326	18.4	1.0	20	1	AR140280	ACCESSION: AR140280
C 254	19	1.1	19	1	19	1	BD274440	ACCESSION: BD274440	C 327	18.4	1.0	20	1	AR140281	ACCESSION: AR140281
C 255	19	1.1	19	1	19	1	BD274441	ACCESSION: BD274441	C 328	18.4	1.0	20	1	AR140558	ACCESSION: AR140558
C 256	19	1.1	19	1	19	1	BD274449	ACCESSION: BD274449	C 329	18.4	1.0	20	1	AR140559	ACCESSION: AR140559
C 257	19	1.1	19	1	19	1	AR205798	ACCESSION: AR205798	C 330	18.4	1.0	20	1	AR211367	ACCESSION: AR211367
C 258	19	1.1	19	1	19	1	AR205799	ACCESSION: AR205799	C 331	18.4	1.0	20	1	AX067205	ACCESSION: AX067205
C 259	19	1.1	19	1	19	1	AR205800	ACCESSION: AR205800	C 332	18.4	1.0	20	1	AX136903	ACCESSION: AX136903
C 260	19	1.1	19	1	19	1	AR205801	ACCESSION: AR205801	C 333	18.4	1.0	21	1	AR241831	ACCESSION: AR241831
C 261	19	1.1	19	1	19	1	AR205809	ACCESSION: AR205809	C 334	18.4	1.0	21	1	AX825104	ACCESSION: AX825104
C 262	19	1.1	19	1	19	1	AR213490	ACCESSION: AR213490	C 335	18.4	1.0	21	1	AX825105	ACCESSION: AX825105
C 263	19	1.1	19	1	19	1	AR213491	ACCESSION: AR213491	C 336	18.4	1.0	21	1	AX825106	ACCESSION: AX825106
C 264	19	1.1	19	1	19	1	AR213492	ACCESSION: AR213492	C 337	18.4	1.0	21	1	AX825107	ACCESSION: AX825107
C 265	19	1.1	19	1	19	1	AR213493	ACCESSION: AR213493	C 338	18.4	1.0	21	1	AX825108	ACCESSION: AX825108
C 266	19	1.1	19	1	19	1	AR213494	ACCESSION: AR213494	C 339	18.4	1.0	21	1	AX825109	ACCESSION: AX825109
C 267	19	1.1	19	1	19	1	AR213495	ACCESSION: AR213495	C 340	18.4	1.0	21	1	AX825117	ACCESSION: AX825117
C 268	19	1.1	19	1	19	1	AR213496	ACCESSION: AR213496	C 341	18.4	1.0	21	1	AX825118	ACCESSION: AX825118
C 269	19	1.1	19	1	19	1	AR213497	ACCESSION: AR213497	C 342	18.4	1.0	21	1	AX825119	ACCESSION: AX825119
C 270	19	1.1	19	1	19	1	AR213501	ACCESSION: AR213501	C 343	18.4	1.0	21	1	AX825140	ACCESSION: AX825140
C 271	19	1.1	19	1	19	1	AR213502	ACCESSION: AR213502	C 344	18.4	1.0	21	1	AX825141	ACCESSION: AX825141
C 272	19	1.1	19	1	19	1	AR213503	ACCESSION: AR213503	C 345	18.4	1.0	21	1	AX825149	ACCESSION: AX825149
C 273	19	1.1	19	1	19	1	AR213512	ACCESSION: AR213512	C 346	18.4	1.0	21	1	AX825150	ACCESSION: AX825150
C 274	19	1.1	19	1	19	1	AR222465	ACCESSION: AR222465	C 347	18.4	1.0	22	1	AX478523	ACCESSION: AX478523
C 275	19	1.1	19	1	19	1	AR237463	ACCESSION: AR237463	C 348	18.4	1.0	23	1	BD244863	ACCESSION: BD244863
C 276	19	1.1	19	1	19	1	AR321589	ACCESSION: AR321589	C 349	18.4	1.0	23	1	BD244865	ACCESSION: BD244865
C 277	19	1.1	19	1	19	1	AR359804	ACCESSION: AR359804	C 350	18.4	1.0	23	1	AX053001	ACCESSION: AX053001
C 278	19	1.1	19	1	19	1	AR359805	ACCESSION: AR359805	C 351	18.2	1.0	19	1	AR102020	ACCESSION: AR102020
C 279	19	1.1	19	1	19	1	AR359806	ACCESSION: AR359806	C 352	18.2	1.0	19	1	AR134802	ACCESSION: AR134802
C 280	19	1.1	19	1	19	1	AR367447	ACCESSION: AR367447	C 353	18.2	1.0	20	1	E28098	ACCESSION: E28098
C 281	19	1.1	19	1	19	1	AR399177	ACCESSION: AR399177	C 354	18	1.0	18	1	AR034896	ACCESSION: AR034896
C 282	19	1.1	19	1	19	1	AR399178	ACCESSION: AR399178	C 355	18	1.0	18	1	AR034899	ACCESSION: AR034899
C 283	19	1.1	19	1	19	1	AR403601	ACCESSION: AR403601	C 356	18	1.0	18	1	AR058305	ACCESSION: AR058305
C 284	19	1.1	19	1	19	1	AR403602	ACCESSION: AR403602	C 357	18	1.0	18	1	AR097579	ACCESSION: AR097579
C 285	19	1.1	19	1	19	1	AR403603	ACCESSION: AR403603	C 358	18	1.0	18	1	AR106506	ACCESSION: AR106506
C 286	19	1.1	19	1	19	1	AR403604	ACCESSION: AR403604	C 359	18	1.0	18	1	E28535	ACCESSION: E28535
C 287	19	1.1	19	1	19	1	AR403605	ACCESSION: AR403605	C 360	18	1.0	18	1	E28536	ACCESSION: E28536
C 288	19	1.1	19	1	19	1	AR403606	ACCESSION: AR403606	C 361	18	1.0	18	1	I79509	ACCESSION: I79509
C 289	19	1.1	19	1	19	1	AR403607	ACCESSION: AR403607	C 362	18	1.0	18	1	AR208426	ACCESSION: AR208426
C 290	19	1.1	19	1	19	1	AR403608	ACCESSION: AR403608	C 363	18	1.0	18	1	AR215435	ACCESSION: AR215435
C 291	19	1.1	19	1	19	1	AR403612	ACCESSION: AR403612	C 364	18	1.0	18	1	AR222464	ACCESSION: AR222464
C 292	19	1.1	19	1	19	1	AR403613	ACCESSION: AR403613	C 365	18	1.0	18	1	AR412363	ACCESSION: AR412363
C 293	19	1.1	19	1	19	1	AR403614	ACCESSION: AR403614	C 366	18	1.0	18	1	AX004875	ACCESSION: AX004875
C 294	19	1.1	19	1	19	1	AR403623	ACCESSION: AR403623	C 367	18	1.0	18	1	AX004879	ACCESSION: AX004879
C 295	19	1.1	19	1	19	1	AR412338	ACCESSION: AR412338	C 368	18	1.0	18	1	AX008117	ACCESSION: AX008117
C 296	19	1.1	19	1	19	1	AR432616	ACCESSION: AR432616	C 369	18	1.0	18	1	AX008118	ACCESSION: AX008118
C 297	19	1.1	19	1	19	1	AX349249	ACCESSION: AX349249	C 370	18	1.0	18	1	AX008122	ACCESSION: AX008122
C 298	19	1.1	19	1	19	1	BD087505	ACCESSION: BD087505	C 371	18	1.0	18	1	AX008123	ACCESSION: AX008123
C 299	19	1.1	19	1	19	1	BD196900	ACCESSION: BD196900	C 372	18	1.0	18	1	AX028845	ACCESSION: AX028845
C 300	19	1.1	20	1	19	1	AR139960	ACCESSION: AR139960	C 373	18	1.0	18	1	AX047271	ACCESSION: AX047271
C 301	19	1.1	20	1	19	1	AR140279	ACCESSION: AR140279	C 374	18	1.0	18	1	AX047273	ACCESSION: AX047273
C 302	19	1.1	20	1	19	1	AR140557	ACCESSION: AR140557	C 375	18	1.0	18	1	AX085252	ACCESSION: AX085252
C 303	19	1.1	21	1	19	1	AR118155	ACCESSION: AR118155	C 376	18	1.0	18	1	AX104721	ACCESSION: AX104721
C 304	19	1.1	21	1	19	1	I84433	ACCESSION: I84433	C 377	18	1.0	18	1	AX104747	ACCESSION: AX104747
C 305	19	1.1	21	1	19	1	AX825120	ACCESSION: AX825120	C 378	18	1.0	18	1	AX105651	ACCESSION: AX105651
C 306	19	1.1	21	1	19	1	AX825121	ACCESSION: AX825121	C 379	18	1.0	18	1	AX108642	ACCESSION: AX108642
C 307	19	1.1	21	1	19	1	AX825122	ACCESSION: AX825122	C 380	18	1.0	18	1	AX268883	ACCESSION: AX268883
C 308	19	1.1	21	1	19	1	AX825124	ACCESSION: AX825124	C 381	18	1.0	18	1	AX355809	ACCESSION: AX355809
C 309	19	1.1	21	1	19	1	AX825125	ACCESSION: AX825125	C 382	18	1.0	18	1	AX547774	ACCESSION: AX547774
C 310	19	1.1	21	1	19	1	AX825128	ACCESSION: AX825128	C 383	18	1.0	18	1	AX547800	ACCESSION: AX547800
C 311	19	1.1	21	1	19	1	AX825129	ACCESSION: AX825129	C 384	18	1.0	18	1	AX814716	ACCESSION: AX814716
C 312	19	1.1	21	1	19	1	AX825130	ACCESSION: AX825130	C 385	18	1.0	18	1	AX814723	ACCESSION: AX814723
C 313	19	1.1	21	1	19	1	AX825153	ACCESSION: AX825153	C 386	18	1.0	18	1	AX814724	ACCESSION: AX814724
C 314	19	1.1	21	1	19	1	AX825159	ACCESSION: AX825159	C 387	18	1.0	18	1	AX814725	ACCESSION: AX814725
C 315	19	1.1	21	1	19	1	AX825161	ACCESSION: AX825161	C 388	18	1.0	18	1	AX814736	ACCESSION: AX814736
C 316	19	1.1	22	1	19	1	BD085544	ACCESSION: BD085544	C 389	18	1.0	18	1	BD085545	ACCESSION: BD085545
C 317	19	1.1	23	1	19	1	BD245230	ACCESSION: BD245230	C 390	18	1.0	18	1	BD222596	ACCESSION: BD222596
C 318	19	1.1	24	1	19	1	AR431312	ACCESSION: AR431312	C 391	18	1.0	19	1	AR432617	ACCESSION: AR432617
C 319	19	1.1	24	1	19	1	BD097127	ACCESSION: BD097127	C 392	18	1.0	20	1	BD234126	ACCESSION: BD234126
C 320	19	1.1	24	1	19	1	BD161931	ACCESSION: BD161931	C 393	18	1.0	21	1	AX095299	ACCESSION: AX095299
C 321	19	1.1	25	1	19	1	AX196979	ACCESSION: AX196979	C 394	18	1.0	21	1	AX095303	ACCESSION: AX095303
C 322	18.8	1.1	24	1	19	1	AR431308	ACCESSION: AR431308	C 395	18	1.0	21	1	AX825111	ACCESSION: AX825111
C 323	18.8	1.1	25	1	19	1	AX043119	ACCESSION: AX043119	C 396	18	1.0	21	1	AX825112	ACCESSION: AX825112
C 324	18.4	1.0	20	1	19	1	AR139961	ACCESSION: AR139961	C 397	18	1.0	21	1	AX825113	ACCESSION: AX825113
C 325	18.4	1.0	20	1	19	1	AR139962	ACCESSION: AR139962	C 398	18	1.0	21	1	AX825114	ACCESSION: AX825114

C 545	15.4	0.9	17	1	AX692523	618	15	0.9	15	1	AR222461	ACCESSION: AR222461
C 546	15.4	0.9	17	1	AX692524	C 619	15	0.9	15	1	AR266630	ACCESSION: AR266630
C 547	15.4	0.9	17	1	AX723348	C 620	15	0.9	15	1	AR371280	ACCESSION: AR371280
C 548	15.4	0.9	18	1	AR079076	C 621	15	0.9	15	1	AR371281	ACCESSION: AR371281
C 549	15.4	0.9	18	1	AX32450	C 622	15	0.9	15	1	AR410213	ACCESSION: AR410213
C 550	15.4	0.9	18	1	E32452	C 623	15	0.9	15	1	AX004877	ACCESSION: AX004877
C 551	15.4	0.9	18	1	E32453	C 624	15	0.9	15	1	AX026066	ACCESSION: AX026066
C 552	15.4	0.9	18	1	E32455	C 625	15	0.9	15	1	AX048407	ACCESSION: AX048407
C 553	15.4	0.9	18	1	E32456	C 626	15	0.9	15	1	AX106973	ACCESSION: AX106973
C 554	15.4	0.9	18	1	AR264176	C 627	15	0.9	15	1	AX127272	ACCESSION: AX127272
C 555	15.4	0.9	18	1	AX014428	C 628	15	0.9	15	1	AX127273	ACCESSION: AX127273
C 556	15.4	0.9	19	1	AX039283	C 629	15	0.9	15	1	AX180140	ACCESSION: AX180140
C 557	15.4	0.9	20	1	AR086109	C 630	15	0.9	15	1	AX180141	ACCESSION: AX180141
C 558	15.4	0.9	20	1	AR086110	C 631	15	0.9	15	1	AX429224	ACCESSION: AX429224
C 559	15.4	0.9	20	1	AR086111	C 632	15	0.9	15	1	AX525141	ACCESSION: AX525141
C 560	15.4	0.9	20	1	E13187	C 633	15	0.9	15	1	AX525143	ACCESSION: AX525143
C 561	15.4	0.9	20	1	E13188	C 634	15	0.9	15	1	AX633197	ACCESSION: AX633197
C 562	15.4	0.9	20	1	E13189	C 635	15	0.9	15	1	AX633199	ACCESSION: AX633199
C 563	15.4	0.9	20	1	E40060	C 636	15	0.9	15	1	AX696087	ACCESSION: AX696087
C 564	15.4	0.9	20	1	E40064	C 637	15	0.9	15	1	AX711176	ACCESSION: AX711176
C 565	15.4	0.9	20	1	E40868	C 638	15	0.9	15	1	BD074424	ACCESSION: BD074424
C 566	15.4	0.9	20	1	E40872	C 639	15	0.9	15	1	BD084687	ACCESSION: BD084687
C 567	15.4	0.9	20	1	E43414	C 640	15	0.9	15	1	BD184668	ACCESSION: BD184668
C 568	15.4	0.9	20	1	E43418	C 641	15	0.9	15	1	BD206432	ACCESSION: BD206432
C 569	15.4	0.9	20	1	AR231312	C 642	15	0.9	15	1	BD209488	ACCESSION: BD209488
C 570	15.4	0.9	20	1	BD090597	C 643	15	0.9	15	1	AR221693	ACCESSION: AR221693
C 571	15.4	0.9	20	1	BD090601	C 644	15	0.9	16	1	AR221694	ACCESSION: AR221694
C 572	15.4	0.9	20	1	BD090706	C 645	15	0.9	16	1	AR221695	ACCESSION: AR221695
C 573	15.4	0.9	20	1	BD090710	C 646	15	0.9	16	1	AR221696	ACCESSION: AR221696
C 574	15.2	0.9	17	1	AR183909	C 647	15	0.9	16	1	AR221697	ACCESSION: AR221697
C 575	15.2	0.9	17	1	AR429726	C 648	15	0.9	16	1	AR221698	ACCESSION: AR221698
C 576	15.2	0.9	20	1	AR066905	C 649	15	0.9	16	1	AR257438	ACCESSION: AR257438
C 577	15.2	0.9	20	1	AR118884	C 650	15	0.9	16	1	AR257439	ACCESSION: AR257439
C 578	15.2	0.9	20	1	AR123336	C 651	15	0.9	16	1	AR257440	ACCESSION: AR257440
C 579	15.2	0.9	20	1	AR125322	C 652	15	0.9	16	1	AR257441	ACCESSION: AR257441
C 580	15.2	0.9	20	1	BD267704	C 653	15	0.9	16	1	AR257442	ACCESSION: AR257442
C 581	15.2	0.9	20	1	E06099	C 654	15	0.9	16	1	AR257443	ACCESSION: AR257443
C 582	15.2	0.9	20	1	E59334	C 655	15	0.9	17	1	AR057478	ACCESSION: AR057478
C 583	15.2	0.9	20	1	AR232303	C 656	15	0.9	17	1	AR115236	ACCESSION: AR115236
C 584	15.2	0.9	20	1	AR294828	C 657	15	0.9	17	1	BD233654	ACCESSION: BD233654
C 585	15.2	0.9	20	1	AR298452	C 658	15	0.9	17	1	E34258	ACCESSION: E34258
C 586	15.2	0.9	20	1	AR360403	C 659	15	0.9	17	1	E34259	ACCESSION: E34259
C 587	15.2	0.9	20	1	AR360430	C 660	15	0.9	17	1	AR187061	ACCESSION: AR187061
C 588	15.2	0.9	20	1	AR382832	C 661	15	0.9	17	1	AR187064	ACCESSION: AR187064
C 589	15.2	0.9	20	1	AX038279	C 662	15	0.9	17	1	AR241830	ACCESSION: AR241830
C 590	15.2	0.9	20	1	AX048436	C 663	15	0.9	17	1	AR266625	ACCESSION: AR266625
C 591	15.2	0.9	20	1	AX441514	C 664	15	0.9	17	1	AR323671	ACCESSION: AR323671
C 592	15.2	0.9	20	1	AX591245	C 665	15	0.9	17	1	AR323674	ACCESSION: AR323674
C 593	15.2	0.9	20	1	BD102552	C 666	15	0.9	17	1	AR401695	ACCESSION: AR401695
C 594	15.2	0.9	20	1	BD196041	C 667	15	0.9	17	1	AX422500	ACCESSION: AX422500
C 595	15	0.9	15	1	AR029402	C 668	15	0.9	17	1	AX422501	ACCESSION: AX422501
C 596	15	0.9	15	1	AR029403	C 669	15	0.9	17	1	AX531994	ACCESSION: AX531994
C 597	15	0.9	15	1	AR034895	C 670	15	0.9	17	1	AX531995	ACCESSION: AX531995
C 598	15	0.9	15	1	AR034898	C 671	15	0.9	17	1	AX531996	ACCESSION: AX531996
C 599	15	0.9	15	1	AR048768	C 672	15	0.9	17	1	AX634505	ACCESSION: AX634505
C 600	15	0.9	15	1	AR049970	C 673	15	0.9	17	1	AX692528	ACCESSION: AX692528
C 601	15	0.9	15	1	AR056157	C 674	15	0.9	17	1	BD011730	ACCESSION: BD011730
C 602	15	0.9	15	1	AR056158	C 675	15	0.9	17	1	BD011731	ACCESSION: BD011731
C 603	15	0.9	15	1	AR056159	C 676	15	0.9	17	1	BD067195	ACCESSION: BD067195
C 604	15	0.9	15	1	AR080676	C 677	15	0.9	17	1	BD091742	ACCESSION: BD091742
C 605	15	0.9	15	1	AR084516	C 678	15	0.9	17	1	BD091743	ACCESSION: BD091743
C 606	15	0.9	15	1	AR084518	C 679	15	0.9	17	1	BD091750	ACCESSION: BD091750
C 607	15	0.9	15	1	AR084520	C 680	15	0.9	17	1	BD091751	ACCESSION: BD091751
C 608	15	0.9	15	1	AR105981	C 681	15	0.9	17	1	BD091773	ACCESSION: BD091773
C 609	15	0.9	15	1	AR113915	C 682	15	0.9	17	1	BD091774	ACCESSION: BD091774
C 610	15	0.9	15	1	AR113916	C 683	15	0.9	17	1	BD097334	ACCESSION: BD097334
C 611	15	0.9	15	1	AR170375	C 684	15	0.9	17	1	BD097335	ACCESSION: BD097335
C 612	15	0.9	15	1	E08522	C 685	15	0.9	17	1	BD142808	ACCESSION: BD142808
C 613	15	0.9	15	1	E12591	C 686	15	0.9	17	1	BD142809	ACCESSION: BD142809
C 614	15	0.9	15	1	I29068	C 687	15	0.9	17	1	BD143834	ACCESSION: BD143834
C 615	15	0.9	15	1	I38641	C 688	15	0.9	17	1	BD143835	ACCESSION: BD143835
C 616	15	0.9	15	1	AR200476	C 689	15	0.9	17	1	BD167835	ACCESSION: BD167835
C 617	15	0.9	15	1	AR200477	C 690	15	0.9	17	1	BD167836	ACCESSION: BD167836

C 691	15	0.9	17	1	BD167907	ACCESSION:BD167907	C 764	14	0.8	14	1	AX048406	ACCESSION:AX048406
C 692	15	0.9	17	1	BD167908	ACCESSION:BD167908	765	14	0.8	14	1	AX827014	ACCESSION:AX827014
C 693	15	0.9	17	1	BD168111	ACCESSION:BD168111	766	14	0.8	14	1	AX839906	ACCESSION:AX839906
C 694	15	0.9	17	1	BD168112	ACCESSION:BD168112	C 767	14	0.8	14	1	BD073890	ACCESSION:BD073890
C 695	15	0.9	17	1	BD171177	ACCESSION:BD171177	768	14	0.8	14	1	BD084127	ACCESSION:BD084127
C 696	15	0.9	17	1	BD171178	ACCESSION:BD171178	C 769	14	0.8	14	1	BD096963	ACCESSION:BD096963
C 697	15	0.9	18	1	E32458	ACCESSION:E32458	C 770	14	0.8	14	1	BD096965	ACCESSION:BD096965
C 698	15	0.9	18	1	E32459	ACCESSION:E32459	C 771	14	0.8	14	1	BD132850	ACCESSION:BD132850
C 699	15	0.9	18	1	E32461	ACCESSION:E32461	C 772	14	0.8	14	1	BD176795	ACCESSION:BD176795
C 700	15	0.9	19	1	BD140103	ACCESSION:BD140103	C 773	14	0.8	14	1	BD176800	ACCESSION:BD176800
C 701	15	0.9	20	1	A46856	ACCESSION:A46856	C 774	14	0.8	14	1	BD176803	ACCESSION:BD176803
C 702	15	0.9	20	1	AR067594	ACCESSION:AR067594	C 775	14	0.8	14	1	BD176804	ACCESSION:BD176804
C 703	15	0.9	20	1	AR226053	ACCESSION:AR226053	C 776	14	0.8	15	1	AR055852	ACCESSION:AR055852
C 704	15	0.9	20	1	AR309844	ACCESSION:AR309844	C 777	14	0.8	15	1	AR056156	ACCESSION:AR056156
C 705	15	0.9	20	1	AR404077	ACCESSION:AR404077	C 778	14	0.8	15	1	AR056159	ACCESSION:AR056159
C 706	15	0.9	20	1	AX498246	ACCESSION:AX498246	C 779	14	0.8	15	1	AR056393	ACCESSION:AR056393
C 707	15	0.9	20	1	BD433336	ACCESSION:BD433336	C 780	14	0.8	15	1	AR113610	ACCESSION:AR113610
C 708	14.8	0.8	18	1	AR016068	ACCESSION:AR016068	C 781	14	0.8	15	1	AR113914	ACCESSION:AR113914
C 709	14.8	0.8	18	1	AR016069	ACCESSION:AR016069	C 782	14	0.8	15	1	AR113917	ACCESSION:AR113917
710	14.8	0.8	18	1	AR074230	ACCESSION:AR074230	C 783	14	0.8	15	1	AR114151	ACCESSION:AR114151
711	14.8	0.8	18	1	AR074246	ACCESSION:AR074246	784	14	0.8	15	1	I29065	ACCESSION:I29065
712	14.8	0.8	18	1	AR074303	ACCESSION:AR074303	785	14	0.8	15	1	I29066	ACCESSION:I29066
C 713	14.8	0.8	18	1	AR075338	ACCESSION:AR075338	786	14	0.8	15	1	I61462	ACCESSION:I61462
C 714	14.8	0.8	18	1	AR075539	ACCESSION:AR075539	C 787	14	0.8	15	1	AX241870	ACCESSION:AX241870
715	14.8	0.8	18	1	AR078882	ACCESSION:AR078882	C 788	14	0.8	15	1	AX632881	ACCESSION:AX632881
716	14.8	0.8	18	1	I20478	ACCESSION:I20478	C 789	14	0.8	15	1	AX633195	ACCESSION:AX633195
C 717	14.8	0.8	18	1	AR187555	ACCESSION:AR187555	C 790	14	0.8	15	1	AX633201	ACCESSION:AX633201
718	14.8	0.8	18	1	AR215621	ACCESSION:AR215621	C 791	14	0.8	15	1	AX633299	ACCESSION:AX633299
C 719	14.8	0.8	18	1	AR231295	ACCESSION:AR231295	C 792	14	0.8	15	1	AX635877	ACCESSION:AX635877
C 720	14.8	0.8	18	1	AR231296	ACCESSION:AR231296	C 793	14	0.8	16	1	AR002257	ACCESSION:AR002257
C 721	14.8	0.8	18	1	AR306483	ACCESSION:AR306483	C 794	14	0.8	16	1	AR045207	ACCESSION:AR045207
C 722	14.8	0.8	18	1	AR306484	ACCESSION:AR306484	C 795	14	0.8	16	1	AR051238	ACCESSION:AR051238
C 723	14.8	0.8	18	1	AR324069	ACCESSION:AR324069	796	14	0.8	16	1	AR089039	ACCESSION:AR089039
724	14.8	0.8	18	1	AX032592	ACCESSION:AX032592	797	14	0.8	16	1	AR089052	ACCESSION:AR089052
725	14.8	0.8	18	1	AX032608	ACCESSION:AX032608	798	14	0.8	16	1	AR140675	ACCESSION:AR140675
726	14.8	0.8	18	1	AX032665	ACCESSION:AX032665	799	14	0.8	16	1	AR140688	ACCESSION:AR140688
C 727	14.8	0.8	18	1	AX082574	ACCESSION:AX082574	C 800	14	0.8	16	1	I16032	ACCESSION:I16032
C 728	14.8	0.8	18	1	BD088263	ACCESSION:BD088263	C 801	14	0.8	16	1	I28367	ACCESSION:I28367
C 729	14.8	0.8	18	1	BD169501	ACCESSION:BD169501	C 802	14	0.8	16	1	AR428275	ACCESSION:AR428275
C 730	14.8	0.8	18	1	BD176184	ACCESSION:BD176184	C 803	14	0.8	16	1	AR428288	ACCESSION:AR428288
C 731	14.8	0.8	18	1	BD176185	ACCESSION:BD176185	C 804	14	0.8	16	1	AX59760	ACCESSION:AX59760
732	14.8	0.8	18	1	AB069090	ACCESSION:AB069090	C 805	14	0.8	17	1	AR187060	ACCESSION:AR187060
733	14.8	0.8	19	1	AX129282	ACCESSION:AX129282	C 806	14	0.8	17	1	AR187065	ACCESSION:AR187065
C 734	14.8	0.8	19	1	AX411902	ACCESSION:AX411902	C 807	14	0.8	17	1	AR323670	ACCESSION:AR323670
C 735	14.4	0.8	16	1	AR1337265	ACCESSION:AR1337265	C 808	14	0.8	17	1	AR323675	ACCESSION:AR323675
C 736	14.4	0.8	16	1	BD231248	ACCESSION:BD231248	C 809	14	0.8	17	1	AX422502	ACCESSION:AX422502
C 737	14.4	0.8	16	1	AX037387	ACCESSION:AX037387	C 810	14	0.8	17	1	AX531993	ACCESSION:AX531993
C 738	14.4	0.8	16	1	BD075139	ACCESSION:BD075139	C 811	14	0.8	17	1	AX531997	ACCESSION:AX531997
739	14.4	0.8	17	1	AX216921	ACCESSION:AX216921	C 812	14	0.8	17	1	AX692529	ACCESSION:AX692529
740	14.4	0.8	17	1	AX218059	ACCESSION:AX218059	C 813	14	0.8	17	1	AX724616	ACCESSION:AX724616
741	14.4	0.8	17	1	AX422499	ACCESSION:AX422499	C 814	14	0.8	17	1	AX728102	ACCESSION:AX728102
C 742	14.4	0.8	17	1	AX692522	ACCESSION:AX692522	C 815	14	0.8	17	1	AX728167	ACCESSION:AX728167
743	14.4	0.8	18	1	A63079	ACCESSION:A63079	816	14	0.8	17	1	AX739654	ACCESSION:AX739654
744	14.4	0.8	18	1	AR095850	ACCESSION:AR095850	817	14	0.8	17	1	AX759905	ACCESSION:AX759905
C 745	14.4	0.8	18	1	AR266237	ACCESSION:AR266237	818	14	0.8	17	1	AX762470	ACCESSION:AX762470
746	14.4	0.8	18	1	AR268656	ACCESSION:AR268656	C 819	14	0.8	17	1	BD198714	ACCESSION:BD198714
C 747	14.4	0.8	18	1	AR392120	ACCESSION:AR392120	C 820	14	0.8	18	1	AX116603	ACCESSION:AX116603
C 748	14.4	0.8	18	1	AX115223	ACCESSION:AX115223	C 821	14	0.8	18	1	AX661797	ACCESSION:AX661797
749	14.4	0.8	18	1	D00269507	ACCESSION:D00269507	C 822	14	0.8	18	1	AX685128	ACCESSION:AX685128
750	14.4	0.8	19	1	AR146849	ACCESSION:AR146849	823	14	0.8	18	1	BD088131	ACCESSION:BD088131
751	14.4	0.8	19	1	AR393609	ACCESSION:AR393609	824	14	0.8	18	1	AB068968	ACCESSION:AB068968
752	14.4	0.8	19	1	AX130721	ACCESSION:AX130721	C 825	13.8	0.8	17	1	AR045403	ACCESSION:AR045403
753	14.4	0.8	19	1	AX659402	ACCESSION:AX659402	826	13.8	0.8	17	1	BD241460	ACCESSION:BD241460
C 754	14.2	0.8	16	1	E52143	ACCESSION:E52143	827	13.8	0.8	17	1	BD241462	ACCESSION:BD241462
C 755	14.2	0.8	16	1	E53842	ACCESSION:E53842	828	13.8	0.8	17	1	BD254403	ACCESSION:BD254403
756	14	0.8	14	1	AR029886	ACCESSION:AR029886	829	13.8	0.8	17	1	BD254747	ACCESSION:BD254747
C 757	14	0.8	14	1	AR029887	ACCESSION:AR029887	C 830	13.8	0.8	17	1	BD255543	ACCESSION:BD255543
C 758	14	0.8	14	1	AR168510	ACCESSION:AR168510	831	13.8	0.8	17	1	BD255580	ACCESSION:BD255580
C 759	14	0.8	14	1	AR174024	ACCESSION:AR174024	C 832	13.8	0.8	17	1	BD257671	ACCESSION:BD257671
760	14	0.8	14	1	BD237464	ACCESSION:BD237464	C 833	13.8	0.8	17	1	BD258579	ACCESSION:BD258579
761	14	0.8	14	1	AR222460	ACCESSION:AR222460	C 834	13.8	0.8	17	1	BD258580	ACCESSION:BD258580
C 762	14	0.8	14	1	AR364948	ACCESSION:AR364948	835	13.8	0.8	17	1	BD272764	ACCESSION:BD272764
763	14	0.8	14	1	AR364949	ACCESSION:AR364949	C 836	13.8	0.8	17	1	I52455	ACCESSION:I52455

C 837	13.8	0.8	0.8	17	1	AR186642	ACCESION:AR186642	910	13.8	0.8	18	1	AR352433	ACCESION:AR352433
C 838	13.8	0.8	0.8	17	1	AR187066	ACCESION:AR187066	911	13.8	0.8	18	1	AR362789	ACCESION:AR362789
C 839	13.8	0.8	0.8	17	1	AR187067	ACCESION:AR187067	912	13.8	0.8	18	1	AX012429	ACCESION:AX012429
C 840	13.8	0.8	0.8	17	1	AR192330	ACCESION:AR192330	913	13.8	0.8	18	1	AX135661	ACCESION:AX135661
C 841	13.8	0.8	0.8	17	1	AR192331	ACCESION:AR192331	914	13.8	0.8	18	1	AX172296	ACCESION:AX172296
C 842	13.8	0.8	0.8	17	1	AR192332	ACCESION:AR192332	915	13.8	0.8	18	1	AX391641	ACCESION:AX391641
C 843	13.8	0.8	0.8	17	1	AR192333	ACCESION:AR192333	916	13.8	0.8	18	1	AX391790	ACCESION:AX391790
C 844	13.8	0.8	0.8	17	1	AR192335	ACCESION:AR192335	917	13.8	0.8	18	1	AX453798	ACCESION:AX453798
C 845	13.8	0.8	0.8	17	1	AR196416	ACCESION:AR196416	918	13.8	0.8	18	1	AX718767	ACCESION:AX718767
C 846	13.8	0.8	0.8	17	1	AR204408	ACCESION:AR204408	919	13.8	0.8	18	1	AX785415	ACCESION:AX785415
C 847	13.8	0.8	0.8	17	1	AR262702	ACCESION:AR262702	920	13.8	0.8	18	1	AX839747	ACCESION:AX839747
C 848	13.8	0.8	0.8	17	1	AR262702	ACCESION:AR262702	921	13.8	0.8	18	1	BD000033	ACCESION:BD000033
C 849	13.8	0.8	0.8	17	1	AR286095	ACCESION:AR286095	922	13.8	0.8	18	1	BD106774	ACCESION:BD106774
C 850	13.8	0.8	0.8	17	1	AR286192	ACCESION:AR286192	923	13.8	0.8	18	1	BD135722	ACCESION:BD135722
C 851	13.8	0.8	0.8	17	1	AR232373	ACCESION:AR232373	924	13.8	0.8	18	1	BD135722	ACCESION:BD135722
C 852	13.8	0.8	0.8	17	1	AR232677	ACCESION:AR232677	925	13.8	0.8	18	1	BD160988	ACCESION:BD160988
C 853	13.8	0.8	0.8	17	1	AR232620	ACCESION:AR232620	926	13.8	0.8	18	1	BD167483	ACCESION:BD167483
C 854	13.8	0.8	0.8	17	1	AR232620	ACCESION:AR232620	927	13.8	0.8	18	1	BD176966	ACCESION:BD176966
C 855	13.8	0.8	0.8	17	1	AR232620	ACCESION:AR232620	928	13.8	0.8	18	1	BD185983	ACCESION:BD185983
C 856	13.8	0.8	0.8	17	1	AR232623	ACCESION:AR232623	929	13.6	0.8	15	1	AX377095	ACCESION:AX377095
C 857	13.8	0.8	0.8	17	1	AR232620	ACCESION:AR232620	930	13.6	0.8	18	1	BD096968	ACCESION:BD096968
C 858	13.8	0.8	0.8	17	1	AR232613	ACCESION:AR232613	931	13.4	0.8	15	1	AR084519	ACCESION:AR084519
C 859	13.8	0.8	0.8	17	1	AR390805	ACCESION:AR390805	932	13.4	0.8	15	1	BD244856	ACCESION:BD244856
C 860	13.8	0.8	0.8	17	1	AR398182	ACCESION:AR398182	933	13.4	0.8	15	1	I28566	ACCESION:I28566
C 861	13.8	0.8	0.8	17	1	AR34061	ACCESION:AR34061	934	13.4	0.8	15	1	I58728	ACCESION:I58728
C 862	13.8	0.8	0.8	17	1	AX039679	ACCESION:AX039679	935	13.4	0.8	15	1	AR241876	ACCESION:AR241876
C 863	13.8	0.8	0.8	17	1	AX215933	ACCESION:AX215933	936	13.4	0.8	15	1	AX147741	ACCESION:AX147741
C 864	13.8	0.8	0.8	17	1	AX216915	ACCESION:AX216915	937	13.4	0.8	16	1	AR141562	ACCESION:AR141562
C 865	13.8	0.8	0.8	17	1	AX216916	ACCESION:AX216916	938	13.4	0.8	16	1	BD266224	ACCESION:BD266224
C 866	13.8	0.8	0.8	17	1	AX216925	ACCESION:AX216925	939	13.4	0.8	16	1	AX598384	ACCESION:AX598384
C 867	13.8	0.8	0.8	17	1	AX218302	ACCESION:AX218302	940	13.4	0.8	17	1	AR090907	ACCESION:AR090907
C 868	13.8	0.8	0.8	17	1	AX218302	ACCESION:AX218302	941	13.4	0.8	17	1	AR010206	ACCESION:AR010206
C 869	13.8	0.8	0.8	17	1	AX272523	ACCESION:AX272523	942	13.4	0.8	17	1	AR043128	ACCESION:AR043128
C 870	13.8	0.8	0.8	17	1	AX272706	ACCESION:AX272706	943	13.4	0.8	17	1	AR045401	ACCESION:AR045401
C 871	13.8	0.8	0.8	17	1	AX272707	ACCESION:AX272707	944	13.4	0.8	17	1	AR074628	ACCESION:AR074628
C 872	13.8	0.8	0.8	17	1	AX272804	ACCESION:AX272804	945	13.4	0.8	17	1	AR098727	ACCESION:AR098727
C 873	13.8	0.8	0.8	17	1	AX272952	ACCESION:AX272952	946	13.4	0.8	17	1	BD238354	ACCESION:BD238354
C 874	13.8	0.8	0.8	17	1	AX361147	ACCESION:AX361147	947	13.4	0.8	17	1	E35686	ACCESION:E35686
C 875	13.8	0.8	0.8	17	1	AX422503	ACCESION:AX422503	948	13.4	0.8	17	1	I32068	ACCESION:I32068
C 876	13.8	0.8	0.8	17	1	AX422924	ACCESION:AX422924	949	13.4	0.8	17	1	I43322	ACCESION:I43322
C 877	13.8	0.8	0.8	17	1	AX423181	ACCESION:AX423181	950	13.4	0.8	17	1	I52453	ACCESION:I52453
C 878	13.8	0.8	0.8	17	1	AX499077	ACCESION:AX499077	951	13.4	0.8	17	1	I5825	ACCESION:I5825
C 879	13.8	0.8	0.8	17	1	AX499340	ACCESION:AX499340	952	13.4	0.8	17	1	AR187288	ACCESION:AR187288
C 880	13.8	0.8	0.8	17	1	AX531998	ACCESION:AX531998	953	13.4	0.8	17	1	AR187289	ACCESION:AR187289
C 881	13.8	0.8	0.8	17	1	AX544715	ACCESION:AX544715	954	13.4	0.8	17	1	AR187290	ACCESION:AR187290
C 882	13.8	0.8	0.8	17	1	AX544716	ACCESION:AX544716	955	13.4	0.8	17	1	AR323898	ACCESION:AR323898
C 883	13.8	0.8	0.8	17	1	AX544717	ACCESION:AX544717	956	13.4	0.8	17	1	AR323899	ACCESION:AR323899
C 884	13.8	0.8	0.8	17	1	AX544744	ACCESION:AX544744	957	13.4	0.8	17	1	AR323900	ACCESION:AR323900
C 885	13.8	0.8	0.8	17	1	AX688347	ACCESION:AX688347	958	13.4	0.8	17	1	AR327688	ACCESION:AR327688
C 886	13.8	0.8	0.8	17	1	AX698573	ACCESION:AX698573	959	13.4	0.8	17	1	AX216923	ACCESION:AX216923
C 887	13.8	0.8	0.8	17	1	AX727700	ACCESION:AX727700	960	13.4	0.8	17	1	AX216923	ACCESION:AX216923
C 888	13.8	0.8	0.8	17	1	AX730844	ACCESION:AX730844	961	13.4	0.8	17	1	AX218294	ACCESION:AX218294
C 889	13.8	0.8	0.8	17	1	AX737376	ACCESION:AX737376	962	13.4	0.8	17	1	AX266015	ACCESION:AX266015
C 890	13.8	0.8	0.8	17	1	AX784081	ACCESION:AX784081	963	13.4	0.8	17	1	AX266016	ACCESION:AX266016
C 891	13.8	0.8	0.8	17	1	AX787049	ACCESION:AX787049	964	13.4	0.8	17	1	AX21847	ACCESION:AX21847
C 892	13.8	0.8	0.8	17	1	BD144764	ACCESION:BD144764	965	13.4	0.8	17	1	AX423210	ACCESION:AX423210
C 893	13.8	0.8	0.8	17	1	BD199007	ACCESION:BD199007	966	13.4	0.8	17	1	AX422498	ACCESION:AX422498
C 894	13.8	0.8	0.8	17	1	BD200582	ACCESION:BD200582	967	13.4	0.8	17	1	AX422545	ACCESION:AX422545
C 895	13.8	0.8	0.8	17	1	BD200583	ACCESION:BD200583	968	13.4	0.8	17	1	AX422546	ACCESION:AX422546
C 896	13.8	0.8	0.8	18	1	A14818	ACCESION:A14818	969	13.4	0.8	17	1	AX423515	ACCESION:AX423515
C 897	13.8	0.8	0.8	18	1	A64610	ACCESION:A64610	970	13.4	0.8	17	1	AX423516	ACCESION:AX423516
C 898	13.8	0.8	0.8	18	1	AR083836	ACCESION:AR083836	971	13.4	0.8	17	1	AX423699	ACCESION:AX423699
C 899	13.8	0.8	0.8	18	1	AR106852	ACCESION:AR106852	972	13.4	0.8	17	1	AX423700	ACCESION:AX423700
C 900	13.8	0.8	0.8	18	1	AR106931	ACCESION:AR106931	973	13.4	0.8	17	1	AX423700	ACCESION:AX423700
C 901	13.8	0.8	0.8	18	1	E40556	ACCESION:E40556	974	13.4	0.8	17	1	AX499341	ACCESION:AX499341
C 902	13.8	0.8	0.8	18	1	E51022	ACCESION:E51022	975	13.4	0.8	17	1	AX499342	ACCESION:AX499342
C 903	13.8	0.8	0.8	18	1	I82163	ACCESION:I82163	976	13.4	0.8	17	1	AX578565	ACCESION:AX578565
C 904	13.8	0.8	0.8	18	1	AR192884	ACCESION:AR192884	977	13.4	0.8	17	1	AX580298	ACCESION:AX580298
C 905	13.8	0.8	0.8	18	1	AR195017	ACCESION:AR195017	978	13.4	0.8	17	1	AX580299	ACCESION:AX580299
C 906	13.8	0.8	0.8	18	1	AR217329	ACCESION:AR217329	979	13.4	0.8	17	1	AX672633	ACCESION:AX672633
C 907	13.8	0.8	0.8	18	1	AR222132	ACCESION:AR222132	980	13.4	0.8	17	1	AX673370	ACCESION:AX673370
C 908	13.8	0.8	0.8	18	1	AR275355	ACCESION:AR275355	981	13.4	0.8	17	1	AX688345	ACCESION:AX688345
C 909	13.8	0.8	0.8	18	1	AR326626	ACCESION:AR326626	982	13.4	0.8	17	1	AX690454	ACCESION:AX690454
C 910	13.8	0.8	0.8	18	1	AR349888	ACCESION:AR349888	983	13.4	0.8	17	1	AX690454	ACCESION:AX690454

983	13.4	0.8	17	1	AX690455	ACCESSION:AX690455	c1056	13	0.7	15	1	AR235555	ACCESSION:AR235555
984	13.4	0.8	17	1	AX690456	ACCESSION:AX690456	1057	13	0.7	15	1	AX377159	ACCESSION:AX377159
c 985	13.4	0.8	17	1	AX692521	ACCESSION:AX692521	c1058	13	0.7	15	1	AX633193	ACCESSION:AX633193
c 986	13.4	0.8	17	1	AX722330	ACCESSION:AX722330	c1059	13	0.7	15	1	AX633203	ACCESSION:AX633203
c 987	13.4	0.8	17	1	AX724812	ACCESSION:AX724812	1060	13	0.7	16	1	AR049816	ACCESSION:AR049816
c 988	13.4	0.8	17	1	AX735928	ACCESSION:AX735928	1061	13	0.7	16	1	AR149710	ACCESSION:AR149710
c 989	13.4	0.8	17	1	AX737170	ACCESSION:AX737170	1062	13	0.7	16	1	I47692	ACCESSION:I47692
c 990	13.4	0.8	17	1	AX738045	ACCESSION:AX738045	c1063	13	0.7	16	1	AR231305	ACCESSION:AR231305
c 991	13.4	0.8	17	1	AX738493	ACCESSION:AX738493	1064	13	0.7	16	1	AR404837	ACCESSION:AR404837
c 992	13.4	0.8	17	1	AX757892	ACCESSION:AX757892	1065	13	0.7	16	1	AR708160	ACCESSION:AR708160
c 993	13.4	0.8	17	1	AX759206	ACCESSION:AX759206	c1066	13	0.7	17	1	AR057435	ACCESSION:AR057435
c 994	13.4	0.8	17	1	AR804339	ACCESSION:AR804339	c1067	13	0.7	17	1	AR057586	ACCESSION:AR057586
c 995	13.4	0.8	17	1	BD000130	ACCESSION:BD000130	c1068	13	0.7	17	1	AR057597	ACCESSION:AR057597
c 996	13.4	0.8	17	1	BD017427	ACCESSION:BD017427	c1069	13	0.7	17	1	AR057619	ACCESSION:AR057619
997	13.4	0.8	17	1	BD203288	ACCESSION:BD203288	c1070	13	0.7	17	1	AR057664	ACCESSION:AR057664
998	13.4	0.8	17	1	BD203289	ACCESSION:BD203289	c1071	13	0.7	17	1	AR115193	ACCESSION:AR115193
c 999	13.2	0.8	14	1	AS2266	ACCESSION:AS2266	c1072	13	0.7	17	1	AR115344	ACCESSION:AR115344
c1000	13.2	0.8	14	1	E13666	ACCESSION:E13666	c1073	13	0.7	17	1	AR115355	ACCESSION:AR115355
c1001	13.2	0.8	14	1	E13671	ACCESSION:E13671	c1074	13	0.7	17	1	AR115377	ACCESSION:AR115377
c1002	13.2	0.8	14	1	AR266627	ACCESSION:AR266627	c1075	13	0.7	17	1	AR115422	ACCESSION:AR115422
c1003	13	0.7	13	1	AR012009	ACCESSION:AR012009	c1076	13	0.7	17	1	BD253932	ACCESSION:BD253932
c1004	13	0.7	13	1	AR012010	ACCESSION:AR012010	c1077	13	0.7	17	1	AR187059	ACCESSION:AR187059
1005	13	0.7	13	1	AR145358	ACCESSION:AR145358	c1078	13	0.7	17	1	AR323669	ACCESSION:AR323669
c1006	13	0.7	13	1	AR179431	ACCESSION:AR179431	1079	13	0.7	17	1	AR327689	ACCESSION:AR327689
1007	13	0.7	13	1	E66853	ACCESSION:E66853	1080	13	0.7	17	1	AR327690	ACCESSION:AR327690
c1008	13	0.7	13	1	E66854	ACCESSION:E66854	1081	13	0.7	17	1	AX216924	ACCESSION:AX216924
c1009	13	0.7	13	1	AR205695	ACCESSION:AR205695	1082	13	0.7	17	1	AX272583	ACCESSION:AX272583
1010	13	0.7	13	1	AR222459	ACCESSION:AR222459	1083	13	0.7	17	1	AX272970	ACCESSION:AX272970
1011	13	0.7	13	1	AR241741	ACCESSION:AR241741	1084	13	0.7	17	1	AX273151	ACCESSION:AX273151
c1012	13	0.7	13	1	AX021144	ACCESSION:AX021144	1085	13	0.7	17	1	AX422887	ACCESSION:AX422887
c1013	13	0.7	13	1	AX048405	ACCESSION:AX048405	1086	13	0.7	17	1	AX423096	ACCESSION:AX423096
c1014	13	0.7	13	1	AX104675	ACCESSION:AX104675	c1087	13	0.7	17	1	AX531992	ACCESSION:AX531992
c1015	13	0.7	13	1	AX104676	ACCESSION:AX104676	c1088	13	0.7	17	1	AX634500	ACCESSION:AX634500
c1016	13	0.7	13	1	AX235509	ACCESSION:AX235509	c1089	13	0.7	17	1	AX634623	ACCESSION:AX634623
c1017	13	0.7	13	1	AX335510	ACCESSION:AX335510	c1090	13	0.7	17	1	AX634645	ACCESSION:AX634645
c1018	13	0.7	13	1	AX355807	ACCESSION:AX355807	c1091	13	0.7	17	1	AX634681	ACCESSION:AX634681
c1019	13	0.7	13	1	AX355808	ACCESSION:AX355808	c1092	13	0.7	17	1	AX634688	ACCESSION:AX634688
c1020	13	0.7	13	1	AX547728	ACCESSION:AX547728	1093	13	0.7	17	1	AX671642	ACCESSION:AX671642
c1021	13	0.7	13	1	AX547729	ACCESSION:AX547729	c1094	13	0.7	17	1	AX674812	ACCESSION:AX674812
c1022	13	0.7	14	1	A88150	ACCESSION:A88150	1095	13	0.7	17	1	AX690457	ACCESSION:AX690457
c1023	13	0.7	14	1	A90117	ACCESSION:A90117	1096	13	0.7	17	1	AX690458	ACCESSION:AX690458
c1024	13	0.7	14	1	A97593	ACCESSION:A97593	c1097	13	0.7	17	1	AX692530	ACCESSION:AX692530
c1025	13	0.7	14	1	AR004935	ACCESSION:AR004935	1098	13	0.7	17	1	AX723881	ACCESSION:AX723881
1026	13	0.7	14	1	AR036791	ACCESSION:AR036791	c1099	13	0.7	17	1	AX736300	ACCESSION:AX736300
1027	13	0.7	14	1	AR051240	ACCESSION:AR051240	1100	13	0.7	17	1	AX739516	ACCESSION:AX739516
c1028	13	0.7	14	1	AR067459	ACCESSION:AR067459	c1101	13	0.7	17	1	AX760808	ACCESSION:AX760808
1029	13	0.7	14	1	AR127787	ACCESSION:AR127787	c1102	12.8	0.7	16	1	A47824	ACCESSION:A47824
c1030	13	0.7	14	1	AR174022	ACCESSION:AR174022	1103	12.8	0.7	16	1	A66860	ACCESSION:A66860
c1031	13	0.7	14	1	AR174023	ACCESSION:AR174023	c1104	12.8	0.7	16	1	AR051248	ACCESSION:AR051248
c1032	13	0.7	14	1	AR174025	ACCESSION:AR174025	c1105	12.8	0.7	16	1	AR066240	ACCESSION:AR066240
1033	13	0.7	14	1	I28369	ACCESSION:I28369	1106	12.8	0.7	16	1	AR074231	ACCESSION:AR074231
c1034	13	0.7	14	1	AR241806	ACCESSION:AR241806	1107	12.8	0.7	16	1	AR074247	ACCESSION:AR074247
c1035	13	0.7	14	1	AR349924	ACCESSION:AR349924	1108	12.8	0.7	16	1	AR074304	ACCESSION:AR074304
c1036	13	0.7	14	1	AR349926	ACCESSION:AR349926	c1109	12.8	0.7	16	1	AR077149	ACCESSION:AR077149
c1037	13	0.7	14	1	AX016298	ACCESSION:AX016298	1110	12.8	0.7	16	1	AR082443	ACCESSION:AR082443
c1038	13	0.7	14	1	AX642208	ACCESSION:AX642208	1111	12.8	0.7	16	1	AR138999	ACCESSION:AR138999
c1039	13	0.7	14	1	AX659630	ACCESSION:AX659630	1112	12.8	0.7	16	1	I13390	ACCESSION:I13390
c1040	13	0.7	14	1	BD065663	ACCESSION:BD065663	1113	12.8	0.7	16	1	I20477	ACCESSION:I20477
c1041	13	0.7	14	1	BD073881	ACCESSION:BD073881	c1114	12.8	0.7	16	1	I28377	ACCESSION:I28377
c1042	13	0.7	14	1	BD073884	ACCESSION:BD073884	c1115	12.8	0.7	16	1	AR233918	ACCESSION:AR233918
c1043	13	0.7	14	1	BD073887	ACCESSION:BD073887	1116	12.8	0.7	16	1	AR281424	ACCESSION:AR281424
c1044	13	0.7	14	1	BD084126	ACCESSION:BD084126	1117	12.8	0.7	16	1	AR285629	ACCESSION:AR285629
1045	13	0.7	14	1	BD176796	ACCESSION:BD176796	1118	12.8	0.7	16	1	AR285649	ACCESSION:AR285649
1046	13	0.7	14	1	BD176797	ACCESSION:BD176797	c1119	12.8	0.7	16	1	AR366072	ACCESSION:AR366072
1047	13	0.7	14	1	BD176798	ACCESSION:BD176798	c1120	12.8	0.7	16	1	AR391428	ACCESSION:AR391428
c1048	13	0.7	14	1	BD176801	ACCESSION:BD176801	c1121	12.8	0.7	16	1	AR391503	ACCESSION:AR391503
c1049	13	0.7	14	1	BD176802	ACCESSION:BD176802	1122	12.8	0.7	16	1	AR397620	ACCESSION:AR397620
1050	13	0.7	14	1	BD209329	ACCESSION:BD209329	1123	12.8	0.7	16	1	AR397640	ACCESSION:AR397640
c1051	13	0.7	15	1	AR056155	ACCESSION:AR056155	c1124	12.8	0.7	16	1	AR408433	ACCESSION:AR408433
c1052	13	0.7	15	1	AR056160	ACCESSION:AR056160	1125	12.8	0.7	16	1	AX032593	ACCESSION:AX032593
c1053	13	0.7	15	1	AR113913	ACCESSION:AR113913	1126	12.8	0.7	16	1	AX032609	ACCESSION:AX032609
c1054	13	0.7	15	1	AR113918	ACCESSION:AR113918	1127	12.8	0.7	16	1	AX032666	ACCESSION:AX032666
1055	13	0.7	15	1	AR180774	ACCESSION:AR180774	c1128	12.8	0.7	16	1	AX194485	ACCESSION:AX194485

c1129	12.8	0.7	16	1	AX281908	ACCESSION:AX281908	1202	12.8	0.7	17	1	AR398144
c1130	12.8	0.7	16	1	AX281983	ACCESSION:AX281983	c1203	12.8	0.7	17	1	AR398176
c1131	12.8	0.7	16	1	AX465435	ACCESSION:AX465435	c1204	12.8	0.7	17	1	AR398177
1132	12.8	0.7	16	1	AX494458	ACCESSION:AX494458	1205	12.8	0.7	17	1	AR398186
1133	12.8	0.7	16	1	AX713247	ACCESSION:AX713247	c1206	12.8	0.7	17	1	AR398443
c1134	12.8	0.7	16	1	BD091347	ACCESSION:BD091347	1207	12.8	0.7	17	1	AR433953
c1135	12.8	0.7	17	1	AX422500	ACCESSION:AX422500	1208	12.8	0.7	17	1	AR433954
c1136	12.8	0.7	17	1	AX422501	ACCESSION:AX422501	1209	12.8	0.7	17	1	AR434060
c1137	12.8	0.7	17	1	AX6769	ACCESSION:AX6769	1210	12.8	0.7	17	1	AR434062
1138	12.8	0.7	17	1	AX6907	ACCESSION:AX6907	1211	12.8	0.7	17	1	AX104223
1139	12.8	0.7	17	1	AR029907	ACCESSION:AR029907	c1212	12.8	0.7	17	1	AX214608
c1140	12.8	0.7	17	1	AR039235	ACCESSION:AR039235	c1213	12.8	0.7	17	1	AX215070
c1141	12.8	0.7	17	1	AR040219	ACCESSION:AR040219	c1214	12.8	0.7	17	1	AX215071
c1142	12.8	0.7	17	1	AR047356	ACCESSION:AR047356	1215	12.8	0.7	17	1	AX215501
c1143	12.8	0.7	17	1	AR057566	ACCESSION:AR057566	c1216	12.8	0.7	17	1	AX215502
c1144	12.8	0.7	17	1	AR057690	ACCESSION:AR057690	1217	12.8	0.7	17	1	AX216917
c1145	12.8	0.7	17	1	AR057780	ACCESSION:AR057780	1218	12.8	0.7	17	1	AX216918
1146	12.8	0.7	17	1	AR097026	ACCESSION:AR097026	1219	12.8	0.7	17	1	AX216919
c1147	12.8	0.7	17	1	AR115324	ACCESSION:AR115324	1220	12.8	0.7	17	1	AX216926
c1148	12.8	0.7	17	1	AR115448	ACCESSION:AR115448	1221	12.8	0.7	17	1	AX216975
c1149	12.8	0.7	17	1	AR115538	ACCESSION:AR115538	1222	12.8	0.7	17	1	AX218301
c1150	12.8	0.7	17	1	AR158452	ACCESSION:AR158452	1223	12.8	0.7	17	1	AX218303
c1151	12.8	0.7	17	1	AR158453	ACCESSION:AR158453	1224	12.8	0.7	17	1	AX227355
1152	12.8	0.7	17	1	AR173612	ACCESSION:AR173612	c1225	12.8	0.7	17	1	AX226655
c1153	12.8	0.7	17	1	BD241455	ACCESSION:BD241455	1226	12.8	0.7	17	1	AX226656
c1154	12.8	0.7	17	1	BD241481	ACCESSION:BD241481	c1227	12.8	0.7	17	1	AX226659
1155	12.8	0.7	17	1	BD254211	ACCESSION:BD254211	1228	12.8	0.7	17	1	AX226660
1156	12.8	0.7	17	1	BD254586	ACCESSION:BD254586	1229	12.8	0.7	17	1	AX227208
c1157	12.8	0.7	17	1	BD254877	ACCESSION:BD254877	c1230	12.8	0.7	17	1	AX227208
c1158	12.8	0.7	17	1	BD255011	ACCESSION:BD255011	c1231	12.8	0.7	17	1	AX227208
c1159	12.8	0.7	17	1	BD255012	ACCESSION:BD255012	1232	12.8	0.7	17	1	AX227208
c1160	12.8	0.7	17	1	BD255013	ACCESSION:BD255013	c1233	12.8	0.7	17	1	AX227208
1161	12.8	0.7	17	1	BD255031	ACCESSION:BD255031	1234	12.8	0.7	17	1	AX227208
c1162	12.8	0.7	17	1	BD255419	ACCESSION:BD255419	1235	12.8	0.7	17	1	AX227208
c1163	12.8	0.7	17	1	BD255420	ACCESSION:BD255420	1236	12.8	0.7	17	1	AX227208
c1164	12.8	0.7	17	1	BD255542	ACCESSION:BD255542	1237	12.8	0.7	17	1	AX227208
1165	12.8	0.7	17	1	BD255581	ACCESSION:BD255581	c1238	12.8	0.7	17	1	AX227208
1166	12.8	0.7	17	1	BD256533	ACCESSION:BD256533	c1239	12.8	0.7	17	1	AX227208
1167	12.8	0.7	17	1	BD256591	ACCESSION:BD256591	c1240	12.8	0.7	17	1	AX227208
c1168	12.8	0.7	17	1	BD256760	ACCESSION:BD256760	c1241	12.8	0.7	17	1	AX227208
c1169	12.8	0.7	17	1	BD257672	ACCESSION:BD257672	c1242	12.8	0.7	17	1	AX227208
c1170	12.8	0.7	17	1	BD258512	ACCESSION:BD258512	1243	12.8	0.7	17	1	AX227208
c1171	12.8	0.7	17	1	BD258578	ACCESSION:BD258578	1244	12.8	0.7	17	1	AX227208
c1172	12.8	0.7	17	1	BD258581	ACCESSION:BD258581	c1245	12.8	0.7	17	1	AX227208
c1173	12.8	0.7	17	1	E37369	ACCESSION:E37369	c1246	12.8	0.7	17	1	AX227208
c1174	12.8	0.7	17	1	I26844	ACCESSION:I26844	c1247	12.8	0.7	17	1	AX227208
c1175	12.8	0.7	17	1	I34408	ACCESSION:I34408	c1248	12.8	0.7	17	1	AX227208
c1176	12.8	0.7	17	1	AR187031	ACCESSION:AR187031	c1249	12.8	0.7	17	1	AX227208
c1177	12.8	0.7	17	1	AR187068	ACCESSION:AR187068	c1250	12.8	0.7	17	1	AX227208
c1178	12.8	0.7	17	1	AR187252	ACCESSION:AR187252	c1251	12.8	0.7	17	1	AX227208
c1179	12.8	0.7	17	1	AR192334	ACCESSION:AR192334	c1252	12.8	0.7	17	1	AX227208
c1180	12.8	0.7	17	1	AR192336	ACCESSION:AR192336	c1253	12.8	0.7	17	1	AX227208
c1181	12.8	0.7	17	1	AR192336	ACCESSION:AR192336	c1254	12.8	0.7	17	1	AX227208
c1182	12.8	0.7	17	1	AR196415	ACCESSION:AR196415	c1255	12.8	0.7	17	1	AX227208
c1183	12.8	0.7	17	1	AR196417	ACCESSION:AR196417	c1256	12.8	0.7	17	1	AX227208
c1184	12.8	0.7	17	1	AR210111	ACCESSION:AR210111	1257	12.8	0.7	17	1	AX227208
1185	12.8	0.7	17	1	AR286154	ACCESSION:AR286154	1258	12.8	0.7	17	1	AX227208
c1186	12.8	0.7	17	1	AR286186	ACCESSION:AR286186	1259	12.8	0.7	17	1	AX227208
c1187	12.8	0.7	17	1	AR286187	ACCESSION:AR286187	1260	12.8	0.7	17	1	AX227208
1188	12.8	0.7	17	1	AR286196	ACCESSION:AR286196	c1261	12.8	0.7	17	1	AX227208
c1189	12.8	0.7	17	1	AR286453	ACCESSION:AR286453	1262	12.8	0.7	17	1	AX227208
c1190	12.8	0.7	17	1	AR322498	ACCESSION:AR322498	1263	12.8	0.7	17	1	AX227208
c1191	12.8	0.7	17	1	AR323641	ACCESSION:AR323641	1264	12.8	0.7	17	1	AX227208
c1192	12.8	0.7	17	1	AR323678	ACCESSION:AR323678	1265	12.8	0.7	17	1	AX227208
c1193	12.8	0.7	17	1	AR323862	ACCESSION:AR323862	c1266	12.8	0.7	17	1	AX227208
c1194	12.8	0.7	17	1	AR326204	ACCESSION:AR326204	c1267	12.8	0.7	17	1	AX227208
c1195	12.8	0.7	17	1	AR326206	ACCESSION:AR326206	c1268	12.8	0.7	17	1	AX227208
c1196	12.8	0.7	17	1	AR327941	ACCESSION:AR327941	1269	12.8	0.7	17	1	AX227208
c1197	12.8	0.7	17	1	AR328074	ACCESSION:AR328074	c1270	12.8	0.7	17	1	AX227208
c1198	12.8	0.7	17	1	AR328160	ACCESSION:AR328160	c1271	12.8	0.7	17	1	AX227208
1199	12.8	0.7	17	1	AR329383	ACCESSION:AR329383	c1272	12.8	0.7	17	1	AX227208
c1200	12.8	0.7	17	1	AR329554	ACCESSION:AR329554	1273	12.8	0.7	17	1	AX227208
1201	12.8	0.7	17	1	AR367363	ACCESSION:AR367363	c1274	12.8	0.7	17	1	AX227208
												AR398144
												AR398176
												AR398177
												AR398186
												AR398443
												AR433953
												AR433954
												AR434060
												AR434062
												AX104223
												AX214608
												AX215070
												AX215071
												AX215501
												AX215502
												AX216917
												AX216918
												AX216919
												AX216926
												AX216975
												AX218301
												AX218303
												AX227355
												AX226655
												AX226656
												AX226659
												AX226660
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
												AX227208
									</			

```
c1275 12.8 0.7 17 1 AX688602
1276 12.8 0.7 17 1 AX688693
1277 12.8 0.7 17 1 AX688694
1278 12.8 0.7 17 1 AX688740
1279 12.8 0.7 17 1 AX688741
1280 12.8 0.7 17 1 AX690554
1281 12.8 0.7 17 1 AX690555
1282 12.8 0.7 17 1 AX691282
1283 12.8 0.7 17 1 AX691283
1284 12.8 0.7 17 1 AX692609
1285 12.8 0.7 17 1 AX692610
1286 12.8 0.7 17 1 AX698570
1287 12.8 0.7 17 1 AX723024
1288 12.8 0.7 17 1 AX723728
1289 12.8 0.7 17 1 AX724111
1290 12.8 0.7 17 1 AX724397
1291 12.8 0.7 17 1 AX724919
1292 12.8 0.7 17 1 AX725040
1293 12.8 0.7 17 1 AX725448
1294 12.8 0.7 17 1 AX725848
1295 12.8 0.7 17 1 AX726840
1296 12.8 0.7 17 1 AX727839
1297 12.8 0.7 17 1 AX728077
1298 12.8 0.7 17 1 AX729967
1299 12.8 0.7 17 1 AX730062
1300 12.8 0.7 17 1 AX730114
1301 12.8 0.7 17 1 AX730625
1302 12.8 0.7 17 1 AX731099
1303 12.8 0.7 17 1 AX731554
1304 12.8 0.7 17 1 AX731857
1305 12.8 0.7 17 1 AX731963
1306 12.8 0.7 17 1 AX735879
1307 12.8 0.7 17 1 AX736107
1308 12.8 0.7 17 1 AX737293
1309 12.8 0.7 17 1 AX737445
1310 12.8 0.7 17 1 AX738613
1311 12.8 0.7 17 1 AX744200
1312 12.8 0.7 17 1 AX744201
1313 12.8 0.7 17 1 AX745047
1314 12.8 0.7 17 1 AX745048
1315 12.8 0.7 17 1 AX757940
1316 12.8 0.7 17 1 AX759934
1317 12.8 0.7 17 1 AX783890
1318 12.8 0.7 17 1 AX783891
1319 12.8 0.7 17 1 AX784080
1320 12.8 0.7 17 1 AX784082
1321 12.8 0.7 17 1 BD104951
1322 12.8 0.7 17 1 BD134134
1323 12.8 0.7 17 1 BD200584
1324 12.8 0.7 17 1 BD201657
1325 12.8 0.7 17 1 BD202792
1326 12.8 0.7 17 1 BD202896
1327 12.8 0.7 17 1 BD202897
1328 12.8 0.7 17 1 BD203006
1329 12.8 0.7 17 1 BD203175
1330 12.8 0.7 17 1 BD203246
1331 12.8 0.7 17 1 BD204781
1332 12.8 0.7 17 1 BD204794
1333 12.4 0.7 16 1 AX598384
1334 12.4 0.7 17 1 AX422502
```

ALIGNMENTS

```
RESULT 1
HSA241944/c HSA241944 29 bp DNA linear PRI 24-FEB-2000
LOCUS Homo sapiens gpl30 gene, partial, intron 14 splice acceptor site.
DEFINITION
AJ241944
VERSION AJ241944.1 GI:7105900
KEYWORDS gpl30 gene; splice acceptor site.
SOURCE Homo sapiens (human)
```

```
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szalai C., Toth, S. and Falus, A.
TITLE Exon-intron organization of the human gpl30 gene
JOURNAL Gene 243 (1-2), 161-166 (2000)
MEDLINE 20156380
PUBMED 10675624
REFERENCE 2 (bases 1 to 29)
AUTHORS Szalai C.
TITLE Direct Submission
JOURNAL Submitted (27-APR-1999) Szalai C., Heim Pal Pediatric Hospital
Budapest, Budapest POBOX 66, H-1958 Hungary
COMMENT Related sequence M57230.
FEATURES
source
1..29
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/maps="5q11"
1..29
/gene="gpl30"
1..24
/gene="gpl30"
/note="splice acceptor site"
/number=14
25..29
/gene="gpl30"
/number=15
Best Match 1.4%; Score 24.2; DB 1; Length 29;
Query Local Similarity 89.7%; Pred. No. 51;
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1726 TCAGTTTACAAAAA 1754
Db 29 TTGAGCTTAAAAA 1
RESULT 2
AR261539 24 bp DNA linear PAT 29-JAN-2003
LOCUS Sequence 6 from patent US 6322971.
DEFINITION AR261539
ACCESSION AR261539
VERSION AR261539.1 GI:28072607
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Chetverin, A. B. and Kramer, F. R.
TITLE Oligonucleotide arrays and their use for sorting, isolating,
sequencing, and manipulating nucleic acids
JOURNAL Patent: US 6322971-A 6 27-NOV-2001;
FEATURES Location/Qualifiers
source
1..24
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 71;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1731 TTTCACAAAAA 1754
Db 1 TTTAAAAA 24
RESULT 3
BD196419/c BD196419 24 bp DNA linear PAT 17-JUL-2003
LOCUS
```



```
DEFINITION
ACCESSION BD196419
VERSION BD196419.1 GI:33006189
KEYWORDS JP 2002516657-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE Prostatic cancer gene
JOURNAL Patent: JP 2002516657-A 8 11-JUN-2002;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002516657-A/8
PD 11-JUN-2002
PF 22-DEC-1998 JP 2000525562
PR 22-DEC-1997 US 08/996306 09-SEP-1998 US 60/099658 PI
DANIEL COHEN,MARTA BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
C12N15/09,C12N15/09,A01K67/027,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
,C12N15/00,C12N5/00,
PC C12N5/00,C12N15/00
CC primer oligonucleotide PGR32
FH Key Location/Qualifiers
FT misc binding 1..24.
FEATURES
source 1..24
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 1.2%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 98;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1732 TTACAAAAA 1754
DB 23 TTTCAAAAA 1
RESULT 4
BD056964/c
LOCUS BD056964 25 bp DNA linear PAT 27-AUG-2002
DEFINITION Sets of labeled energy transfer fluorescent primers and their use
in multi component analysis.
ACCESSION BD056964
VERSION BD056964.1 GI:22602570
KEYWORDS JP 2001509271-A/1.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 25)
AUTHORS Ju,J.
TITLE Sets of labeled energy transfer fluorescent primers and their use
in multi component analysis
JOURNAL Patent: JP 2001509271-A 1 10-JUL-2001;
COMMENT INCYTE PHARMACEUTICALS INC
PN JP 2001509271-A/1
PD 10-JUL-2001
PF 12-DEC-1997 JP 1998534358
PR 15-JAN-1997 US 08/784162
PI JINGYUE JU
PC GO1N21/78,C12N15/09,C12Q1/68,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
source 1..25
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
Query Match 1.2%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1755
DB 24 TAAAAA 2
RESULT 5
ARI74581/c
LOCUS ARI74581 26 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 38 from patent US 6307024.
ACCESSION ARI74581
VERSION ARI74581.1 GI:17914901
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Grose,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Cytokine zalphall Ligand
JOURNAL Patent: US 6307024-A 38 23-OCT-2001;
FEATURES
source 1..26
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1755
DB 26 TAAAAA 4
RESULT 6
BD248974/c
LOCUS BD248974 26 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHALL ligand.
ACCESSION BD248974
VERSION BD248974.1 GI:33058744
KEYWORDS JP 2002537839-A/35.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
Grose,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
Hammond,A.K.
TITLE Novel cytokine ZALPHALL ligand
JOURNAL Patent: JP 2002537839-A 35 12-NOV-2002;
COMMENT ZYMOGENETICS INC
OS Artificial Sequence
PN JP 2002537839-A/35
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603382
PR 09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
01-JUL-1999 US 60/142013
PI JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI
FOSTER,
PI RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
PI STACEY R DILLON,ANGELA K HAMMOND
PC C12N15/09,A61K38/00,A61P35/00,A61P37/00,A61P37/00,C07K14/52,
PC C07K14/53,
PC C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21.
```

```
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Oligonucleotide primer ZC7764a
FH Key Location/Qualifiers
FT source 1..26
FT /organism='Artificial Sequence'.

FEATURES
    source
        1..26
            Location/Qualifiers
                1..26
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 7
I79494/c
LOCUS I79494 26 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5707807.
ACCESSION I79494
VERSION I79494.1 GI:3207784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 1 13-JAN-1998,
FEATURES
    source
        1..26
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 8
AR263648/c
LOCUS AR263648 26 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 7 from patent US 6331413.
ACCESSION AR263648
VERSION AR263648.1 GI:28075581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZSIG63 Polypeptide
JOURNAL Patent: US 6331413-A 7 18-DEC-2001;
FEATURES
    source
        1..26
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
```

```
PC C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC Oligonucleotide primer ZC7764a
FH Key Location/Qualifiers
FT source 1..26
FT /organism='Artificial Sequence'.

FEATURES
    source
        1..26
            Location/Qualifiers
                1..26
                    /organism="synthetic construct"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32630"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 7
I79494/c
LOCUS I79494 26 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 1 from patent US 5707807.
ACCESSION I79494
VERSION I79494.1 GI:3207784
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Kato,K.
TITLE Molecular indexing for expressed gene analysis
JOURNAL Patent: US 5707807-A 1 13-JAN-1998,
FEATURES
    source
        1..26
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 8
AR263648/c
LOCUS AR263648 26 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 7 from patent US 6331413.
ACCESSION AR263648
VERSION AR263648.1 GI:28075581
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZSIG63 Polypeptide
JOURNAL Patent: US 6331413-A 7 18-DEC-2001;
FEATURES
    source
        1..26
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
```

```
Db 26 TAAAAA 4

RESULT 9
AR374073/c
LOCUS AR374073 26 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 38 from patent US 6605272.
ACCESSION AR374073
VERSION AR374073.1 GI:40076645
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 26)
AUTHORS Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.
TITLE Methods of using zaiphal1 ligand
JOURNAL Patent: US 6605272-A 38 12-AUG-2003;
FEATURES
    source
        1..26
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 10
AX106717/c
LOCUS AX106717 26 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 9 from Patent WO0125444.
ACCESSION AX106717
VERSION AX106717.1 GI:13922378
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Presnell,S.R., Novak,J.E. and Gao,Z.
TITLE Human phosphodiesterase zcytor13
JOURNAL Patent: WO 0125444-A 9 12-APR-2001;
FEATURES
    source
        1..26
            Location/Qualifiers
                1..26
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Oligonucleotide primer ZC7764b"

Query Match
    Best Local Similarity 1.2%; Score 21.4; DB 1; Length 26;
    Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 TAAAAA 4

RESULT 11
AR241865/c
LOCUS AR241865 27 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 153 from patent US 6472154.
ACCESSION AR241865
VERSION AR241865.1 GI:27287677
KEYWORDS
SOURCE Unknown.
```

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 27)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 153 29-OCT-2002;
FEATURES
source
1. .27
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.2%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 1.e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1755
DB 24 TAAAAA 2
RESULT 12
AX825131/c
LOCUS AX825131 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 29 from Patent WO03072818.
ACCESSION AX825131
VERSION AX825131.1 GI:39750860
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 29 04-SEP-2003;
DEGUSA Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 ACACAAAA 1754
DB 21 ACACAAAA 1
RESULT 14
AX825164/c
LOCUS AX825164 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 62 from Patent WO03072818.
ACCESSION AX825164
VERSION AX825164.1 GI:39750893
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 62 04-SEP-2003;
DEGUSA Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen Sequenz:Capture-Oligonukleotid"

RESULT 13

```

misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER

Query Match 1.2%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 15
AX817782
LOCUS AX817782 24 bp DNA linear PAT 10-DEC-2003
DEFINITION Sequence 18 from Patent WO02067861.
ACCESSION AX817782
VERSION AX817782.1 GI:39722977
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS
TITLE Oncolytic adenoviral vectors
JOURNAL Patent: WO 02067861-A 18 06-SEP-2002;
FEATURES
source
misc_feature 1.24
polyA_site 3..24

Query Match 1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 2 CAAAAAAAAAAAAAAAAAAAAA 22

RESULT 16
AX838369
LOCUS AX838369 24 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 8 from Patent WO02068627.
ACCESSION AX838369
VERSION AX838369.1 GI:39922050
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.

```

```

REFERENCE 1
AUTHORS Vector constructs
TITLE Patent: WO 02068627-A 8 06-SEP-2002;
JOURNAL Location/Qualifiers
FEATURES
source
misc_feature 1..24
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Viral vector sequence"
polyA_site 3..24
               /note="Fig. 1C. SV40 early Poly(A) site"

Query Match 1.2%; Score 21; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 2 CAAAAAAAAAAAAAAAAAAAAA 22

RESULT 17
I29929
LOCUS I29929 25 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 42 from patent US 5578468.
ACCESSION I29929
VERSION I29929.1 GI:1820720
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 25)
AUTHORS Pickup,D.J., Patel,D. and Antczak,J.B.
TITLE Site-Specific RNA cleavage
JOURNAL Patent: US 5578468-A 42 26-NOV-1996;
FEATURES
source
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match 1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 5 AAAAAAAAAAAAAAAAAAAAAA 25

RESULT 18
AX338548
LOCUS AX338548 25 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 4 from Patent WO0188192.
ACCESSION AX338548
VERSION AX338548.1 GI:18128948
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and
               Kinzler,K.W.
TITLE A method for generating hypermutable organisms
JOURNAL Patent: WO 0188192-A 4 22-NOV-2001;
               The Johns Hopkins University School of Medicine (US) ; Morphotek
               Inc. (US) ; Nicolaides, Nicholas, C. (US) ; Sass, Philip, M. (US) ;
               Grasso, Luigi (US) ; Vogelstein, Bert (US)
FEATURES
source
               /organism="synthetic construct"
               /mol_type="unassigned DNA"

```

```

/db_xref="taxon:32630"
/note="Recombinant DNA"

Query Match      1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1735 CAAAAA..... 1755
      |||||.....
Db    5 CAAAAA..... 25

RESULT 19
LOCUS       AX394507                      25 bp          DNA          linear          PAT 18-MAY-2002
DEFINITION   Sequence 52 from Patent WO0218638.
ACCESSION   AX394507
VERSION     AX394507.1 GI:21065645
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Risinger,C., Andersson,M.K., Lewander,T. and Ollasson,E.
TITLE       Detection of cyp2d6 polymorphisms
JOURNAL     Patent: WO 0218638-A 52 07-MAR-2002;
GEMINI Genomics PLC (GB)
FEATURES    Location/Qualifiers
             source
               1..25
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1735 CAAAAA..... 1755
      |||||.....
Db    2 CAAAAA..... 22

RESULT 20
LOCUS       AX394514/c                    25 bp          DNA          linear          PAT 18-MAY-2002
DEFINITION   Sequence 59 from Patent WO0218638.
ACCESSION   AX394514
VERSION     AX394514.1 GI:21065652
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Risinger,C., Andersson,M.K., Lewander,T. and Ollasson,E.
TITLE       Detection of cyp2d6 polymorphisms
JOURNAL     Patent: WO 0218638-A 59 07-MAR-2002;
GEMINI Genomics PLC (GB)
FEATURES    Location/Qualifiers
             source
               1..25
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic oligonucleotide"

Query Match      1.2%; Score 21; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1735 CAAAAA..... 1755
      |||||.....
Db    24 CAAAAA..... 4

RESULT 21
LOCUS       I79496                       26 bp          DNA          linear          PAT 10-JUN-1998
DEFINITION   Sequence 3 from patent US 5707807.
ACCESSION   I79496
VERSION     I79496.1 GI:3207786
KEYWORDS    .
SOURCE      Unknown.
            Unclassified.
ORGANISM    Kato,K.
REFERENCE   Molecular indexing for expressed gene analysis
            Patent: US 5707807-A 3 13-JAN-1998;
            Location/Qualifiers
             source
               1..26
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1735 CAAAAA..... 1755
      |||||.....
Db    26 CAAAAA..... 6

RESULT 22
LOCUS       AX338547                      26 bp          DNA          linear          PAT 09-JAN-2002
DEFINITION   Sequence 3 from Patent WO0188192.
ACCESSION   AX338547
VERSION     AX338547.1 GI:18128947
KEYWORDS    .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    .
REFERENCE   1
AUTHORS     Nicolaides,N.C., Sass,P.M., Grasso,L., Vogelstein,B. and
            Kinzler,K.W.
TITLE       A method for generating hypermutable organisms
JOURNAL     Patent: WO 0188192-A 3 22-NOV-2001;
            The Johns Hopkins University School of Medicine (US); Morphotek
            Inc. (US); Nicolaides, Nicholas, C. (US); Sass, Philip, M. (US);
            Grasso, Luigi (US); Vogelstein, Bert (US)
FEATURES    Location/Qualifiers
             source
               1..26
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Recombinant DNA"

Query Match      1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1735 CAAAAA..... 1755
      |||||.....
Db    5 CAAAAA..... 25

RESULT 23
LOCUS       BD192375/c                   26 bp          DNA          linear          PAT 17-JUL-2003
DEFINITION   Reagents and methods useful for detecting diseases of the breast.
ACCESSION   BD192375
VERSION     BD192375.1 GI:33002114
KEYWORDS    Mus sp.
SOURCE      Mus sp.
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```



```
Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 27
LOCUS AR263647/c 26 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 6 from patent US 6331413.
ACCESSION AR263647
VERSION AR263647.1 GI:28075580
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Adler,D.A. and Sheppard,P.O.
TITLE Secreted salivary ZSIG63 Polypeptide
JOURNAL Patent: US 6331413-A 6 18-DEC-2001;
FEATURES
    source
        1..26
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 1.4e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 28
LOCUS AX814950 26 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 36 from Patent WO03064691.
ACCESSION AX814950
VERSION AX814950.1 GI:39104088
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and
        Montellius,A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 36 07-AUG-2003;
        Global Genomics AB (SE)
FEATURES
    source
        1..26
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Primer"
        26
            /note="v is a, c or g"
misc_feature
    1..26; Score 20.6; DB 1; Length 26;
    Best Local Similarity 91.3%; Pred. No. 1.4e+02;
    Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 29
LOCUS BD062456/c 26 bp DNA linear PAT 27-AUG-2002
DEFINITION A human 2-19 protein homologue, Z219A.
ACCESSION BD062456
VERSION BD062456.1 GI:22608059
KEYWORDS JP 2001507946-A/4.
```

```
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 26)
AUTHORS Conklin,D.C. and Blumberg,H.
TITLE A human 2-19 protein homologue, Z219A
JOURNAL Patent: JP 2001507946-A 4 19-JUN-2001;
        ZYMOGENETICS INC
COMMENT OS Artificial Sequence
        PN JP 2001507946-A/4
        PD 19-JUN-2001
        PF 06-OCT-1998 JP 1999522287
        PR 06-OCT-1997 US 60/061712
        PI DARRELL C CONKLIN,HAL BLUMBERG
        PC C12N15/12,C12N15/62,C12N5/10,C07K14/47,C07K16/18,C12Q1/69, PC
        A01K67/027
        CC Oligonucleotide primer ZC7231
        FH Key Location/Qualifiers.
FEATURES
    source
        1..26
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"
Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 1.4e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 BAAAAAAAAAAAAAAAAAAAAA 4

RESULT 30
LOCUS AX327980/c 27 bp DNA linear PAT 07-JAN-2002
DEFINITION Sequence 37 from Patent WO0190747.
ACCESSION AX327980
VERSION AX327980.1 GI:18098134
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Rhode,P., Wittman,V., Weidanz,J.A., Burkhardt,M., Card,K.F.,
        Tal,R., Acevedo,J. and Wong,H.C.
TITLE Modulation of t-cell receptor interactions
JOURNAL Patent: WO 0190747-A 37 29-NOV-2001;
        Sunol Molecular Corporation (US)
FEATURES
    source
        1..27
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"
Query Match 1.2%; Score 20.6; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 1.5e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 HAAAAAAAAAAAAAAAAAAAAA 4

RESULT 31
LOCUS AX513052/c 27 bp DNA linear PAT 03-OCT-2002
DEFINITION Sequence 42 from Patent WO02062135.
ACCESSION AX513052
VERSION AX513052.1 GI:23504143
KEYWORDS synthetic construct
SOURCE synthetic construct
```

[illegible]

ORGANISM	synthetic construct	artificial sequences	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	source	Query Match	Best Local Similarity	Score	DB 1;	Length	DB 2;	Mismatches	Indels	Gaps
1	Egglrud, T. and Hansson, L.	Scce modified transgenic mammals and their use as models of human disease	Patent: WO 02062135-A 42 15-AUG-2002;	Egglrud, Torbjorn (SE); Hansson, Lennart (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="unassigned DNA"	1755	1	95.5%;	Pred. No. 1.2e+02;	22	1	0;	0;	0;
26	BAA	AAAAAAAAAAAAAAAAAAAAA	1755	1	AAAAAAAAAAAAAAAAAAAAA	22	1	AAAAAAAAAAAAAAAAAAAAA	22	1	95.5%;	Pred. No. 1.2e+02;	22	1	0;	0;	0;
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956.1	GI:29787747																
synthetic construct																	
artificial sequences																	
1	Tuvemo, H.T., Frisk, G.E. and Yin, H.	Enterovirus nucleic acids	Patent: WO 02103060-A 35 27-DEC-2002;	Innoventus Project AB (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="genomic DNA"	1755	1	91.3%;	Pred. No. 1.5e+02;	27	1	0;	0;	0;
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956.1	GI:29787747																
synthetic construct																	
artificial sequences																	
1	Tuvemo, H.T., Frisk, G.E. and Yin, H.	Enterovirus nucleic acids	Patent: WO 02103060-A 35 27-DEC-2002;	Innoventus Project AB (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="genomic DNA"	1755	1	91.3%;	Pred. No. 1.5e+02;	27	1	0;	0;	0;
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956.1	GI:29787747																
synthetic construct																	
artificial sequences																	
1	Tuvemo, H.T., Frisk, G.E. and Yin, H.	Enterovirus nucleic acids	Patent: WO 02103060-A 35 27-DEC-2002;	Innoventus Project AB (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="genomic DNA"	1755	1	91.3%;	Pred. No. 1.5e+02;	27	1	0;	0;	0;
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956.1	GI:29787747																
synthetic construct																	
artificial sequences																	
1	Tuvemo, H.T., Frisk, G.E. and Yin, H.	Enterovirus nucleic acids	Patent: WO 02103060-A 35 27-DEC-2002;	Innoventus Project AB (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="genomic DNA"	1755	1	91.3%;	Pred. No. 1.5e+02;	27	1	0;	0;	0;
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956.1	GI:29787747																
synthetic construct																	
artificial sequences																	
1	Tuvemo, H.T., Frisk, G.E. and Yin, H.	Enterovirus nucleic acids	Patent: WO 02103060-A 35 27-DEC-2002;	Innoventus Project AB (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="genomic DNA"	1755	1	91.3%;	Pred. No. 1.5e+02;	27	1	0;	0;	0;
AX711956	Sequence 35 from Patent WO02103060.	27 bp	DNA	linear	PAT 12-MAY-2003												
AX711956.1	GI:29787747																
synthetic construct																	
artificial sequences																	
1	Tuvemo, H.T., Frisk, G.E. and Yin, H.	Enterovirus nucleic acids	Patent: WO 02103060-A 35 27-DEC-2002;	Innoventus Project AB (SE)	Location/Qualifiers	1. .27	/organism="synthetic construct"	/mol_type="genomic DNA"	1755	1	91.3%;						

VERSION BD244857.1 GI:33054627
KEYWORDS JP 2002532063-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier, J. and Dae, M.
TITLE Oligonucleotide primer capable of making the non-specific double strand formation unstable
JOURNAL Patent: JP 2002532063-A 2 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
PN JP 2002532063-A/2
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PI 07-OCT-1998 CA 2246623
PR JERRY PELLETIER, MANJULA DAS
PC C12N15/09, C12O1/68, C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source 1..23
Location/Qualifiers
FEATURES
source 1..23
Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1..23; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 23 AAAAAAAAAAAAAAAAAAAAAA 2
RESULT 37
AR010037
LOCUS AR010037 24 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 50 from patent US 5756684.
ACCESSION AR010037
VERSION AR010037.1 GI:3968842
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson, E.M. and Bergemann, A.D.
TITLE Cloning and expression of PUR protein
JOURNAL Patent: US 5756684-A 50 26-MAY-1998;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1..24; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 38
AR034772
LOCUS AR034772 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 50 from patent US 5869622.
ACCESSION AR034772
VERSION AR034772.1 GI:5950377
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Johnson, E.M. and Bergemann, A.D.
TITLE Monoclonal antibodies to the pur protein
JOURNAL Patent: US 5869622-A 50 09-FEB-1999;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1..24; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 39
AR068465
LOCUS AR068465 24 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5853993.
ACCESSION AR068465
VERSION AR068465.1 GI:600672
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger, D.J., Dahm, S.C. and Troll, M.A.
TITLE Signal enhancement method and kit
JOURNAL Patent: US 5853993-A 1 29-DEC-1998;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1..24; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 40
AR105984
LOCUS AR105984 24 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 7 from patent US 6103474.
ACCESSION AR105984
VERSION AR105984.1 GI:12820049
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dellinger, D.J., Dahm, S.C., Ilseley, D.D., Ach, R.A. and Troll, M.A.
TITLE Hybridization assay signal enhancement
JOURNAL Patent: US 6103474-A 7 15-AUG-2000;
FEATURES
source 1..24
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1..24; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 41

LOCUS AR107972 24 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 1 from patent US 6110682.

ACCESSION AR107972

VERSION AR107972.1 GI:12823459

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Dellinger,D.J., Dahm,S.C. and Troll,M.A.

TITLE Signal enhancement method and kit

JOURNAL Patent: US 6110682-A 1 29-AUG-2000;

FEATURES

source Location/Qualifiers

1..24

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.4; DB 1; Length 24;

Best Local Similarity 95.5%; Pred. No. 1.3e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 42

LOCUS BD234330/c 24 bp DNA linear PAT 17-JUL-2003

DEFINITION Improved method for inserting nucleic acid into cyclic vector.

ACCESSION BD234330

VERSION BD234330.1 GI:33044100

KEYWORDS JP 2002532085-A/3.

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1 (bases 1 to 24)

AUTHORS Romantchikov,Y.

TITLE Improved method for inserting nucleic acid into cyclic vector

JOURNAL Patent: JP 2002532085-A 3 02-OCT-2002;

COMMENT YURI ROMANTCHIKOV

OS Artificial Sequence

PN JP 2002532085-A/3

PD 02-OCT-2002

PF 17-DEC-1999 JP 2000588337

PR 17-DEC-1998 US 09/213834

PI YURI ROMANTCHIKOV

PC C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/00

CC Cloning Vector

CC Key

FH Key

FT source 1..24

FT Location/Qualifiers

1..24

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

FEATURES

source Location/Qualifiers

1..24

/organism="Artificial Sequence"

Query Match 1.2%; Score 20.4; DB 1; Length 24;

Best Local Similarity 95.5%; Pred. No. 1.3e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 43

LOCUS I24762 24 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 25 from patent US 5545551.

ACCESSION I24762

VERSION I24762.1 GI:1604632

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Johnson,E.M. and Bergmann,A.D.

TITLE Cloning and expression of pur protein

JOURNAL Patent: US 5545551-A 25 13-AUG-1996;

FEATURES

source Location/Qualifiers

1..24

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.4; DB 1; Length 24;

Best Local Similarity 95.5%; Pred. No. 1.3e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 44

LOCUS AR184443 24 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 11 from patent US 6346384.

ACCESSION AR184443

VERSION AR184443.1 GI:20230408

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Pollner,R.B.

TITLE Real-time monitoring of PCR using LOCI

JOURNAL Patent: US 6346384-A 11 12-FEB-2002;

FEATURES

source Location/Qualifiers

1..24

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 1.2%; Score 20.4; DB 1; Length 24;

Best Local Similarity 95.5%; Pred. No. 1.3e+02;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 45

LOCUS AR202876 24 bp DNA linear PAT 20-JUN-2002

DEFINITION Sequence 4 from patent US 6365346.

ACCESSION AR202876

VERSION AR202876.1 GI:21499117

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 24)

AUTHORS Patel,R. and Kurn,N.

TITLE Quantitative determination of nucleic acid amplification products

JOURNAL Patent: US 6365346-A 4 02-APR-2002;

FEATURES

source Location/Qualifiers

1..24

/organism="unknown"


```
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 56
AX354553
LOCUS AX354553 24 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 11 from Patent WO0173129.
ACCESSION AX354553
VERSION AX354553.1 GI:18619355
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Pollner,R.B.
TITLE Real time monitoring of PCR using loci
JOURNAL Patent: WO 0173129-A 11 04-OCT-2001;
DADE BEHRING INC. (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide attached to beads"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 57
AX355813/c
LOCUS AX355813 24 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 841 from Patent WO0197843.
ACCESSION AX355813
VERSION AX355813.1 GI:18620481
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 841 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 58
AX427163/c
LOCUS AX427163 24 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 12 from Patent WO0210374.
ACCESSION AX427163
VERSION AX427163.1 GI:21530544
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Lin,S.L., Chung,C.M. and Widelitz,R.B.
TITLE Gene silencing using mrna-cdna hybrids
JOURNAL Patent: WO 0210374-A 12 07-FEB-2002;
UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Poly(dT)24 primer"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 59
AX428574
LOCUS AX428574 24 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 1 from Patent WO0184157.
ACCESSION AX428574
VERSION AX428574.1 GI:21538485
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Pease,J.S., Cromer,R., Patel,R., Kurn,N. and de Keczzer,S.
TITLE Compositions for detection of multiple analytes
JOURNAL Patent: WO 0184157-A 1 08-NOV-2001;
Dade Behring Marburg GmbH (DE)
FEATURES
source
Location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthesized"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACNAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 60
AX547294/c
LOCUS AX547294 24 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 433 from Patent WO02053141.
ACCESSION AX547294
VERSION AX547294.1 GI:25812438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
```

```
artificial sequences.
1
REFERENCE
AUTHORS      Bratzler,R.L.
TITLE        Inhibition of angiogenesis by nucleic acids
JOURNAL      Patent: WO 02053141-A 433 11-JUL-2002;
FEATURES     Coley Pharmaceutical Group, Inc. (US)
SOURCE       Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic Sequence"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
DB 24 AAAAAAAAA 3

RESULT 61
LOCUS      AX547822/c
DEFINITION Sequence 961 from Patent WO02053141.
ACCESSION  AX547822
VERSION     AX547822.1 GI:25812966
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS     Bratzler,R.L.
TITLE       Inhibition of angiogenesis by nucleic acids
JOURNAL     Patent: WO 02053141-A 961 11-JUL-2002;
FEATURES    Coley Pharmaceutical Group, Inc. (US)
SOURCE      Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic Sequence"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
DB 24 AAAAAAAAA 3

RESULT 62
LOCUS      AX547823
DEFINITION Sequence 962 from Patent WO02053141.
ACCESSION  AX547823
VERSION     AX547823.1 GI:25812967
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS     Bratzler,R.L.
TITLE       Inhibition of angiogenesis by nucleic acids
JOURNAL     Patent: WO 02053141-A 962 11-JUL-2002;
FEATURES    Coley Pharmaceutical Group, Inc. (US)
SOURCE      Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

artificial sequences.
1
REFERENCE
AUTHORS      Bratzler,R.L.
TITLE        Inhibition of angiogenesis by nucleic acids
JOURNAL      Patent: WO 02053141-A 433 11-JUL-2002;
FEATURES     Coley Pharmaceutical Group, Inc. (US)
SOURCE       Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic Sequence"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
DB 24 AAAAAAAAA 3

RESULT 63
LOCUS      AX684290/c
DEFINITION Sequence 13 from Patent WO02059609.
ACCESSION  AX684290
VERSION     AX684290.1 GI:29371160
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS     Mack,D.H., Gish,K.C. and Wilson,K.E.
TITLE       Methods of diagnosing colorectal cancer and/or breast cancer,
            compositions, and methods of screening for colorectal cancer and/or
            breast cancer modulators
JOURNAL     Patent: WO 02059609-A 13 01-AUG-2002;
FEATURES    EOS Biotechnology, Inc. (US)
SOURCE      Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="T7-(dT)-24 primer"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
DB 24 AAAAAAAAA 3

RESULT 64
LOCUS      AX750585/c
DEFINITION Sequence 11 from Patent WO0221134.
ACCESSION  AX750585
VERSION     AX750585.1 GI:32133003
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS     Mack,D. and Gish,K.C.
TITLE       Methods of diagnosing breast cancer and screening for modulators
JOURNAL     Patent: WO 0221134-A 11 14-MAR-2002;
FEATURES    EOS Biotechnology, Inc. (US)
SOURCE      Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="T7-(dT)-24 primer"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
DB 24 AAAAAAAAA 3

RESULT 65
LOCUS      AX750585/c
DEFINITION Sequence 11 from Patent WO0221134.
ACCESSION  AX750585
VERSION     AX750585.1 GI:32133003
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
REFERENCE  1
AUTHORS     Mack,D. and Gish,K.C.
TITLE       Methods of diagnosing breast cancer and screening for modulators
JOURNAL     Patent: WO 0221134-A 11 14-MAR-2002;
FEATURES    EOS Biotechnology, Inc. (US)
SOURCE      Location/Qualifiers
1. .24
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="T7-(dT)-24 primer"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
DB 24 AAAAAAAAA 3
```

```

Db      1  AAAAAAAAAAAAAAAAAAAAAA 22
|||||

RESULT 67
AR105982/c
LOCUS   AR105982               25 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION   Sequence 5 from patent US 6103474.
ACCESSION   AR105982
VERSION     AR105982.1  GI:12820047
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 25)
AUTHORS    Dellinger,D.J., Dahm,S.C., Irsley,D.D., Ach,R.A. and Troll,M.A.
TITLE      Hybridization assay signal enhancement
JOURNAL
PATENT     US 6103474-A 5 15-AUG-2000;
FEATURES
             Location/Qualifiers
             1..25
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734  AAAAAAAAAAAAAAAAAAAAAA 1755
Db      25  AAAAAAAAAAAAAAAAAAAAAA 4
|||||

RESULT 68
BD234336/c
LOCUS   BD234336               25 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION   Improved method for inserting nucleic acid into cyclic vector.
ACCESSION   BD234336
VERSION     BD234336.1  GI:33044106
KEYWORDS    JP 2002532085-A/9.
SOURCE      synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1 (bases 1 to 25)
AUTHORS    Romantchikov,Y.
TITLE      Improved method for inserting nucleic acid into cyclic vector
JOURNAL
COMMENT
OS        YURI ROMANTCHIKOV
PN        JP 2002532085-A/9
PD        02-OCT-2002
PF        17-DEC-1999  JP 2000588337
PI        17-DEC-1998  US 09/213834
PR        YURI ROMANTCHIKOV
PC        C12N15/09,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/00,C12N5/7
PC        00
CC        Cloning Vector
FH        Key
FT        source
            Location/Qualifiers
            1..25
            /organism='Artificial Sequence'.

FEATURES
             Location/Qualifiers
             1..25
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

Query Match      1.2%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1734  AAAAAAAAAAAAAAAAAAAAAA 1755
Db      25  AAAAAAAAAAAAAAAAAAAAAA 4
|||||

```


FEATURES	source	FT	Key	Location/Qualifiers
Query Match				1. .25
Best Local Similarity				/organism='Artificial Sequence'
Matches	21; Conservative	0; Mismatches	1; Indels	0; Gaps
QY	1734	ACAAAAA	Score 20.4; DB 1; Length 25;	
DB	25	AAAAA	Pred. No. 1.4e+02;	
			Location/Qualifiers	
			1. .25	
			/organism="synthetic construct"	
			/mol_type="genomic DNA"	
			/db_xref="taxon:32630"	
			1.2%; Score 20.4; DB 1; Length 25;	
			Best Local Similarity	
			95.5%; Pred. No. 1.4e+02;	
			Matches	21; Conservative
			0; Mismatches	1; Indels
			0; Gaps	0;
RESULT 76				
AR137712/c				
LOCUS	AR137712		26 bp	DNA
DEFINITION	Sequence 5 from patent US 6197554.			linear
ACCESSION	AR137712			
VERSION	AR137712.1		GI:14479221	
KEYWORDS			Location/Qualifiers	
SOURCE			Unknown.	
ORGANISM			Unknown.	
REFERENCE			1 (bases 1 to 26)	
AUTHORS	Lin,S.-L., Chuong,C.-M. and Ying,S.-Y.			
TITLE	Method for generating full-length cDNA library from single cells			
JOURNAL	Patent: US 6197554-A 5 06-MAR-2001;			
FEATURES				
source			1. .26	
			/organism="unknown"	
			/mol_type="unassigned DNA"	
Query Match			1.2%; Score 20.4; DB 1; Length 26;	
Best Local Similarity			95.5%; Pred. No. 1.5e+02;	
Matches	21; Conservative	0; Mismatches	1; Indels	0; Gaps
QY	1734	ACAAAAA	Score 20.4; DB 1; Length 26;	
DB	26	AAAAA	Pred. No. 1.5e+02;	
			Location/Qualifiers	
			1. .26	
			/organism="unknown"	
			/mol_type="unassigned DNA"	
RESULT 77				
AR174582/c				
LOCUS	AR174582		26 bp	DNA
DEFINITION	Sequence 39 from patent US 6307024.			linear
ACCESSION	AR174582			
VERSION	AR174582.1		GI:17914902	
KEYWORDS			Location/Qualifiers	
SOURCE			Unknown.	
ORGANISM			Unknown.	
REFERENCE			1 (bases 1 to 26)	
AUTHORS	Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D., Gross,J.A., Johnson,J.V., Nelson,A.J., Dillon,S.R. and Hammond,A.K.			
TITLE	Cytokine zalphall Ligand			
JOURNAL	Patent: US 6307024-A 39 23-OCT-2001;			
FEATURES				
source			1. .25	
			/organism="unknown"	
			/mol_type="unassigned DNA"	
Query Match			1.2%; Score 20.4; DB 1; Length 26;	
Best Local Similarity			95.5%; Pred. No. 1.5e+02;	
Matches	21; Conservative	0; Mismatches	1; Indels	0; Gaps
QY	1734	ACAAAAA	Score 20.4; DB 1; Length 26;	
DB	26	AAAAA	Pred. No. 1.5e+02;	
			Location/Qualifiers	
			1. .25	
			/organism="unknown"	
			/mol_type="unassigned DNA"	

```
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 78
BD248975/c
LOCUS      26 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Novel cytokine ZALPHA11 ligand.
ACCESSION BD248975
VERSION    1 GI:33058745
KEYWORDS   JP 2002537839-A/36.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 26)
AUTHORS    Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
TITLE      Novel cytokine ZALPHA11 ligand
JOURNAL    Patent: JP 2002537839-A 36 12-NOV-2002;
COMMENT    ZYMOGENETICS INC
OS         JP 2002537839-A/36
PD         12-NOV-2002 JP 200603382
PF         09-MAR-2000 JP 200603382
PR         09-MAR-1999 US 09/264908,11-MAR-1999 US 09/265992 PR
PI         01-JUL-1999 US 60/142013
PI         JULIA E NOVAK,SCOTT R PRESNELL,CINDY A SPRECHER,DONALD C PI
FOSTER,
PI         RICHARD D HOLLY,JANE A GROSS,JANET V JOHNSTON,ANDREW J NELSON,
PI         STACEY R DILLON,ANGELA K HAMMOND
PC         C12N15/09,A61K38/00,A61K45/00,A61P35/00,A61P37/00,C07K14/52,
PC         C07K14/53,
PC         C07K14/54,C07K14/55,C07K16/24,C07K19/00,C12N1/15,C12N1/19, PC
C12N1/21,
PC         C12N5/10,C12P21/02,C12P21/02,G01N33/53,C12N15/00,C12N5/00, PC
A61K37/02
CC         Oligonucleotide primer ZC7764b
FH         Key
FT         source
FT         Location/Qualifiers
            1..26
            /organism="Artificial Sequence".

FEATURES
    source
    1..26
    Location/Qualifiers
    1..26
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 ACACAAAAA 1755
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 79
I79495/c
LOCUS      26 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 2 from patent US 5707807.
ACCESSION I79495
VERSION    1 GI:3207785
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 26)
AUTHORS    Kato,K.
TITLE      Molecular indexing for expressed gene analysis
JOURNAL    Patent: US 5707807-A 2 13-JAN-1998;
COMMENT    Location/Qualifiers
            1..26
            /organism="unknown"
            /mol_type="unassigned DNA"

FEATURES
    source
    1..26
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 ACACAAAAA 1755
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 80
AR279358/c
LOCUS      26 bp      DNA      linear      PAT 10-APR-2003
DEFINITION Sequence 2 from patent US 6514699.
ACCESSION AR279358
VERSION    1 GI:29714110
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 26)
AUTHORS    O'Neill,R.A., Chen,J.-K., Chiesa,C. and Fry,G.
TITLE      Multiplex polynucleotide capture methods and compositions
JOURNAL    Patent: US 6514699-A 2 04-FEB-2003;
COMMENT    Location/Qualifiers
            1..26
            /organism="unknown"
            /mol_type="genomic DNA"

FEATURES
    source
    1..26
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 ACACAAAAA 1755
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 81
AR374074/c
LOCUS      26 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 39 from patent US 6605272.
ACCESSION AR374074
VERSION    1 GI:40076646
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 26)
AUTHORS    Novak,J.E., Presnell,S.R., Sprecher,C.A., Foster,D.C., Holly,R.D.,
            Gross,J.A., Johnston,J.V., Nelson,A.J., Dillon,S.R. and
            Hammond,A.K.
TITLE      Methods of using zalphall ligand
JOURNAL    Patent: US 6605272-A 39 12-AUG-2003;
COMMENT    Location/Qualifiers
            1..26
            /organism="unknown"
            /mol_type="genomic DNA"

FEATURES
    source
    1..26
    Location/Qualifiers
    1..26
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 ACACAAAAA 1755
Db      25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 82
AR404597/c
LOCUS      26 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6627748.
ACCESSION AR404597
```

```
VERSION AR404597.1 GI:40153233
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Ju,J., Li,Z., Tong,A. and Russo,J.J.
TITLE Combinatorial fluorescence energy transfer tags and their
        applications for multiplex genetic analyses
JOURNAL Patent: US 6627748-A 1 30-SEP-2003;
FEATURES
    source
        1..26
        /organism="unknown"
        /mol_type="genomic DNA"
Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACAAACAAAAA 1755
Db 25 AAAAAA 4
RESULT 83
AX427154/c
LOCUS
DEFINITION Sequence 3 from Patent WO0210374.
ACCESSION AX427154
VERSION AX427154.1 GI:21530535
KEYWORDS
SOURCE synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Lin,S.L., Chung,C.M. and Widelitz,R.B.
TITLE Gene silencing using mrna-cdna hybrids
JOURNAL Patent: WO 0210374-A 3 07-FEB-2002;
        UNIVERSITY OF SOUTHERN CALIFORNIA (US)
FEATURES
    source
        1..26
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Poly(dT)-26mer primer"
Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACAAACAAAAA 1755
Db 26 AAAAAA 5
RESULT 84
AX528804/c
LOCUS
DEFINITION Sequence 53 from Patent WO02059357.
ACCESSION AX528804
VERSION AX528804.1 GI:25172859
KEYWORDS
SOURCE synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Pedersen,M.L.
TITLE Assay and kit for analyzing gene expression
JOURNAL Patent: WO 02059357-A 53 01-AUG-2002;
        Location/Qualifiers
FEATURES
    source
        1..26
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
```

```

/db_xref="taxon:32630"
/note="synthetic construct"
Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACAAACAAAAA 1755
Db 26 AAAAAA 5
RESULT 85
BD007174/c
LOCUS
DEFINITION Method and composition for capturing multiple polynucleotide.
ACCESSION BD007174
VERSION BD007174.1 GI:18635545
KEYWORDS JP 2001503973-A/2.
SOURCE unidentified
        unidentified
        unclassified.
REFERENCE 1 (bases 1 to 26)
AUTHORS Ogneill,R.A., Chen,J.C., Chiesa,C. and Fry,G.
TITLE Method and composition for capturing multiple polynucleotide
JOURNAL Patent: JP 2001503973-A 2 27-MAR-2001;
        THE PERKIN ELMAR CORP
COMMENT OS Unidentified
        PN JP 2001503973-A/2
        PD 27-MAR-2001
        PF 02-OCT-1997 JP 199816839
        PR 04-OCT-1996 US 60/027832,12-JUN-1997 US 08/873437 PI
        ROGER A O'NEILL,JAR CAIN CHEN,CLAUDIA CHIESA,GEORGE FRY PC
        C12Q1/68,C12N15/09,C12N15/00
        CC Strandedness: Single;
        CC Topology: Linear;
        FH Key Location/Qualifiers
        FT source
            1..26
            /organism="Unidentified".
            Location/Qualifiers
                1..26
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"
Query Match
Best Local Similarity 1.2%; Score 20.4; DB 1; Length 26;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACAAACAAAAA 1755
Db 25 AAAAAA 4
RESULT 86
E04985
LOCUS
DEFINITION DNA sequence of 3'terminal fragment of ITR.
ACCESSION E04985
VERSION E04985.1 GI:2173180
KEYWORDS JP 1993103673-A/79.
SOURCE synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE 1 (bases 1 to 27)
AUTHORS Sengu,K.Y. and Ito,S.
TITLE REPLICATION OF DNA
JOURNAL Patent: JP 1993103673-A 79 27-APR-1993;
        ARIZONA BOARD OF REGENTS
COMMENT OS Artificial gene
        PN JP 1993103673-A/79
        PD 27-APR-1993
```



```
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 91
AX492939/c
LOCUS AX492939 27 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 16 from Patent EP1227150.
ACCESSION AX492939
VERSION AX492939.1 GI:23338609
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Tai-Jay, C.
TITLE Androgen receptor complex-associated protein
JOURNAL Patent: EP 1227150-A 16 31-JUL-2002;
Veterans General Hospital (TW)
FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetically generated primer"

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 92
AX547772/c
LOCUS AX547772 27 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 911 from Patent WO02053141.
ACCESSION AX547772
VERSION AX547772.1 GI:25812916
KEYWORDS
SOURCE
synthetic construct
artificial sequences.
ORGANISM
1
REFERENCE
1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 911 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1..27
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 93
BD175131/c
LOCUS BD175131 27 bp DNA linear PAT 18-MAR-2003
```

```
DEFINITION Androgen receptor complex-associated protein.
ACCESSION BD175131
VERSION BD175131.1 GI:29120825
KEYWORDS JP 2002262871-A/12.
SOURCE
synthetic construct
artificial sequences.
ORGANISM
1 (bases 1 to 27)
REFERENCE
1
AUTHORS Chan, T.Z.
TITLE Androgen receptor complex-associated protein
JOURNAL Patent: JP 2002262871-A 12 17-SEP-2002;
VETERANS GENERAL HOSPITAL
COMMENT OS Artificial Sequence
PN JP 2002262871-A/12
PD 17-SEP-2002
PF 28-FEB-2001 JP 2001055192
PI TAI ZHAI CHAN
PC C12N15/09,C07K14/47,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
,C12P21/02,C12Q1/68,
PC G01N33/15,G01N33/50,G01N33/566,C12N15/00,C12N5/00 CC n =
A,T,C or G
CC synthetically generated primer
FH Key Location/Qualifiers
FT misc feature (1)..(27).
Location/Qualifiers
1..27
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 94
S64862S3
LOCUS S64862S3 27 bp DNA linear PRI 17-DEC-1993
DEFINITION alpha 1-theta 1 globin intergenic region {3' alpha 1-Alu 1 repeat}
[Hylobates sp.=gibbons, Genomic, 27 nt, segment 3 of 5].
ACCESSION S64864
VERSION S64864.1 GI:415419
KEYWORDS
SEGMENT
3 of 5
SOURCE
Hylobates sp. (gibbon)
ORGANISM
Hylobates sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
REFERENCE
1 (bases 1 to 27)
AUTHORS Bailey, A.D. and Shen, C.K.
TITLE Sequential insertion of Alu family repeats into specific genomic
sites of higher primates
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90 (15), 7205-7209 (1993)
MEDLINE 93348242
PUBMED 8394013
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI Gibseq 13653] from the original journal article.
This sequence comes from Fig. 2A.
FEATURES
source
1..27
/organism="Hylobates sp."
/mol_type="genomic DNA"
/db_xref="taxon:9581"

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
```



```
Db      20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 100
AR093312 LOCUS AR093312 20 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 83 from patent US 6001361.
ACCESSION AR093312
VERSION AR093312.1 GI:10020062
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan, P., Hiyama, J., Visser, E., Skinner, M., Scott, L. and Prestidge, R.
TITLE Mycobacterium vaccae antigens
JOURNAL Patent: US 6001361-A 83 14-DEC-1999;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
|||||
RESULT 101
AR118970 LOCUS AR118970 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 96 from patent US 6150092.
ACCESSION AR118970
VERSION AR118970.1 GI:14100880
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Uchida, K., Uchida, T., Tanaka, Y., Matsuda, Y. and Kondo, S.
TITLE Antisense nucleic acid compound targeted to VEGF
JOURNAL Patent: US 6150092-A 96 21-NOV-2000;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
|||||
RESULT 102
AR121692 LOCUS AR121692 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 83 from patent US 6160093.
ACCESSION AR121692
VERSION AR121692.1 GI:14105268
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Visser, E.
TITLE Compounds and methods for treatment and diagnosis of mycobacterial
```

```
infections
JOURNAL Patent: US 6160093-A 83 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
|||||
RESULT 103
AR123335 LOCUS AR123335 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6169176.
ACCESSION AR123335
VERSION AR123335.1 GI:14108301
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Bruice, T. C. and Dev, A. P.
TITLE Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL Patent: US 6169176-A 1 02-JAN-2001;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
|||||
RESULT 104
AR141070 LOCUS AR141070 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 1 from patent US 6207819.
ACCESSION AR141070
VERSION AR141070.1 GI:14483566
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Manoharan, M. and Maier, M. A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 1 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/mol_type="unknown"
/mol_type="unassigned DNA"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
```

```
RESULT 105
LOCUS       AR154115/c                20 bp    DNA        linear    PAT 08-AUG-2001
DEFINITION   Sequence 14 from patent US 6238865.
ACCESSION   AR154115
VERSION     AR154115.1  GI:15122168
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Huang,Z. and Szostak,J.W.
TITLE      Simple and efficient method to label and modify 3'-termini of RNA
           using DNA polymerase and a synthetic template with defined overhang
           nucleotides
JOURNAL     Patent: US 6238865-A 14 29-MAY-2001;
FEATURES    Location/Qualifiers
             source          1..20
             /organism="unknown"
             /mol_type="unassigned DNA"
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 106
LOCUS       AR164658                20 bp    DNA        linear    PAT 17-OCT-2001
DEFINITION   Sequence 13 from patent US 6274321.
ACCESSION   AR164658
VERSION     AR164658.1  GI:16237754
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Blumberg,B.
TITLE      High throughput functional screening of cDNAs
JOURNAL     Patent: US 6274321-A 13 14-AUG-2001;
FEATURES    Location/Qualifiers
             source          1..20
             /organism="unknown"
             /mol_type="unassigned DNA"
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 107
LOCUS       E12676/c                20 bp    DNA        linear    PAT 27-APR-1998
DEFINITION   Anti-HTLV-1 antisense oligonucleotide.
ACCESSION   E12676
VERSION     E12676.1  GI:3251508
KEYWORDS    JP1997052898-A/10.
SOURCE      unidentified
ORGANISM    unidentified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Mizuguchi,M., Kurosaki,N., Makino,K., Koyanagi,Y. and Yamamoto,N.
TITLE      ANTI-HTLV-I ANTI-SENSE OLIGONUCLEOTIDE
JOURNAL     Patent: JP 1997052898-A 10 25-FEB-1997;
           SOYAKU GIJUTSU KENKYUSHO:KK

COMMENT     OS None
            OC Artificial sequences.
            PN JP 1997052898-A/10
            PD 25-FEB-1997
            PF 09-AUG-1995 JP 1995224606
            PI MIZUGUCHI MASATSUGU, KUROSAKI NAKO, MAKINO KEISUKE, PI
            KOYANAGI YOSHIO,
            YAMAMOTO NAKO
            PC C07H21/04//A61K31/70;
            CC strandedness: Single;
            CC topology: Linear;
            CC hypothetical: No;
            CC anti-sense: Yes;
            FH Key
            FT source          1..20
            FT /organism='Artificial sequences'.
FEATURES    Location/Qualifiers
             source          1..20
             /organism="unidentified"
             /mol_type="genomic DNA"
             /db_xref="taxon:32644"
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 108
LOCUS       I36180/c                20 bp    DNA        linear    PAT 13-MAY-1997
DEFINITION   Sequence 16 from patent US 5605662.
ACCESSION   I36180
VERSION     I36180.1  GI:2086693
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Heller,M.J. and Tu,E.
TITLE      Active programmable electronic devices for molecular biological
           analysis and diagnostics
JOURNAL     Patent: US 5605662-A 16 25-FEB-1997;
FEATURES    Location/Qualifiers
             source          1..20
             /organism="unknown"
             /mol_type="unassigned DNA"
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 109
LOCUS       AR213738                20 bp    DNA        linear    PAT 25-SEP-2002
DEFINITION   Sequence 83 from patent US 6406704.
ACCESSION   AR213738
VERSION     AR213738.1  GI:23311025
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 20)
AUTHORS    Tan,P., Visser,E., Prestidge,R. and Watson,J.D.
```



```
thereof
JOURNAL Patent: US 6582921-A 55 24-JUN-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 115
AR365970
LOCUS AR365970 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 83 from patent US 6328978.
ACCESSION AR365970
VERSION AR365970.1 GI:34598223
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Watson,J.D., Tan,P.L.J. and Prestidge,R.
TITLE Methods for the treatment of immunologically-mediated skin disorders
JOURNAL Patent: US 6328978-A 83 11-DEC-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 116
AR382312
LOCUS AR382312 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 55 from patent US 6610491.
ACCESSION AR382312
VERSION AR382312.1 GI:40090724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: US 6610491-A 55 26-AUG-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

thereof
JOURNAL Patent: US 6582921-A 55 24-JUN-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 117
AR429653
LOCUS AR429653 20 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 55 from patent US 6645721.
ACCESSION AR429653
VERSION AR429653.1 GI:40189949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R. and Taton,T.A.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: US 6645721-A 55 11-NOV-2003;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 118
AX004876/C
LOCUS AX004876 20 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 5 from Patent WO9910527.
ACCESSION AX004876
VERSION AX004876.1 GI:9928276
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bayer,R. and Schwietz,J.
TITLE Method for isolating anionic organic substances from aqueous systems using cationic polymer nanoparticles
JOURNAL Patent: WO 9910527-A 5 04-MAR-1999;
FEATURES SUBDEUTSCHE KALKSTICKSTOFF (DE); BAYER ERNST (DE)
Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="phosphorothioate oligonucleotide"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 119
AX045779/C
LOCUS AX045779 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 9 from Patent WO0067023.
ACCESSION AX045779
VERSION AX045779.1 GI:11344146
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
```

```
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 9 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
misc_feature 1
/note="modified with digoxigenin"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 120
AX045787/c
LOCUS AX045787 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 17 from Patent WO0067023.
ACCESSION AX045787
VERSION AX045787.1 GI:11344154
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 17 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
misc_feature 1
/note="phosphorothioate backbone"
misc_feature 1
/note="modified with digoxigenin"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 121
AX045790/c
LOCUS AX045790 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 20 from Patent WO0067023.
ACCESSION AX045790
VERSION AX045790.1 GI:11344157
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Noll,B.O., Schetter,C. and Krieg,A.M.
artificial sequences.
TITLE Screening for immunostimulatory dna functional modifiers
JOURNAL Patent: WO 0067023-A 20 09-NOV-2000;
CPG Immunopharmaceuticals GmbH (DE) ; UNIVERSITY OF IOWA RESEARCH
FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic oligonucleotide"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 123
AX104364/c
LOCUS AX104364 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 556 from Patent WO0122972.
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 123
AX104364/c
LOCUS AX104364 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 556 from Patent WO0122972.
ACCESSION AX104364
VERSION AX104364.1 GI:13920561
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 556 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 124
LOCUS AX104368 20 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 560 from Patent WO0122972.
ACCESSION AX104368
VERSION AX104368.1 GI:13920565
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 560 05-APR-2001;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
          GmbH (DE)
FEATURES
    source
    Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 125
LOCUS AX196224 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 55 from Patent WO0151665.
ACCESSION AX196224
VERSION AX196224.1 GI:15386427
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
          Elghanian,R., Taton,T.A. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
          therefor
JOURNAL Patent: WO 0151665-A 55 19-JUL-2001;
          Nanosphere, Inc. (US)
FEATURES
    source
    Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="random synthetic sequence"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 126
LOCUS AX196239 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 70 from Patent WO0151665.
ACCESSION AX196239
VERSION AX196239.1 GI:15386442
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
          Elghanian,R., Taton,T.A. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
          therefor
JOURNAL Patent: WO 0151665-A 70 19-JUL-2001;
          Nanosphere, Inc. (US)
FEATURES
    source
    Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="random synthetic sequence"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 127
LOCUS AX354974 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 2 from Patent WO0197843.
ACCESSION AX354974
VERSION AX354974.1 GI:18619641
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
          cancer
JOURNAL Patent: WO 0197843-A 2 27-DEC-2001;
          UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
    source
    Location/Qualifiers
    1..20
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 128
LOCUS AX355810 20 bp DNA linear PAT -06-FEB-2002
DEFINITION Sequence 838 from Patent WO0197843.
ACCESSION AX355810
VERSION AX355810.1 GI:18620478
KEYWORDS .
SOURCE synthetic construct
```

ORGANISM synthetic construct
REFERENCE artificial sequences.
1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 838 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 129
AX355811/c
LOCUS AX355811 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 839 from Patent WO0197843.
ACCESSION AX355811
VERSION AX355811.1 GI:18620479
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 839 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphodiester backbone"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 130
AX440125
LOCUS AX440125 20 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 55 from Patent WO0173123.
ACCESSION AX440125
VERSION AX440125.1 GI:21664936
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0173123-A 55 04-OCT-2001;

Nanosphere, Inc. (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 131
AX440140
LOCUS AX440140 20 bp DNA linear PAT 28-JUN-2002
DEFINITION Sequence 70 from Patent WO0173123.
ACCESSION AX440140
VERSION AX440140.1 GI:21664951
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R., Taton,T.A., Park,S.J. and Li,Z.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0173123-A 70 04-OCT-2001;
Nanosphere, Inc. (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 132
AX465311
LOCUS AX465311 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 55 from Patent WO0218643.
ACCESSION AX465311
VERSION AX465311.1 GI:21899674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J., Elghanian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses therefor
JOURNAL Patent: WO 0218643-A 55 07-MAR-2002;
Nanosphere, Inc. (US)
FEATURES Location/Qualifiers
source
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 133
LOCUS AX465326 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 70 from Patent WO0218643.
ACCESSION AX465326
VERSION AX465326.1 GI:21899689
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 556 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 136
LOCUS AX547421 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 560 from Patent WO02053141.
ACCESSION AX547421
VERSION AX547421.1 GI:25812565
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 560 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 134
LOCUS AX547087/c 20 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 226 from Patent WO02053141.
ACCESSION AX547087
VERSION AX547087.1 GI:25812231
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Bratzler, R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 226 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 137
LOCUS AX556124 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 55 from Patent WO0246472.
ACCESSION AX556124
VERSION AX556124.1 GI:25899506
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
```

REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghamian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 55 13-JUN-2002;
Nanosphere, Inc. (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 138
AX556139
LOCUS AX556139 20 bp DNA linear PAT 27-NOV-2002
DEFINITION Sequence 70 from Patent WO0246472.
ACCESSION AX556139
VERSION AX556139.1 GI:25899521
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mirkin,C.A., Letsinger,R.L., Mucic,R.C., Storhoff,J.J.,
Elghamian,R., Taton,T.A., Garimella,V., Li,Z. and Park,S.J.
TITLE Nanoparticles having oligonucleotides attached thereto and uses
therefor
JOURNAL Patent: WO 0246472-A 70 13-JUN-2002;
Nanosphere, Inc. (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="random synthetic sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 139
AX664307
LOCUS AX664307 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 5 from Patent WO0246398.
ACCESSION AX664307
VERSION AX664307.1 GI:29164237
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Willson,R.C. and Murphy,J.C.
TITLE Nucleic acid separation using immobilized metal affinity
chromatography
JOURNAL Patent: WO 0246398-A 5 13-JUN-2002;
The University of Houston System (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 140
AX664308/c
LOCUS AX664308 20 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 6 from Patent WO0246398.
ACCESSION AX664308
VERSION AX664308.1 GI:29164238
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Willson,R.C. and Murphy,J.C.
TITLE Nucleic acid separation using immobilized metal affinity
chromatography
JOURNAL Patent: WO 0246398-A 6 13-JUN-2002;
The University of Houston System (US)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Oligonucleotide Sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 141
AX741040/c
LOCUS AX741040 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 14 from Patent WO03027328.
ACCESSION AX741040
VERSION AX741040.1 GI:30523901
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Kirteen,N.V., Hyldig-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of
detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 14 03-APR-2003;
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES
source Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;

```

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 142
AX741052 AX741052 20 bp DNA linear PAT 10-MAY-2003
DEFINITION Sequence 26 from Patent WO03027328.
ACCESSION AX741052
VERSION AX741052.1 GI:30523913
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kirszen,N.V., Hyldeg-Nielsen,J.J. and Williams,B.F.
TITLE Methods, kits and compositions pertaining to the suppression of
detectable probe binding to randomly distributed repeat sequences
in genomic nucleic acid
JOURNAL Patent: WO 03027328-A 26 03-APR-2003;
Boston Probes, Inc. (US) ; DakoCytomation Denmark A/S (DK)
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/notes="Description of Combined DNA/RNA Molecule:Synthetic
Oligomer Sequence-Synthetic Probe Sequence"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 143
BD008523 BD008523 20 bp DNA linear PAT 31-JAN-2002
LOCUS Compounds and methods for treatment and diagnosis of Mycobacterial
DEFINITION infections.
ACCESSION BD008523
VERSION BD008523.1 GI:18636896
KEYWORDS JP 2001503969-A/26.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Tan,P., Hiyaama,J., Visser,E.S., Skinner,M.A., Scott,L.M. and
Prestidge,R.L.
TITLE Compounds and methods for treatment and diagnosis of Mycobacterial
infections
JOURNAL Patent: JP 2001503969-A 26 27-MAR-2001;
GENESIS RESEARCH & DEVELOPMENT CO LTD
COMMENT OS Unidentified
PN JP 2001503969-A/26
PD 27-MAR-2001
PF 28-AUG-1997 JP 1998511516
PR PAUL TAN,JUN HIYAMA,ELIZABETH S VISSER,MARGOT A SKINNER, PI
LINDA M SCOTT,
PI ROSS L PRESTIDGE
PC A61K39/04,A61K35/74,C07K14/35,C12N15/63
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20

Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 144
BD008522 BD008522 20 bp RNA linear PAT 27-AUG-2002
LOCUS Ribonucleoside-derivative and method for preparing the same.
DEFINITION
ACCESSION BD008522
VERSION BD008522.1 GI:22626125
KEYWORDS JP 2001515087-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Pitsch,S., Weiss,P.A. and Jenny,L.
TITLE Ribonucleoside-derivative and method for preparing the same
JOURNAL Patent: JP 2001515087-A 1 18-SEP-2001;
STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
COMMENT OS Artificial Sequence
PN JP 2001515087-A/1
PD 18-SEP-2001
PF 17-AUG-1998 JP 2000509723
PR 18-AUG-1997 CH 1931/97
PI STEFAN PITTSCH,PATRICK A WEISS,LUZI JENNY
PC C07H19/06,C07H19/16,C07H21/02,C07H23/00 CC
Description of Artificial Sequence:synthetic polynucleotide PH
Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".

FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1

RESULT 145
BD107450 BD107450 20 bp DNA linear PAT 18-SEP-2002
LOCUS Method of detecting single base polymorphism.
DEFINITION
ACCESSION BD107450
VERSION BD107450.1 GI:23202268
KEYWORDS JP 2002034599-A/9.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Segawa,M., Takarada,H., Aono,T. and Yoshiga,S.
TITLE Method of detecting single base polymorphism
JOURNAL Patent: JP 2002034599-A 9 05-FEB-2002;
TOYOBO CO LTD
COMMENT OS Artificial Sequence

```



```

source
1. .21
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 155
AR322245/c
LOCUS AR322245 21 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 13 from patent US 6566072.
ACCESSION AR322245
VERSION AR322245.1 GI:33707814
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 21)
AUTHORS Watson,M.A. and Fleming,T.P.
TITLE Mamaglobin, a secreted mammary-specific breast cancer protein
JOURNAL Patent: US 6566072-A 13 20-MAY-2003;
FEATURES
Location/Qualifiers
source
1. .21
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 156
AX104720/c
LOCUS AX104720 21 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 912 from Patent WO0122972.
ACCESSION AX104720
VERSION AX104720.1 GI:13920917
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 912 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
Location/Qualifiers
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 157
AX825132/c
LOCUS AX825132 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 30 from Patent WO03072818.
ACCESSION AX825132
VERSION AX825132.1 GI:39750861
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

```

```

AX355812/c
LOCUS AX355812 21 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 840 from Patent WO0197843.
ACCESSION AX355812
VERSION AX355812.1 GI:18620480
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 840 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
Location/Qualifiers
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate
backbone"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 158
AX547773/c
LOCUS AX547773 21 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 912 from Patent WO02053141.
ACCESSION AX547773
VERSION AX547773.1 GI:25812917
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 912 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
Location/Qualifiers
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match
Best Local Similarity 1.1%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 159
AX825132/c
LOCUS AX825132 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 30 from Patent WO03072818.
ACCESSION AX825132
VERSION AX825132.1 GI:39750861
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

```



```
RESULT 162
AX825155/c
LOCUS AX825155 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 53 from Patent WO03072818.
ACCESSION AX825155
VERSION AX825155.1 GI:39750884
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 53 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 20 CAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 163
AX825156/c
LOCUS AX825156 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 54 from Patent WO03072818.
ACCESSION AX825156
VERSION AX825156.1 GI:39750885
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 54 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 20 CAAAAAAAAAAAAAAAAAAAAA 1
|||||
RESULT 164
AX825157/c
LOCUS AX825157 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 55 from Patent WO03072818.
ACCESSION AX825157
VERSION AX825157.1 GI:39750886
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 55 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
Location/Qualifiers
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base 18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
|||||
Db 20 CAAAAAAAAAAAAAAAAAAAAA 1
|||||
```



```

modified_base      /mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
/modified_base      /mod_base=OTHER
18
/modified_base      /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 168
BD080832/c
LOCUS      Mamaglobin, a secreted mammary specific breast cancer protein.
DEFINITION
ACCESSION  BD080832
VERSION     JP 2001516569-A/10.
KEYWORDS   unidentifed
SOURCE      unidentifed
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Watson,M.A. and Fleming,T.P.
TITLE       Mamaglobin, a secreted mammary specific breast cancer protein
JOURNAL     Patent: JP 2001516569-A 10 02-OCT-2001;
            WASHINGTON UNIVERSITY
COMMENT     OS Unidentifed
            PN JP 2001516569-A/10
            PD 02-OCT-2001
            PF 18-SEP-1998 US 08/933149
            PR 18-SEP-1998 US 08/933149
            PI MARK A WATSON,TIMOTHY P FLEMING
            PC C12N15/09,A61K35/26,A61K39/00,A61K39/395,A61K39/395,
            A61P35/00,
            PC C07K14/47,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Mamaglobin, a secreted mammary specific breast cancer protein
            FH Key Location/Qualifiers
            FT source 1..21
            /organism='Unidentifed'.
FEATURES
source
1..21
/organism='unidentifed'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 169
BD087491
LOCUS      Mamaglobin, a secreted mammary specific breast cancer protein.
DEFINITION
ACCESSION  BD087491
VERSION     JP 2002525098-A/10.
KEYWORDS   unidentifed
SOURCE      unidentifed
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Watson,M.A. and Fleming,T.P.
TITLE       Mamaglobin, a secreted mammary specific breast cancer protein
JOURNAL     Patent: JP 2002525098-A 10 13-AUG-2002;
            WASHINGTON UNIVERSITY
COMMENT     OS Artificial Sequence
            PN JP 2002525098-A/10
            PD 13-AUG-2002
            PF 29-SEP-1999 US 09/162622
            PR 29-SEP-1998 US 09/162622
            PI MARK A WATSON,TIMOTHY P FLEMING
            PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
            C12N15/00
            CC Description of Artificial Sequence:Synthetic
            FH Key Location/Qualifiers
            FT source 1..21
            /organism='Artificial Sequence'.
FEATURES
source
1..21
/organism='Artificial Sequence'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 170
BD224108/c
LOCUS      Mamaglobin, breast cancer secretory protein specific to mamma.
DEFINITION
ACCESSION  BD224108
VERSION     BD224108.1 GI:33033878
KEYWORDS   JP 2002525098-A/10.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Watson,M.A. and Fleming,T.P.
TITLE       Mamaglobin, breast cancer secretory protein specific to mamma
JOURNAL     Patent: JP 2002525098-A 10 13-AUG-2002;
            WASHINGTON UNIVERSITY
COMMENT     OS Artificial Sequence
            PN JP 2002525098-A/10
            PD 13-AUG-2002
            PF 29-SEP-1999 US 09/162622
            PR 29-SEP-1998 US 09/162622
            PI MARK A WATSON,TIMOTHY P FLEMING
            PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
            C12N15/00
            CC Description of Artificial Sequence:Synthetic
            FH Key Location/Qualifiers
            FT source 1..21
            /organism='Artificial Sequence'.
FEATURES
source
1..21
/organism='Artificial Sequence'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

KEYWORDS          JP 2001525193-A/2.
SOURCE            synthetic construct
ORGANISM          artificial construct
REFERENCE         1 (bases 1 to 21)
AUTHORS           Sosnowski,R.G., Butler,W.F., Tu,E., Nerenberg,M.I., Heller,M.J. and
                  Edman,C.F.
TITLE            Self-assembling microelectronic integration system capable of
                  designation self address, compartment device, mechanism, method and
                  operation for molecular biological analysis and diagnosis
JOURNAL          Patent: JP 2001525193-A 2 11-DEC-2001;
                  NANOGEN INC
COMMENT          OS Artificial Sequence
                  PN JP 2001525193-A/2
                  PD 11-DEC-2001
                  PR 01-DEC-1998 US 08/986065
                  PI RONALD G SOSNOWSKI,WILLIAM F BUTLER,EUGENE TU,MICHAEL I PI
                  NERENBERG,
                  PI MICHAEL J HELLER,CARL F EDMAN
                  PC C12Q1/68,C12N15/09,C12N15/00
                  CC Description of Artificial Sequence: Synthesized with u at 3'
                  CC terminus to
                  CC provide ribonucleic acid base for reactivity; Poly A sequence
                  CC for reduced
                  CC secondary structure
                  CC Location/Qualifiers
                  FH Key 1..21
                  FT source 1..21
                  /organism='Artificial Sequence'.
FEATURES
source
1..21
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 170
BD224108/c
LOCUS      Mamaglobin, breast cancer secretory protein specific to mamma.
DEFINITION
ACCESSION  BD224108
VERSION     BD224108.1 GI:33033878
KEYWORDS   JP 2002525098-A/10.
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1 (bases 1 to 21)
AUTHORS     Watson,M.A. and Fleming,T.P.
TITLE       Mamaglobin, breast cancer secretory protein specific to mamma
JOURNAL     Patent: JP 2002525098-A 10 13-AUG-2002;
            WASHINGTON UNIVERSITY
COMMENT     OS Artificial Sequence
            PN JP 2002525098-A/10
            PD 13-AUG-2002
            PF 29-SEP-1999 US 09/162622
            PR 29-SEP-1998 US 09/162622
            PI MARK A WATSON,TIMOTHY P FLEMING
            PC C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/577//G01N33/574, PC
            C12N15/00
            CC Description of Artificial Sequence:Synthetic
            FH Key Location/Qualifiers
            FT source 1..21
            /organism='Artificial Sequence'.
FEATURES
source
1..21
/organism='Artificial Sequence'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

```

```

source
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 171
AX825103/c
LOCUS AX825103 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 1 from Patent WO03072818.
ACCESSION AX825103
VERSION AX825103.1 GI:39750832
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 1 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 21
Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAAAAAAAAAAAAAAAAA 1754
Db 21 ACTAAAAAAAAAAAAAAAAAAAAA 1

RESULT 173
AX825115/c
LOCUS AX825115 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 13 from Patent WO03072818.
ACCESSION AX825115
VERSION AX825115.1 GI:39750844
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 13 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 21
Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTCACAAAAAAAAAAAAAAAAAAAA 1751
Db 21 TTTCACAAAAAAAAAAAAAAAAAAAA 1

RESULT 172
AX825110/c
LOCUS AX825110 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 8 from Patent WO03072818.
ACCESSION AX825110
VERSION AX825110.1 GI:39750839
KEYWORDS

```


/note="LNA-T (Locked Nucleic Acid)"		
modified_base	9	/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"		
modified_base	12	/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"		
modified_base	15	/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"		
modified_base	18	/mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"		
/mod_base=OTHER		
Query Match		
Best Local Similarity 1.1%; Score 19.4; DB 1; Length 21;		
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1733	TACAAAAA 1753
Db	21	TATAAAAA 1
RESULT 174		
AX825116/c		
LOCUS		
AX825116 21 bp DNA linear PAT 11-DEC-2003		
DEFINITION Sequence 14 from Patent WO03072818.		
ACCESSION AX825116		
VERSION AX825116.1 GI:39750845		
KEYWORDS		
SOURCE		
ORGANISM		
synthetic construct		
synthetic construct		
artificial sequences.		
REFERENCE	1	
AUTHORS	Beckenkamp, D., Dieck, T.H. and Hoppe, H.U.	
TITLE	Method for sorting single-stranded nucleic acids	
JOURNAL	Patent: WO 03072818-A 14 04-SEP-2003;	
DEGUS	Degussa Bioactives GmbH (DE)	
FEATURES	Location/Qualifiers	
source	1..21	
/organism="synthetic construct"		
/mol_type="unassigned DNA"		
/db_xref="taxon:32630"		
/note="Beschreibung der kuenstlichen		
Sequenz:Capture-Oligonukleotid"		
misc_binding	1	/bound_moiety="Biotin"
modified_base	3	/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER		
modified_base	6	/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER		
modified_base	9	/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER		
modified_base	12	/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER		
modified_base	15	/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER		
modified_base	18	/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER		
Query Match		
Best Local Similarity 1.1%; Score 19.4; DB 1; Length 21;		
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
Qy	1735	CAAAAAA 1755


```

RESULT 182
AX825151/c
LOCUS AX825151 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 49 from Patent WO03072818.
ACCESSION AX825151
VERSION AX825151.1 GI:39750880
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 49 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAACAAAAA 1755
Db 21 CTAACAAAAA 1

RESULT 183
AX825152/c
LOCUS AX825152 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 50 from Patent WO03072818.
ACCESSION AX825152
VERSION AX825152.1 GI:39750881
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 50 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1752
Db 21 TTAAAAA 1

RESULT 184
AX825154/c
LOCUS AX825154 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 52 from Patent WO03072818.
ACCESSION AX825154
VERSION AX825154.1 GI:39750883
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 52 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding
1 /bound_moiety="Biotin"
modified_base
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
modified_base
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAACAAAAA 1755
Db 21 CTAACAAAAA 1

```

```

/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1754
Db 21 ATAAAAAAAAAAAAAAAAAAAA 1

RESULT 185
AX825160/c      21 bp. DNA linear PAT 11-DEC-2003
LOCUS           Sequence 58 from Patent WO03072818.
DEFINITION      AX825160
ACCESSION       AX825160
VERSION         AX825160.1 GI:39750889
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS         Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE           Method for sorting single-stranded nucleic acids
JOURNAL         Patent: WO 03072818-A 58 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES        Location/Qualifiers
                 source
                 1..21
                 /organism="synthetic construct"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:32630"
                 /note="Beschreibung der kuenstlichen
                 Sequenz:Capture-Oligonukleotid"
                 misc_binding
                 1
                 /bound_moiety="Biotin"
                 modified_base
                 3
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 6
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 9
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 12
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 15
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 18
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 21
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1754
Db 21 AGAAAAAAAAAAAAAAAAAAAA 1

RESULT 187
E13209/c      24 bp DNA linear PAT 27-APR-1998
LOCUS         E13209
DEFINITION    DNA probe.
ACCESSION     E13209
VERSION       E13209.1 GI:3252014
KEYWORDS      JP 1997149799-A/1.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1. (bases 1 to 24)
AUTHORS       Kanbara,H., Okano,K. and Umetsu,K.
TITLE         ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
              DEVICE OF NUCLEIC ACID
JOURNAL       Patent: JP 1997149799-A 1 10-JUN-1997;
              HITACHI LTD
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1997149799-A/1
              PD 10-JUN-1997
              PF 30-NOV-1995 JP 1995311949
              PI KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
              C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
              G01N27/447,
              PC G01N27/447,G01N33/50;
              CC strandedness: Single;
              CC topology: Linear;
              FH Key
              FH Key
              FT source

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1755
Db 21 CAAAAAAAAAAAAAAAAAAAA 1

RESULT 186
AX825162/c      21 bp DNA linear PAT 11-DEC-2003
LOCUS           Sequence 60 from Patent WO03072818.
DEFINITION      AX825162
ACCESSION       AX825162
VERSION         AX825162.1 GI:39750891
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS         Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE           Method for sorting single-stranded nucleic acids
JOURNAL         Patent: WO 03072818-A 58 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES        Location/Qualifiers
                 source
                 1..21
                 /organism="synthetic construct"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:32630"
                 /note="Beschreibung der kuenstlichen
                 Sequenz:Capture-Oligonukleotid"
                 misc_binding
                 1
                 /bound_moiety="Biotin"
                 modified_base
                 3
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 6
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 9
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 12
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 15
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 18
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 21
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1755
Db 21 CAAAAAAAAAAAAAAAAAAAA 1

RESULT 186
AX825162/c      21 bp DNA linear PAT 11-DEC-2003
LOCUS           Sequence 60 from Patent WO03072818.
DEFINITION      AX825162
ACCESSION       AX825162
VERSION         AX825162.1 GI:39750891
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE       1
AUTHORS         Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE           Method for sorting single-stranded nucleic acids
JOURNAL         Patent: WO 03072818-A 60 04-SEP-2003;
                Degussa Bioactives GmbH (DE)
FEATURES        Location/Qualifiers
                 source
                 1..21
                 /organism="synthetic construct"
                 /mol_type="unassigned DNA"
                 /db_xref="taxon:32630"
                 /note="Beschreibung der kuenstlichen
                 Sequenz:Capture-Oligonukleotid"
                 misc_binding
                 1
                 /bound_moiety="Biotin"
                 modified_base
                 3
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 6
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 9
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 12
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 15
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 18
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER
                 modified_base
                 21
                 /note="LNA-T (Locked Nucleic Acid)"
                 /mod_base=OTHER

Query Match      1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1754
Db 21 AGAAAAAAAAAAAAAAAAAAAA 1

RESULT 187
E13209/c      24 bp DNA linear PAT 27-APR-1998
LOCUS         E13209
DEFINITION    DNA probe.
ACCESSION     E13209
VERSION       E13209.1 GI:3252014
KEYWORDS      JP 1997149799-A/1.
SOURCE        unidentified
ORGANISM      unclassified.
REFERENCE     1. (bases 1 to 24)
AUTHORS       Kanbara,H., Okano,K. and Umetsu,K.
TITLE         ANALYSIS OR DETECTION OF NUCLEIC ACID AND ANALYSER OR INSPECTION
              DEVICE OF NUCLEIC ACID
JOURNAL       Patent: JP 1997149799-A 1 10-JUN-1997;
              HITACHI LTD
COMMENT       OS None
              OC Artificial sequences.
              PN JP 1997149799-A/1
              PD 10-JUN-1997
              PF 30-NOV-1995 JP 1995311949
              PI KANBARA HIDEKI, OKANO KAZUNOBU, UEMATSU KAZUMUNE PC
              C12Q1/68,C07H21/04,C12M1/00,C12N15/09,C12Q1/44,C12Q1/48, PC
              G01N27/447,
              PC G01N27/447,G01N33/50;
              CC strandedness: Single;
              CC topology: Linear;
              FH Key
              FH Key
              FT source

```

```
FT      /organism='Artificial sequences'.
source  Location/Qualifiers
        1..24
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

Query Match
Best Local Similarity 1.1%; Score 19.4; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA..... 1755
Db 21 CGAAAAA..... 1

RESULT 188
AX708815
LOCUS AX708815 24 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 31 from Patent WO02095071.
ACCESSION AX708815
VERSION AX708815.1 GI:29564542
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Plasterk,R.H.
TITLE Means and methods for identifying genes and proteins involved in
JOURNAL the prevention and/or repair of a replication error
        Patent: WO 02095071-A 31 28-NOV-2002;
        Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES
source Location/Qualifiers
        1..24
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="sequence to demonstrate the principle of how to
        detect somatic repeat instability-##N# stands for any
        number of nucleotides selected from A, C, T or G#"

Query Match
Best Local Similarity 1.1%; Score 19.4; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TACAAAAA..... 1755
Db 2 TGNAAAAA..... 24

RESULT 189
AX708814
LOCUS AX708814 25 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 30 from Patent WO02095071.
ACCESSION AX708814
VERSION AX708814.1 GI:29564541
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Plasterk,R.H.
TITLE Means and methods for identifying genes and proteins involved in
JOURNAL the prevention and/or repair of a replication error
        Patent: WO 02095071-A 30 28-NOV-2002;
        Koninklijke Nederlandse Akademie van Wetenschappen (NL)
FEATURES
source Location/Qualifiers
        1..25
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="sequence to demonstrate the principle of how to
        detect somatic repeat instability-##N# stands for any

number of nucleotides selected from A, C, T or G#"

number of nucleotides selected from A, C, T or G#"

Query Match
Best Local Similarity 1.1%; Score 19.4; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1733 TACAAAAA..... 1755
Db 2 TGNAAAAA..... 24

RESULT 190
AX704227
LOCUS AR074227 24 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 35 from patent US 5952490.
ACCESSION AR074227
VERSION AR074227.1 GI:10000982
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
        Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
        Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 35 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..24
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 191
AR074235
LOCUS AR074235 24 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 43 from patent US 5952490.
ACCESSION AR074235
VERSION AR074235.1 GI:10000990
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
        Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
        Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 43 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..24
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 192
AR074301
```



```
RESULT 197
AR307275
LOCUS AR307275 24 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 32 from patent US 6551774.
ACCESSION AR307275
VERSION AR307275.1 GI:31697802
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 24)
AUTHORS West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 32 22-APR-2003;
FEATURES
source
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
|||||
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 198
AR307277
LOCUS AR307277 24 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 34 from patent US 6551774.
ACCESSION AR307277
VERSION AR307277.1 GI:31697804
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 24)
AUTHORS West,M.D., Harley,C.B., Weinrich,S.L., Strahl,C.M., McEachern,M.J.,
Shay,J., Wright,W.E., Blackburn,E.H., Kim,N.W. and Vaziri,H.
TITLE Diagnostic methods for conditions associated with elevated cellular
levels of telomerase activity
JOURNAL Patent: US 6551774-A 34 22-APR-2003;
FEATURES
source
Location/Qualifiers
1..24
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
|||||
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 199
AR302589
LOCUS AR302589 24 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 35 from Patent EP1016715.
ACCESSION AR302589
VERSION AR302589.1 GI:10279527
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 109 05-JUL-2000;
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
```

```
Wyatt,J.R.
Oligonucleotides having a conserved g4 core sequence
Patent: EP 1016715-A 35 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
|||||
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 200
AR302597
LOCUS AR302597 24 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 43 from Patent EP1016715.
ACCESSION AR302597
VERSION AR302597.1 GI:10279535
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 43 05-JUL-2000;
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGGGCTGGGGTTGTGG 1042
|||||
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 201
AR302663
LOCUS AR302663 24 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 109 from Patent EP1016715.
ACCESSION AR302663
VERSION AR302663.1 GI:10279601
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE
1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 109 05-JUL-2000;
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
```



```
Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGTTGGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 202
AX032670
LOCUS AX032670 24 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 116 from Patent EP1016715.
ACCESSION AX032670
VERSION AX032670.1 GI:10279608
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
AUTHORS Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: EP 1016715-A 116 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
Location/Qualifiers
1..24
/organism="unidentified"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 24;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGTTGGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 203
AR074225
LOCUS AR074225 25 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 33 from patent US 5952490.
ACCESSION AR074225
VERSION AR074225.1 GI:10000980
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 33 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGTTGGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 204
AR074226
LOCUS AR074226 25 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 34 from patent US 5952490.
ACCESSION AR074226
VERSION AR074226.1 GI:10000981
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 25)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 34 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..25
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGTTGGG 1042
Db 1 TTGGGGTTGGGTTGGGTTGGG 24

RESULT 205
BD244864
LOCUS BD244864 25 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double
strand formation unstable.
ACCESSION BD244864
VERSION BD244864.1 GI:33054634
KEYWORDS JP 2002532063-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 (bases 1 to 25)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double
strand formation unstable
JOURNAL Patent: JP 2002532063-A 9 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
OS Artificial Sequence
PN JP 2002532063-A/9
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
FT source
1..25
/organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 1.1%; Score 19.2; DB 1; Length 25;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1732 TTACAAAAAATTTTAAAAA 1755
Db 1 TTTAAAAAACAAAAAAGAAAAA 24

RESULT 206
```

AX032587
LOCUS AX032587 25 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 33 from Patent EP1016715.
ACCESSION AX032587
VERSION AX032587.1 GI:10279525
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 33 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
1. .25
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGATGGGCTGGGTTGTGG 1042
||||| ||||| ||||| ||||| |||||
Db 1 TTGGGTTGGGTTGGGTTGGG 24
RESULT 207
AX032588
LOCUS AX032588 25 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 34 from Patent EP1016715.
ACCESSION AX032588
VERSION AX032588.1 GI:10279526
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 34 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
1. .25
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGATGGGCTGGGTTGTGG 1042
||||| ||||| ||||| ||||| |||||
Db 1 TTGGGTTGGGTTGGGTTGGG 24
RESULT 208
AX042937/c
LOCUS AX042937 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 503 from Patent WO0065088.
ACCESSION AX042937
VERSION AX042937.1 GI:11341545
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 503 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="16S rRNA Homozygote Primer Sequence"
Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1724 CTCGAGTTTACAAAAA 1747
||||| ||||| ||||| ||||| |||||
Db 24 CCTCGCGGTACAAAAA 1
RESULT 209
AX043114/c
LOCUS AX043114 25 bp DNA linear PAT 23-NOV-2000
DEFINITION Sequence 680 from Patent WO0065089.
ACCESSION AX043114
VERSION AX043114.1 GI:11341722
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Ulfendahl,P.J. and Wong,K.C.
TITLE Primers for identifying typing or classifying nucleic acids
JOURNAL Patent: WO 0065088-A 680 02-NOV-2000;
Amersham Pharmacia Biotech AB (SE)
FEATURES
source
1. .25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DPAL Heterozygote Primer Sequence"
Query Match 1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.1e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1727 CGAGTTTACAAAAA 1750
||||| ||||| ||||| ||||| |||||
Db 24 CGTCTGTACAAAAA 1
RESULT 210
A68209/c
LOCUS A68209 19 bp DNA linear PAT 06-MAY-1999
DEFINITION Sequence 4 from Patent WO9747636.
ACCESSION A68209
VERSION A68209.1 GI:4759376
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P., Moser,H.E., Altmann,K. and Douglas,M.E.
TITLE INTERMEDIATES FOR OLIGONUCLEOTIDE SYNTHESIS
JOURNAL Patent: WO 9747636-A 4 18-DEC-1997;
CIBA GEIGY AG (CH)
FEATURES
source
1. .19
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

[illegible]

```
Db      19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 216
AR111949/c
LOCUS   AR111949          19 bp    DNA          linear      PAT 14-FEB-2001
DEFINITION   Sequence 23 from patent US 6127533.
ACCESSION   AR111949
VERSION     AR111949.1 GI:12828797
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE       2'-O-aminooxy-modified oligonucleotides
JOURNAL     Patent: US 6127533-A 23 03-OCT-2000;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 217
AR111950/c
LOCUS   AR111950          19 bp    DNA          linear      PAT 14-FEB-2001
DEFINITION   Sequence 24 from patent US 6127533.
ACCESSION   AR111950
VERSION     AR111950.1 GI:12828798
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE       2'-O-aminooxy-modified oligonucleotides
JOURNAL     Patent: US 6127533-A 24 03-OCT-2000;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 218
AR111951/c
LOCUS   AR111951          19 bp    DNA          linear      PAT 14-FEB-2001
DEFINITION   Sequence 25 from patent US 6127533.
ACCESSION   AR111951
VERSION     AR111951.1 GI:12828799
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE       2'-O-aminooxy-modified oligonucleotides
JOURNAL     Patent: US 6127533-A 25 03-OCT-2000;

FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 219
AR111952/c
LOCUS   AR111952          19 bp    DNA          linear      PAT 14-FEB-2001
DEFINITION   Sequence 26 from patent US 6127533.
ACCESSION   AR111952
VERSION     AR111952.1 GI:12828800
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE       2'-O-aminooxy-modified oligonucleotides
JOURNAL     Patent: US 6127533-A 26 03-OCT-2000;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 220
AR111953/c
LOCUS   AR111953          19 bp    DNA          linear      PAT 14-FEB-2001
DEFINITION   Sequence 27 from patent US 6127533.
ACCESSION   AR111953
VERSION     AR111953.1 GI:12828801
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE       2'-O-aminooxy-modified oligonucleotides
JOURNAL     Patent: US 6127533-A 27 03-OCT-2000;
FEATURES    Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 221
AR111957/c
LOCUS   AR111957          19 bp    DNA          linear      PAT 14-FEB-2001
DEFINITION   Sequence 28 from patent US 6127533.
ACCESSION   AR111957
VERSION     AR111957.1 GI:12828802
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE       2'-O-aminooxy-modified oligonucleotides
JOURNAL     Patent: US 6127533-A 28 03-OCT-2000;
```

```
DEFINITION Sequence 31 from patent US 6127533.
ACCESSION AR111957
VERSION AR111957.1 GI:12828805
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 31 03-OCT-2000;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 222
AR111959/c
LOCUS AR111959
DEFINITION Sequence 33 from patent US 6127533.
ACCESSION AR111959
VERSION AR111959.1 GI:12828807
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 33 03-OCT-2000;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 223
AR111960/c
LOCUS AR111960
DEFINITION Sequence 34 from patent US 6127533.
ACCESSION AR111960
VERSION AR111960.1 GI:12828808
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 34 03-OCT-2000;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 224
AR111970/c
LOCUS AR111970
DEFINITION Sequence 44 from patent US 6127533.
ACCESSION AR111970
VERSION AR111970.1 GI:12828818
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook, P. Dan., Manoharan, M. and Kawasaki, A. Mamoru.
TITLE 2'-O-aminooxy-modified oligonucleotides
JOURNAL Patent: US 6127533-A 44 03-OCT-2000;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 225
AR124843/c
LOCUS AR124843
DEFINITION Sequence 20 from patent US 6172209.
ACCESSION AR124843
VERSION AR124843.1 GI:14110204
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan, M.; Cook, P. Dan., Prakash, T. P. and Kawasaki, A. M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 20 09-JAN-2001;
FEATURES Location/Qualifiers
source
    1..19
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
    |||||
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 226
AR124844/c
LOCUS AR124844
DEFINITION Sequence 21 from patent US 6172209.
ACCESSION AR124844
VERSION AR124844.1 GI:14110205
KEYWORDS
SOURCE
ORGANISM
```

Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 21 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 227
ARI24845/c
LOCUS ARI24845 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6172209.
ACCESSION ARI24845
VERSION ARI24845.1 GI:14110206
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 22 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 228
ARI24846/c
LOCUS ARI24846 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6172209.
ACCESSION ARI24846
VERSION ARI24846.1 GI:14110207
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 23 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 229
ARI24847/c
LOCUS ARI24847 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6172209.
ACCESSION ARI24847
VERSION ARI24847.1 GI:14110208
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 24 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 230
ARI24848/c
LOCUS ARI24848 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6172209.
ACCESSION ARI24848
VERSION ARI24848.1 GI:14110209
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 25 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 231
ARI24849/c
LOCUS ARI24849 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 26 from patent US 6172209.
ACCESSION ARI24849
VERSION ARI24849.1 GI:14110210
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.Dan., Prakash,T.P. and Kawasaki,A.M.
TITLE Aminoxy-modified oligonucleotides and methods for making same
JOURNAL Patent: US 6172209-A 26 09-JAN-2001;
FEATURES Location/Qualifiers
source
1. .19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1


```
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 237
ARI35291/c
LOCUS ARI35291 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 20 from patent US 6194598.
ACCESSION ARI35291
VERSION ARI35291.1 GI:14124196
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 20 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 238
ARI35292/c
LOCUS ARI35292 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 21 from patent US 6194598.
ACCESSION ARI35292
VERSION ARI35292.1 GI:14124197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 21 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 239
ARI35293/c
LOCUS ARI35293 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6194598.
ACCESSION ARI35293
VERSION ARI35293.1 GI:14124198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
```

```
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 22 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 240
ARI35294/c
LOCUS ARI35294 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 23 from patent US 6194598.
ACCESSION ARI35294
VERSION ARI35294.1 GI:14124199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 23 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 241
ARI35295/c
LOCUS ARI35295 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 24 from patent US 6194598.
ACCESSION ARI35295
VERSION ARI35295.1 GI:14124200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 24 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 242
ARI35296/c
LOCUS ARI35296 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 25 from patent US 6194598.
ACCESSION ARI35296
VERSION ARI35296.1 GI:14124201
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL Patent: US 6194598-A 25 27-FEB-2001;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1..1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
```



```

VERSION      AR135305.1  GI:14124210
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE        Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL      Patent: US 6194598-A 34 27-FEB-2001;
FEATURES     Location/Qualifiers
             source
             1..19
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 248
LOCUS      AR135315/c
DEFINITION Sequence 44 from patent US 6194598.
ACCESSION  AR135315
VERSION     AR135315.1  GI:14124220
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Cook,P.Dan., Manoharan,M. and Kawasaki,A.Mamoru.
TITLE      Aminoxy-modified oligonucleotide synthetic intermediates
JOURNAL    Patent: US 6194598-A 44 27-FEB-2001;
FEATURES   Location/Qualifiers
             source
             1..19
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 249
LOCUS      AR141898/c
DEFINITION Sequence 4 from patent US 6147200.
ACCESSION  AR141898
VERSION     AR141898.1  GI:15101414
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Manoharan,M., Kawasaki,A.M., Cook,P.Dan., Fraser,A.S. and
            Prakash,T.P.
TITLE      2'-O-acetamido modified monomers and oligomers
JOURNAL    Patent: US 6147200-A 4 14-NOV-2000;
FEATURES   Location/Qualifiers
             source
             1..19
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 250
LOCUS      AR153863/c
DEFINITION Sequence 16 from patent US 6238624.
ACCESSION  AR153863
VERSION     AR153863.1  GI:15121916
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Heller,M.J., Tu,E., Evans,G.A. and Sosnowski,R.G.
TITLE      Methods for transport in molecular biological analysis and
            diagnostics
JOURNAL    Patent: US 6238624-A 16 29-MAY-2001;
FEATURES   Location/Qualifiers
             source
             1..19
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 251
LOCUS      AR164173/c
DEFINITION Sequence 6 from patent US 6271358.
ACCESSION  AR164173
VERSION     AR164173.1  GI:16235162
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 19)
AUTHORS    Manoharan,M., Mohan,V. and Boswell,H.
TITLE      RNA targeted 2'-modified oligonucleotides that are conformationally
            preorganized
JOURNAL    Patent: US 6271358-A 6 07-AUG-2001;
FEATURES   Location/Qualifiers
             source
             1..19
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 252
LOCUS      BD274438/c
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformationally
            geometry.
ACCESSION  BD274438
VERSION     BD274438.1  GI:33084206
KEYWORDS   JP 2002543215-A/15.

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 253
LOCUS      BD274438
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformationally
            geometry.
ACCESSION  BD274438
VERSION     BD274438.1  GI:33084206
KEYWORDS   JP 2002543215-A/15.

```

```

SOURCE          synthetic construct
ORGANISM        synthetic construct
REFERENCE       1 (bases 1 to 19)
AUTHORS        Manoharan,M. and Mohan,V.
TITLE          Oligonucleotides having A-DNA form and B-DNA form confirmational
JOURNAL        Patent: JP 2002543215-A 15 17-DEC-2002;
COMMENT        ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002543215-A/15
                PD 17-DEC-2002
                PF 03-MAY-2000 JP 2000615638
                PR 03-MAY-1999 US 09/303586
                PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
                PC C07H21/02, A61K48/00, A61P35/00, A61P43/00, C12N15/09,
                PC C12N15/00
                CC Oligonucleotide
                CC 3' - O-MOE linkage
                CC 3' - O-MOE linkage
                CC 3' - O-MOE linkage
                FH Key Location/Qualifiers
                FT misc_feature (16)..(17)
                FT misc_feature (17)..(18)
                FT misc_feature (18)..(19)
FEATURES       1..19
               source
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match   1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 253
BD274439/c
LOCUS          19 bp DNA linear PAT 17-JUL-2003
DEFINITION    Oligonucleotides having A-DNA form and B-DNA form confirmational
ACCESSION     BD274439
VERSION       BD274439.1 GI:33084207
KEYWORDS      JP 2002543215-A/16.
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE     1 (bases 1 to 19)
AUTHORS       Manoharan,M. and Mohan,V.
TITLE        Oligonucleotides having A-DNA form and B-DNA form confirmational
JOURNAL      Patent: JP 2002543215-A 16 17-DEC-2002;
COMMENT      ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002543215-A/16
                PD 17-DEC-2002
                PF 03-MAY-2000 JP 2000615638
                PR 03-MAY-1999 US 09/303586
                PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
                PC C07H21/02, A61K48/00, A61P35/00, A61P43/00, C12N15/09,
                PC C12N15/00
                CC Oligonucleotide
                CC 2' - O-MOE linkage
                CC 2' - O-MOE linkage
                CC 2' - O-MOE linkage
                FH Key Location/Qualifiers
                FT misc_feature (16)..(17)
                FT misc_feature (17)..(18)
                FT misc_feature (18)..(19)

```

```

FEATURES       1..19
               source
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match   1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 254
BD274440/c
LOCUS          19 bp DNA linear PAT 17-JUL-2003
DEFINITION    Oligonucleotides having A-DNA form and B-DNA form confirmational
ACCESSION     BD274440
VERSION       BD274440.1 GI:33084208
KEYWORDS      JP 2002543215-A/17.
SOURCE        synthetic construct
ORGANISM      synthetic construct
REFERENCE     1 (bases 1 to 19)
AUTHORS       Manoharan,M. and Mohan,V.
TITLE        Oligonucleotides having A-DNA form and B-DNA form confirmational
JOURNAL      Patent: JP 2002543215-A 17 17-DEC-2002;
COMMENT      ISIS PHARMACEUTICALS INC
                OS Artificial Sequence
                PN JP 2002543215-A/17
                PD 17-DEC-2002
                PF 03-MAY-2000 JP 2000615638
                PR 03-MAY-1999 US 09/303586
                PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
                PC C07H21/02, A61K48/00, A61P35/00, A61P43/00, C12N15/09,
                PC C12N15/00
                CC Oligonucleotide
                CC sub O linkage
                CC 3' - O-MOE linkage; sub O linkage
                CC 3' - O-MOE linkage; sub O linkage
                CC 3' - O-MOE linkage; sub O linkage
                CC 3' - O-MOE linkage
                FH Key Location/Qualifiers
                FT misc_feature (15)..(16)
                FT misc_feature (16)..(17)
                FT misc_feature (17)..(18)
                FT misc_feature (18)..(19)
                FT misc_feature (19)..(19)
FEATURES       1..19
               source
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match   1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 255
BD274441/c
LOCUS          19 bp DNA linear PAT 17-JUL-2003
DEFINITION    Oligonucleotides having A-DNA form and B-DNA form confirmational
ACCESSION     BD274441

```

```

VERSION      BD274441.1  GI:33084209
KEYWORDS     JP 2002543215-A/18.
SOURCE       synthetic construct
ORGANISM     synthetic construct
             artificial sequences.
REFERENCE    1 (bases 1 to 19)
AUTHORS      Manoharan,M. and Mohan,V.
TITLE        Oligonucleotides having A-DNA form and B-DNA form conformational
             geometry
JOURNAL      Patent: JP 2002543215-A 18 17-DEC-2002;
COMMENT      ISIS PHARMACEUTICALS INC
             OS Artificial Sequence
             PN JP 2002543215-A/18
             PD 17-DEC-2002
             PF 03-MAY-2000 JP 2000615638
             PR 03-MAY-1999 US 09/303586.
             PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
             PC C07H21/02,A61K48/00,A61P35/00,A61P43/00,C12N15/09,
             CC C12N15/00
             CC Oligonucleotide
             CC sub O linkage
             CC 2'- O-MOE; sub O linkage
             CC 2'- O-MOE; sub O linkage
             CC 2'- O-MOE; sub O linkage
             CC 2'- O-MOE
             FT Key Location/Qualifiers
             FT misc feature (15) . (16)
             FT misc feature (16) . (17)
             FT misc feature (17) . (18)
             FT misc feature (18) . (19)
             FT misc feature (19) . (19)
             FT Location/Qualifiers
             1. .19
             /organism="synthetic construct"
             /mol_type="genomic DNA"
             /db_xref="taxon:32630"

FEATURES     source
             source
             Query Match 1.1%; Score 19; DB 1; Length 19;
             Best Local Similarity 100.0%; Pred. No. 1.6e+02;
             Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 257
BD274449/c
LOCUS       AR205798 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 15 from patent US 6369209.
ACCESSION  AR205798
VERSION     AR205798.1 GI:21503472
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Manoharan,M. and Mohan,V.
TITLE       Oligonucleotides having A-DNA form and B-DNA form conformational
             geometry
JOURNAL     Patent: US 6369209-A 15 09-APR-2002;
FEATURES    Location/Qualifiers
             source
             1. .19
             /organism="unknown"
             /mol_type="unassigned DNA"

             Query Match 1.1%; Score 19; DB 1; Length 19;
             Best Local Similarity 100.0%; Pred. No. 1.6e+02;
             Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 258
BD274449/c
LOCUS       AR205799 19 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 16 from patent US 6369209.
ACCESSION  AR205799
VERSION     AR205799.1 GI:21503473
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Manoharan,M. and Mohan,V.
TITLE       Oligonucleotides having A-DNA form and B-DNA form conformational
             geometry
JOURNAL     Patent: US 6369209-A 16 09-APR-2002;
FEATURES    Location/Qualifiers
             source
             1. .19
             /organism="unknown"
             /mol_type="unassigned DNA"

             Query Match 1.1%; Score 19; DB 1; Length 19;
             Best Local Similarity 100.0%; Pred. No. 1.6e+02;
             Matches 19; Conservative 0; Mismatches 0; Indels 19;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 256
BD274449/c
LOCUS       BD274449 19 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotides having A-DNA form and B-DNA form conformational
             geometry.
ACCESSION  BD274449
VERSION     BD274449.1 GI:33084217
KEYWORDS   JP 2002543215-A/26.
SOURCE     synthetic construct
ORGANISM   synthetic construct
             artificial sequences.
REFERENCE   1 (bases 1 to 19)
AUTHORS      Manoharan,M. and Mohan,V.
TITLE        Oligonucleotides having A-DNA form and B-DNA form conformational
             geometry
JOURNAL      Patent: JP 2002543215-A 26 17-DEC-2002;
COMMENT      ISIS PHARMACEUTICALS INC
             OS Artificial Sequence
             PN JP 2002543215-A/26
             PD 17-DEC-2002
             PF 03-MAY-2000 JP 2000615638
             PR 03-MAY-1999 US 09/303586
             PI MUTHIAH MANOHARAN, VENKATRAMAN MOHAN
             PC C07H21/02,A61K48/00,A61P35/00,A61P43/00,C12N15/09,
             CC C12N15/00
             CC Oligonucleotide
             CC 2'-modified T linkage
```

SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 19)
AUTHORS	Manoharan,M. and Mohan,V.
TITLE	Oligonucleotides having A-DNA form and B-DNA form conformational geometry
JOURNAL	US 6369209-A 26 09-APR-2002;
FEATURES	Patent: US 6369209-A 26 09-APR-2002;
source	Location/Qualifiers 1..19 /organism="unknown" /mol_type="unassigned DNA"
Query Match	1.i.%; Score 19; DB 1; Length 19;
Best Local Similarity	100.0%; Pred. No. 1.6e+02;
.Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 262	
LOCUS	AR213490 19 bp DNA linear PAT 25-SEP-2002
DEFINITION	Sequence 1 from patent US 6403779.
ACCESSION	AR213490
VERSION	AR213490.1 GI:23310721
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 19)
AUTHORS	Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE	Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL	Patent: US 6403779-A 1 11-JUN-2002;
FEATURES	Location/Qualifiers 1..19 /organism="unknown" /mol_type="genomic DNA"
source	
Query Match	1.i.%; Score 19; DB 1; Length 19;
Best Local Similarity	100.0%; Pred. No. 1.6e+02;
.Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 263	
LOCUS	AR213491/c 19 bp DNA linear PAT 25-SEP-2002
DEFINITION	Sequence 2 from patent US 6403779.
ACCESSION	AR213491
VERSION	AR213491.1 GI:23310722
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 19)
AUTHORS	Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE	Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL	Patent: US 6403779-A 2 11-JUN-2002;
FEATURES	Location/Qualifiers 1..19 /organism="unknown" /mol_type="genomic DNA"
source	
Query Match	1.i.%; Score 19; DB 1; Length 19;
Best Local Similarity	100.0%; Pred. No. 1.6e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 264
AR213492/c
LOCUS AR213492 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 3 from patent US 6403779.
ACCESSION AR213492
VERSION AR213492.1 GI:23310723
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 3 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 265
AR213493/c
LOCUS AR213493 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 4 from patent US 6403779.
ACCESSION AR213493
VERSION AR213493.1 GI:23310724
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 4 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 266
AR213494/c
LOCUS AR213494 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 5 from patent US 6403779.
ACCESSION AR213494
VERSION AR213494.1 GI:23310725
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 5 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 267
AR213495/c
LOCUS AR213495 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 6 from patent US 6403779.
ACCESSION AR213495
VERSION AR213495.1 GI:23310726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 6 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 268
AR213496/c
LOCUS AR213496 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 7 from patent US 6403779.
ACCESSION AR213496
VERSION AR213496.1 GI:23310727
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 7 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 269
AR213497/c
LOCUS AR213497 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6403779.
ACCESSION AR213497
VERSION AR213497.1 GI:23310728
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 8 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 269
AR213497/c
LOCUS AR213497 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 8 from patent US 6403779.
ACCESSION AR213497
VERSION AR213497.1 GI:23310728
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 270
AR213501/c
LOCUS AR213501 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 12 from patent US 6403779.
ACCESSION AR213501
VERSION AR213501.1 GI:23310732
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 12 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 271
AR213502/c
LOCUS AR213502 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 14 from patent US 6403779.
ACCESSION AR213502
VERSION AR213502.1 GI:23310733
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 272
AR213503/c
LOCUS AR213503 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 15 from patent US 6403779.
ACCESSION AR213503
VERSION AR213503.1 GI:23310734
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 15 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 273
AR213512/c
LOCUS AR213512 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 25 from patent US 6403779.
ACCESSION AR213512
VERSION AR213512.1 GI:23310743
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 277
AR213502/c
LOCUS AR213502 19 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 14 from patent US 6403779.
ACCESSION AR213502
VERSION AR213502.1 GI:23310733
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6403779-A 25 11-JUN-2002;
FEATURES Location/Qualifiers
source 1..19
/mol_type="genomic DNA"

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754 	19 bp DNA linear PAT 26-SEP-2002			
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1				
<hr/>					
RESULT 274					
AR222465	AR222465	Sequence 25 from patent US 6429300.			
LOCUS	AR222465	1 (bases 1 to 19)			
DEFINITION	AR222465	Peptide acceptor ligation methods			
ACCESSION	AR222465.1	GI:23329996			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Kurz,M., Lohse,P. and Wagner,R.				
TITLE	Peptide acceptor ligation methods				
JOURNAL	Patent: US 6429300-A 25 06-AUG-2002;				
FEATURES	Location/Qualifiers				
source	1..19				
<hr/>					
Query Match	1.1%; Score 19; DB 1; Length 19;				
Best Local Similarity	100.0%; Pred. No. 1.6e+02;				
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<hr/>					
QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754 	19 bp DNA linear PAT 20-DEC-2002			
Db	1 AAAAAAAAAAAAAAAAAAAAAA 19				
<hr/>					
RESULT 275					
AR237463/c	AR237463	Sequence 1 from patent US 6465628.			
LOCUS	AR237463	1 (bases 1 to 19)			
DEFINITION	AR237463	Process for the synthesis of oligomeric compounds			
ACCESSION	AR237463.1	GI:27282213			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Ravikumar,V.T., Manoharan,M., Capaldi,D.C., Krotz,A., Cole,D.L. and Guzaev,A.				
TITLE	Process for the synthesis of oligomeric compounds				
JOURNAL	Patent: US 6465628-A 1 15-OCT-2002;				
FEATURES	Location/Qualifiers				
source	1..19				
<hr/>					
Query Match	1.1%; Score 19; DB 1; Length 19;				
Best Local Similarity	100.0%; Pred. No. 1.6e+02;				
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<hr/>					
QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754 	19 bp DNA linear PAT 17-AUG-2003			
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1				
<hr/>					
RESULT 276					
AR321589/c	AR321589	Sequence 10 from patent US 6562960.			
LOCUS	AR321589	1 (bases 1 to 19)			
DEFINITION	AR321589	Unclassified.			
ACCESSION	AR321589.1	GI:33706818			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 19)				
<hr/>					
Query Match	1.1%; Score 19; DB 1; Length 19;				
Best Local Similarity	100.0%; Pred. No. 1.6e+02;				
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<hr/>					
QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754 	19 bp DNA linear PAT 17-AUG-2003			
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1				
<hr/>					
RESULT 277					
AR359804/c	AR359804	Sequence 3 from patent US 6593466.			
LOCUS	AR359804	1 (bases 1 to 19)			
DEFINITION	AR359804	Unclassified.			
ACCESSION	AR359804.1	GI:33766602			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.				
TITLE	Guanidinium functionalized nucleotides and precursors thereof				
JOURNAL	Patent: US 6593466-A 3 15-JUL-2003;				
FEATURES	Location/Qualifiers				
source	1..19				
<hr/>					
Query Match	1.1%; Score 19; DB 1; Length 19;				
Best Local Similarity	100.0%; Pred. No. 1.6e+02;				
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
<hr/>					
QY	1736 AAAAAAAAAAAAAAAAAAAAAA 1754 	19 bp DNA linear PAT 17-AUG-2003			
Db	19 AAAAAAAAAAAAAAAAAAAAAA 1				
<hr/>					
RESULT 278					
AR359805/c	AR359805	Sequence 4 from patent US 6593466.			
LOCUS	AR359805	1 (bases 1 to 19)			
DEFINITION	AR359805	Unclassified.			
ACCESSION	AR359805.1	GI:33766603			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 19)				
AUTHORS	Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.				
TITLE					

RESULT 279
AR359806/c
LOCUS AR359806 19 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 5 from patent US 6593466.
ACCESSION AR359806
VERSION AR359806.1 GI:33766604
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D., Prakash,T.P. and Mohan,V.
TITLE Guanidinilum functionalized nucleotides and precursors thereof
JOURNAL Patent: US 6593466-A 5 15-JUL-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 280
AR367447/c
LOCUS AR367447 19 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6329519.
ACCESSION AR367447
VERSION AR367447.1 GI:34600659
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Collingwood,S.P., Moser,H.E., Altmann,K.-H. and Douglas,M.E.
TITLE Intermediates for oligonucleotide synthesis
JOURNAL Patent: US 6329519-A 4 11-DEC-2001;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 281
AR399177/c
LOCUS AR399177 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 17 from patent US 6617442.
ACCESSION AR399177
VERSION AR399177.1 GI:40137667
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase H1 and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 17 09-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"

/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 282
AR399178/c
LOCUS AR399178 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 18 from patent US 6617442.
ACCESSION AR399178
VERSION AR399178.1 GI:40137669
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Crooke,S.T., Lima,W.F., Wu,H. and Monoharan,M.
TITLE Human RNase H1 and oligonucleotide compositions thereof
JOURNAL Patent: US 6617442-A 18 09-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 283
AR403601/c
LOCUS AR403601 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6624294.
ACCESSION AR403601
VERSION AR403601.1 GI:40151187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawaaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 1 23-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 284
AR403602/c
LOCUS AR403602 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6624294.
ACCESSION AR403602

```
VERSION AR403602.1 GI:40151188
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
          Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 2 23-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 287
AR403605/c
LOCUS AR403605
DEFINITION Sequence 5 from patent US 6624294.
ACCESSION AR403605
VERSION AR403605.1 GI:40151191
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
          Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 5 23-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 288
AR403606/c
LOCUS AR403606
DEFINITION Sequence 6 from patent US 6624294.
ACCESSION AR403606
VERSION AR403606.1 GI:40151192
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
          Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 6 23-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 289
AR403607/c
LOCUS AR403607
DEFINITION Sequence 7 from patent US 6624294.
ACCESSION AR403607
VERSION AR403607.1 GI:40151193
```

```
VERSION AR403603/c
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
          Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 3 23-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 285
AR403603/c
LOCUS AR403603
DEFINITION Sequence 3 from patent US 6624294.
ACCESSION AR403603
VERSION AR403603.1 GI:40151189
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
          Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 3 23-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..19
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 19; DB 1; Length 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 286
AR403604/c
LOCUS AR403604
DEFINITION Sequence 4 from patent US 6624294.
ACCESSION AR403604
VERSION AR403604.1 GI:40151190
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
          Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 4 23-SEP-2003;
FEATURES Location/Qualifiers
          source
            1..19
              /organism="unknown"
              /mol_type="genomic DNA"
```

```
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 7 23-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 290
AR403608/c
LOCUS AR403608 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6624294.
ACCESSION AR403608
VERSION AR403608.1 GI:40151194
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 8 23-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 291
AR403612/c
LOCUS AR403612 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12 from patent US 6624294.
ACCESSION AR403612
VERSION AR403612.1 GI:40151198
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 12 23-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 292
AR403613/c
LOCUS AR403613 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6624294.
ACCESSION AR403613
VERSION AR403613.1 GI:40151199
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 14 23-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 293
AR403614/c
LOCUS AR403614 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 15 from patent US 6624294.
ACCESSION AR403614
VERSION AR403614.1 GI:40151200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Kawasaki,A.M., Fraser,A.S., Manoharan,M., Cook,P.D. and
Prakash,T.P.
TITLE Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL Patent: US 6624294-A 15 23-SEP-2003;
FEATURES
source
1. .19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 294
AR403623/c
LOCUS AR403623 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 25 from patent US 6624294.
ACCESSION AR403623
VERSION AR403623.1 GI:40151209
KEYWORDS
```

```

SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Kawasaki A.M., Fraser, A.S., Mancharan, M., Cook, P.D. and
            Prakash, F.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL    Patent: US 6624294-A 25 23-SEP-2003;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 295
LOCUS      AR412338
DEFINITION Sequence 1 from patent US 6639061.
ACCESSION  AR412338
VERSION     AR412338.1 GI:40167448
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
AUTHORS    Cook, P.D., Mancharan, M., Maier, M. and An, H.
TITLE      C3'-methylene hydrogen phosphonate oligomers and related compounds
JOURNAL    Patent: US 6639061-A 1 28-OCT-2003;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 296
LOCUS      AR432616/c
DEFINITION Sequence 6 from patent US 6653458.
ACCESSION  AR432616
VERSION     AR432616.1 GI:40195149
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Mancharan, M., Cook, P.D. and Guinasso, C.J.
TITLE      Modified oligonucleotides
JOURNAL    Patent: US 6653458-A 6 25-NOV-2003;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Kawasaki A.M., Fraser, A.S., Mancharan, M., Cook, P.D. and
            Prakash, F.P.
TITLE      Regioselective synthesis of 2'-O-modified nucleosides
JOURNAL    Patent: US 6624294-A 25 23-SEP-2003;
FEATURES   Location/Qualifiers
            source
            1..19
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 297
LOCUS      AX349249/c
DEFINITION Sequence 33 from Patent WO0202810.
ACCESSION  AX349249
VERSION     AX349249.1 GI:18615281
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Bickel, R., Ehrlich, R., Ellinger, T., Ermantraut, E., Kaiser, T.,
            Schulz, T. and Wagner, G.
REFERENCE   1 Method for qualitative and/or quantitative detecting of molecular
            interactions on probe arrays
            TITLE Patent: WO 0202810-A 33 10-JAN-2002;
            JOURNAL Clondiag Chip Technologies GmbH (DE)
            FEATURES Location/Qualifiers
                    source
                    1..19
                    /organism="synthetic construct"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:32630"
                    /note="Oligonukleotidsonde"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 298
LOCUS      BD087505/c
DEFINITION Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis.
ACCESSION  BD087505
VERSION     BD087505.1 GI:22633115
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Sonowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and
            Edman, C.F.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Sonowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and
            Edman, C.F.
TITLE      Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis
            JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
            COMMENT NANOGEN INC
                    OS Artificial Sequence
                    PN JP 2001525193-A/16
                    PD 11-DEC-2001
                    PF 01-DEC-1998 JP 2000524303
                    PR 05-DEC-1997 US 08/986065
                    PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
                    NERENBERG,
                    PI MICHAEL J HELLER, CARL F EDMAN
                    PC C1201/68, C12N15/09, C12N15/00
                    CC Description of Artificial Sequence: Amine
                    conjugate to provide
                    CC with dyes
                    CC Key
                    FT source
                    1..19
                    Location/Qualifiers

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 299
LOCUS      BD087505/c
DEFINITION Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis.
ACCESSION  BD087505
VERSION     BD087505.1 GI:22633115
KEYWORDS   .
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM    Sonowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and
            Edman, C.F.
REFERENCE   1 (bases 1 to 19)
AUTHORS    Sonowski, R.G., Butler, W.F., Tu, E., Nerenberg, M.I., Heller, M.J. and
            Edman, C.F.
TITLE      Self-assembling microelectronic integration system capable of
            designating self address, compartment device, mechanism, method and
            operation for molecular biological analysis and diagnosis
            JOURNAL Patent: JP 2001525193-A 16 11-DEC-2001;
            COMMENT NANOGEN INC
                    OS Artificial Sequence
                    PN JP 2001525193-A/16
                    PD 11-DEC-2001
                    PF 01-DEC-1998 JP 2000524303
                    PR 05-DEC-1997 US 08/986065
                    PI RONALD G SOSNOWSKI, WILLIAM F BUTLER, EUGENE TU, MICHAEL I PI
                    NERENBERG,
                    PI MICHAEL J HELLER, CARL F EDMAN
                    PC C1201/68, C12N15/09, C12N15/00
                    CC Description of Artificial Sequence: Amine
                    conjugate to provide
                    CC with dyes
                    CC Key
                    FT source
                    1..19
                    Location/Qualifiers
```

```
FT          /organism='Artificial Sequence'.
FEATURES    Location/Qualifiers
  source    1..19
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 299
AR139960/c
LOCUS      BD196900                19 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Protostatic cancer gene.
ACCESSION  BD196900
VERSION    BD196900.1 GI:33006670
KEYWORDS  JP 2002516657-A/489.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  1 (bases 1 to 19)
AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I. and Bougueleret,L.
TITLE     Protostatic cancer gene
JOURNAL   Patent: JP 2002516657-A 489 11-JUN-2002;
COMMENT   OS Homo sapiens (human)
          PN JP 2002516657-A/489
          PD 11-JUN-2002
          PF 22-DEC-1998 JP 2000525562
          PR 22-DEC-1997 US 08/996306,09-SEP-1998 US 60/099658 PI
          DANIEL COHEN,MARTY BLUMENFELD,ILYA CHUMAKOV,LYDIE BOUGUELERET PC
          C12N15/09,C12N15/09,A01K67/02,C07K14/47,C07K16/18,C12N1/15, PC
          C12N1/19,
          PC C12N1/21,C12N5/10,C12N5/10,C12P21/08,C12Q1/68,G01N33/50 PC
          ,C12N15/00,C12N5/00,
          CC C12N5/00,C12N15/00
          CC potential microsequencing oligo for 4-4-187.mis2 FH Key
          Location/Qualifiers
          FT primer bind 1..19.
          Location/Qualifiers
          source    1..19
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 300
AR139960/c
LOCUS      AR139960                20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 32 from patent US 6207417.
ACCESSION  AR139960
VERSION    AR139960.1 GI:14482456
KEYWORDS  JP 2002516657-A/489.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE     Stem cell factor and compositions
JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES    Location/Qualifiers
  source    1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 301
AR140279/c
LOCUS      AR140279                20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 32 from patent US 6207454.
ACCESSION  AR140279
VERSION    AR140279.1 GI:14482775
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE     Method for enhancing the efficiency of gene transfer with stem cell
          factor (SCF) polypeptide
JOURNAL   Patent: US 6207454-A 32 27-MAR-2001;
FEATURES    Location/Qualifiers
  source    1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 302
AR140557/c
LOCUS      AR140557                20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 32 from patent US 6207802.
ACCESSION  AR140557
VERSION    AR140557.1 GI:14483053
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE     Stem cell factor and compositions
JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES    Location/Qualifiers
  source    1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 303
AR139960/c
LOCUS      AR139960                20 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 32 from patent US 6207417.
ACCESSION  AR139960
VERSION    AR139960.1 GI:14482456
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE  1 (bases 1 to 20)
AUTHORS   Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE     Stem cell factor and compositions
JOURNAL   Patent: US 6207802-A 32 27-MAR-2001;
FEATURES    Location/Qualifiers
  source    1..20
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1
```

<p>RESULT 303</p> <p>AR118155/c</p> <p>LOCUS</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>DEFINITION</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>ACCESSION</p> <p>Version 1</p> <p>AR118155.1</p> <p>GI:14099061</p> <p>KEYWORDS</p> <p>Unknown.</p> <p>SOURCE</p> <p>Unknown.</p> <p>ORGANISM</p> <p>Unclassified.</p> <p>REFERENCE</p> <p>1 (bases 1 to 21)</p> <p>Brenner, S.</p> <p>AUTHORS</p> <p>Compositions for sorting polynucleotides</p> <p>TITLE</p> <p>Patent: US 6140489-A 23 31-OCT-2000;</p> <p>JOURNAL</p> <p>Location/Qualifiers</p> <p>FEATURES</p> <p>1..21</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>	<p>linear</p> <p>21 bp</p> <p>DNA</p> <p>PAT 16-MAY-2001</p>	<p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 1; Length 21;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1736</p> <p>AAAAAAAAAAAAAAAAAAAA 1754</p> <p> </p> <p>Db 21</p> <p>AAAAAAAAAAAAAAAAAAAA 3</p>	<p>RESULT 304</p> <p>AR118155/c</p> <p>LOCUS</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>DEFINITION</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>ACCESSION</p> <p>Version 1</p> <p>AR118155.1</p> <p>GI:14099061</p> <p>KEYWORDS</p> <p>Unknown.</p> <p>SOURCE</p> <p>Unknown.</p> <p>ORGANISM</p> <p>Unclassified.</p> <p>REFERENCE</p> <p>1 (bases 1 to 21)</p> <p>Brenner, S.</p> <p>AUTHORS</p> <p>Compositions for sorting polynucleotides</p> <p>TITLE</p> <p>Patent: US 6140489-A 23 31-OCT-2000;</p> <p>JOURNAL</p> <p>Location/Qualifiers</p> <p>FEATURES</p> <p>1..21</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>	<p>linear</p> <p>21 bp</p> <p>DNA</p> <p>PAT 04-APR-1998</p>	<p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 1; Length 21;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1735</p> <p>AAAAAAAAAAAAAAAAAAAA 1753</p> <p> </p> <p>Db 19</p> <p>AAAAAAAAAAAAAAAAAAAA 1</p>	<p>RESULT 305</p> <p>AR118155/c</p> <p>LOCUS</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>DEFINITION</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>ACCESSION</p> <p>Version 1</p> <p>AR118155.1</p> <p>GI:14099061</p> <p>KEYWORDS</p> <p>Unknown.</p> <p>SOURCE</p> <p>Unknown.</p> <p>ORGANISM</p> <p>Unclassified.</p> <p>REFERENCE</p> <p>1 (bases 1 to 21)</p> <p>Brenner, S.</p> <p>AUTHORS</p> <p>Compositions for sorting polynucleotides</p> <p>TITLE</p> <p>Patent: US 6140489-A 23 31-OCT-2000;</p> <p>JOURNAL</p> <p>Location/Qualifiers</p> <p>FEATURES</p> <p>1..21</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>	<p>linear</p> <p>21 bp</p> <p>DNA</p> <p>PAT 11-DEC-2003</p>	<p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 1; Length 21;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1736</p> <p>AAAAAAAAAAAAAAAAAAAA 1754</p> <p> </p> <p>Db 21</p> <p>AAAAAAAAAAAAAAAAAAAA 3</p>	<p>RESULT 306</p> <p>AR118155/c</p> <p>LOCUS</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>DEFINITION</p> <p>Sequence 23 from patent US 6140489.</p> <p>AR118155</p> <p>ACCESSION</p> <p>Version 1</p> <p>AR118155.1</p> <p>GI:14099061</p> <p>KEYWORDS</p> <p>Unknown.</p> <p>SOURCE</p> <p>Unknown.</p> <p>ORGANISM</p> <p>Unclassified.</p> <p>REFERENCE</p> <p>1 (bases 1 to 21)</p> <p>Brenner, S.</p> <p>AUTHORS</p> <p>Compositions for sorting polynucleotides</p> <p>TITLE</p> <p>Patent: US 6140489-A 23 31-OCT-2000;</p> <p>JOURNAL</p> <p>Location/Qualifiers</p> <p>FEATURES</p> <p>1..21</p> <p>/organism="unknown"</p> <p>/mol_type="unassigned DNA"</p>	<p>linear</p> <p>21 bp</p> <p>DNA</p> <p>PAT 11-DEC-2003</p>	<p>Query Match</p> <p>Best Local Similarity 1.1%; Score 19; DB 1; Length 21;</p> <p>Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>	<p>QY 1737</p> <p>AAAAAAAAAAAAAAAAAAAA 1755</p> <p> </p> <p>Db 19</p> <p>AAAAAAAAAAAAAAAAAAAA 1</p>
---	--	---	---	---	--	---	---	---	--	---	---	---	--	---	---

```

modified_base
18 /mod_base=OTHER
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match
1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 307
AX825122/c
LOCUS AX825122 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 20 from Patent WO03072818.
ACCESSION AX825122
VERSION AX825122.1 GI:39750851
KEYWORDS
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 20 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
modified_base 12 /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
modified_base 18 /mod_base=OTHER

Query Match
1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 309
AX825125/c
LOCUS AX825125 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 23 from Patent WO03072818.
ACCESSION AX825125
VERSION AX825125.1 GI:39750854
KEYWORDS
SOURCE
ORGANISM
artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 23 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
modified_base 6 /mod_base=OTHER

```

```
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
|||||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 310
AX825128/c
LOCUS AX825128 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 26 from Patent WO03072818.
ACCESSION AX825128
VERSION AX825128.1 GI:39750857
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 26 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
1
misc_binding /bound_moiety="Biotin"
3
modified_base /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6
modified_base /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9
modified_base /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12
modified_base /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
modified_base /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
modified_base /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
|||||
Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 312
AX825130/c
LOCUS AX825130 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 28 from Patent WO03072818.
ACCESSION AX825130
VERSION AX825130.1 GI:39750859
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
1
REFERENCE Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
AUTHORS Method for sorting single-stranded nucleic acids
TITLE Patent: WO 03072818-A 28 04-SEP-2003;
JOURNAL Degussa Bioactives GmbH (DE)
FEATURES Location/Qualifiers
source
1..21
/organism="synthetic construct"
```



```

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/bound_moiety="Biotin"
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match      1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAA 1754
Db 19 CAAAAAAAAAAAAAAAAAAAA 1

RESULT 313
AX825153/c
LOCUS AX825153 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 51 from Patent WO03072818.
ACCESSION AX825153
VERSION AX825153.1 GI:39750882
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 51 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1
/bound_moiety="Biotin"
3
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18
/note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

misc_binding
modified_base
modified_base
modified_base
modified_base
modified_base
modified_base
modified_base

Query Match      1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 315
AX825161/c
LOCUS AX825161 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 59 from Patent WO03072818.
ACCESSION AX825161
VERSION AX825161.1 GI:39750890
KEYWORDS
SOURCE synthetic construct

```

ORGANISM	synthetic construct									
REFERENCE	artificial sequences.									
AUTHORS	1 Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.									
TITLE	Method for sorting single-stranded nucleic acids									
JOURNAL	Patent: WO 03072818-A 59 04-SEP-2003;									
	Degussa Bioactives GmbH (DE)									
FEATURES	Location/Qualifiers									
source	1..21									
misc_binding	1 /organism="synthetic construct"									
	/mol_type="unassigned DNA"									
	/db_xref="taxon:32630"									
modified_base	3 /note="LNA-T (Locked Nucleic Acid)"									
	/mod_base=OTHER									
modified_base	6 /note="LNA-T (Locked Nucleic Acid)"									
	/mod_base=OTHER									
modified_base	9 /note="LNA-T (Locked Nucleic Acid)"									
	/mod_base=OTHER									
modified_base	12 /note="LNA-T (Locked Nucleic Acid)"									
	/mod_base=OTHER									
modified_base	15 /note="LNA-T (Locked Nucleic Acid)"									
	/mod_base=OTHER									
modified_base	18 /note="LNA-T (Locked Nucleic Acid)"									
	/mod_base=OTHER									
Query Match	1.1%; Score 19; DB 1; Length 21;									
Best Local Similarity	100.0%; Pred. No. 1.8e+02;									
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1736 AAAAAAAAAAAAAAAAAA 1754									
Db	19 AAAAAAAAAAAAAAAAAA 1									
RESULT 316										
LOCUS	BD085544 22 bp RNA linear PAT 27-AUG-2002									
DEFINITION	Method of comparison and detection of RNA amount and DNA amount.									
ACCESSION	BD085544									
VERSION	BD085544.1 GI:22631154									
KEYWORDS	JP 2001333800-A/1.									
SOURCE	Homo sapiens (human)									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;									
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.									
JOURNAL	Shimada,K.									
COMMENT	Method of comparison and detection of RNA amount and DNA amount									
LOCUS	1 (bases 1 to 22)									
DEFINITION	OS Homo sapiens (human)									
ACCESSION	PN JP 2001333800-A/1									
VERSION	PD 04-DEC-2001									
KEYWORDS	PF 30-MAY-2000 JP 2000160324									
SOURCE	PI KAO RI SHIMADA									
ORGANISM	PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00									
REFERENCE	CC Method of comparison and detection of RNA amount and DNA CC									
AUTHORS	amount									
JOURNAL	FH Key Location/Qualifiers									
COMMENT	FT source 1..22									
LOCUS	/organism='Homo sapiens (human)'									
DEFINITION	Location/Qualifiers									
ACCESSION	1..22									
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										
DEFINITION										
ACCESSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
REFERENCE										
AUTHORS										
JOURNAL										
COMMENT										
LOCUS										

```

FEATURES
  source      Location/Qualifiers
    1..24
    /organism="unknown"
    /mol_type="genomic DNA"

  Query Match      1.1%; Score 19; DB 1; Length 24;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 20 ACAAAAAAAAAAAAAAAAAA 2

RESULT 319
BD097127/c
LOCUS      24 bp DNA linear PAT 27-AUG-2002
DEFINITION Support for immobilizing nucleotide and process for producing the
same.
ACCESSION  BD097127
VERSION     BD097127.1 GI:22642701
KEYWORDS   WO 0155365-A/1.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Tanga,M., Okamura,H., Takagi,K. and Takahashi,K.
TITLE     Support for immobilizing nucleotide and process for producing the
JOURNAL   Patent: WO 0155365-A 1 02-AUG-2001;
          TOYO KOHAN CO LTD, MICHIFUMI TANGA, HIROSHI OKAMURA, KENICHI TAKAGI,
          KOJIRO TAKAHASHI
COMMENT    OS Artificial Sequence
          PN WO 0155365-A/1
          PD 02-AUG-2001
          PF 24-JAN-2001 WO 2001JP000443
          PR 27-JAN-2000 JP OOP 019301
          PI MICHIFUMI TANGA, HIROSHI OKAMURA, KENICHI TAKAGI, KOJIRO PI
          TAKAHASHI
          PC C12N15/10, C07H21/04//G01N33/50, C12Q1/68
          CC Support for immobilizing nucleotide and process for producing
          the same
          FH Key      Location/Qualifiers
          FT source  1..24
                   /organism="Artificial Sequence".

FEATURES
  source      Location/Qualifiers
    1..24
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

  Query Match      1.1%; Score 19; DB 1; Length 24;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 24 CAAAAAAAAAAAAAAAAA 6

RESULT 320
BD161931/c
LOCUS      24 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized
substrate.
ACCESSION  BD161931
VERSION     BD161931.1 GI:27867689
KEYWORDS   JP 2002191369-A/8.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 24)
AUTHORS   Tanga,M., Okamura,H. and Takahashi,K.
TITLE     Method for carrying out thermal cycle of PCR using DNA-immobilized

```

```

substrate
Patent: JP 2002191369-A 8 09-JUL-2002;
TOYO KOHAN CO LTD, KOJIRO TAKAHASHI
OS Artificial Sequence
PN JP 2002191369-A/8
PD 09-JUL-2002
PF 27-DEC-2000 JP 2000399573
PI MICHIFUMI TANGA, HIROSHI OKAMURA, KOJIRO TAKAHASHI PC
C12N15/09, C12N15/68, C12Q1/68, C12N15/00, C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
immobilized
CC substrate
FH Key      Location/Qualifiers
FT source  1..24
           /organism="Artificial Sequence".

FEATURES
  source      Location/Qualifiers
    1..24
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

  Query Match      1.1%; Score 19; DB 1; Length 24;
  Best Local Similarity 100.0%; Pred. No. 2.1e+02;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 24 CAAAAAAAAAAAAAAAAA 6

RESULT 321
AX196979
LOCUS      25 bp DNA linear PAT 07-SEP-2001
DEFINITION Sequence 686 from Patent WO0151627.
ACCESSION  AX196979
VERSION     AX196979.1 GI:15387185
KEYWORDS   Glycine max (soybean)
SOURCE     Glycine max
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
          Glycine.
REFERENCE  1
AUTHORS   Hauge,B.M., Wang,M.L., Parsons,J.D. and Parnell,L.D.
TITLE     Nucleic acid molecules and other molecules associated with soybean
          cyst nematode resistance
JOURNAL   Patent: WO 0151627-A 686 19-JUL-2001;
          MONSANTO COMPANY (US)
FEATURES
  source      Location/Qualifiers
    1..25
    /organism="Glycine max"
    /mol_type="unassigned DNA"
    /db_xref="taxon:3847"
    /note="Seq ID:
          318013_seq ID:
          318013_A3_151839_17_Reverse_Primer_Seq"

  Query Match      1.1%; Score 19; DB 1; Length 25;
  Best Local Similarity 100.0%; Pred. No. 2.2e+02;
  Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 860 CAGGAAGAGGAAGAGGAGG 878
Db 1 CAGGAAGAGGAAGAGGAGG 19

RESULT 322
AR431308/c
LOCUS      24 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6651008.
ACCESSION  AR431308
VERSION     AR431308.1 GI:40193276
KEYWORDS

```

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 24)
AUTHORS      Vaisberg,E.A., Adams,C.L., Sabry,J.H. and Crompton,A.M.
TITLE        Database system including computer code for predictive cellular
              bioinformatics
JOURNAL      Patent: US 6651008-A 2 18-NOV-2003;
FEATURES     Location/Qualifiers
              source
              1..24
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 24;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAATAAAAAA 3

RESULT 323
LOCUS      AX043119/c
DEFINITION Sequence 685 from Patent WO0065088.
ACCESSION  AX043119
VERSION     AX043119.1 GI:11341727
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 24)
AUTHORS    Ulfendahl,P.J. and Wong,K.C.
TITLE      Primers for identifying typing or classifying nucleic acids
JOURNAL    Patent: WO 0065088-A 685 02-NOV-2000;
           Amersham Pharmacia Biotech AB (SE)
FEATURES   Location/Qualifiers
           source
           1..25
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32630"
           /note="DPaI Heterozygote Primer Sequence"

Query Match
Best Local Similarity 1.1%; Score 18.8; DB 1; Length 25;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTCACAAAAAAAAAAAAAAAAA 1752
Db 22 TGTACACACAAAAAAAAAAAAAAAAA 1

RESULT 324
LOCUS      AR139961/c
DEFINITION Sequence 33 from patent US 6207417.
ACCESSION  AR139961
VERSION     AR139961.1 GI:14482457
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE      DNA encoding stem cell factor
JOURNAL    Patent: US 6207417-A 33 27-MAR-2001;
FEATURES   Location/Qualifiers
           source
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 325
LOCUS      AR139962/c
DEFINITION Sequence 34 from patent US 6207417.
ACCESSION  AR139962
VERSION     AR139962.1 GI:14482458
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE      DNA encoding stem cell factor
JOURNAL    Patent: US 6207417-A 34 27-MAR-2001;
FEATURES   Location/Qualifiers
           source
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 326
LOCUS      AR140280/c
DEFINITION Sequence 33 from patent US 6207454.
ACCESSION  AR140280
VERSION     AR140280.1 GI:14482776
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 20)
AUTHORS    Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE      Method for enhancing the efficiency of gene transfer with stem cell
           factor (SCF) polypeptide
JOURNAL    Patent: US 6207454-A 33 27-MAR-2001;
FEATURES   Location/Qualifiers
           source
           1..20
           /organism="unknown"
           /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 18.4; DB 1; Length 20;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 327
LOCUS      AR140281/c
DEFINITION Sequence 34 from patent US 6207454.
ACCESSION  AR140281
VERSION     AR140281.1 GI:14482777
KEYWORDS   .
SOURCE     Unknown.

```

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Method for enhancing the efficiency of gene transfer with stem cell factor (SCF) polypeptide
JOURNAL Patent: US 6207454-A 34 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAA...AAAAAAAAA 1754
Db 20 CGAAAAA...AAAAAAAAA 1

RESULT 328
AR140558/c
LOCUS AR140558 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 33 from patent US 6207802.
ACCESSION AR140558
VERSION AR140558.1 GI:14483054
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 33 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAA...AAAAAAAAA 1754
Db 20 CTA...AAAAAAAAA 1

RESULT 329
AR140559/c
LOCUS AR140559 20 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 34 from patent US 6207802.
ACCESSION AR140559
VERSION AR140559.1 GI:14483055
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 34 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAA...AAAAAAAAA 1754
Db 20 CTA...AAAAAAAAA 1

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zsebo,K.M., Bosselman,R.A., Suggs,S.V. and Martin,F.H.
TITLE Stem cell factor and compositions
JOURNAL Patent: US 6207802-A 34 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAA...AAAAAAAAA 1754
Db 20 CTA...AAAAAAAAA 1

Db 20 CGAAAAA...AAAAAAAAA 1

RESULT 330
AR211367/c
LOCUS AR211367 20 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 5 from patent US 6399305.
ACCESSION AR211367
VERSION AR211367.1 GI:21514670
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Makino,Y., Abe,Y., Takagi,M., Takenaka,S., Yamashita,K. and Ogawa,M.
TITLE Protection of partial complementary nucleic acid fragment using a electroconductive chip and intercalator
JOURNAL Patent: US 6399305-A 5 04-JUN-2002;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1736 AAAAAA...AAAAAAAAA 1755
Db 20 AAAAAA...AAAAAAAAA 1

RESULT 331
AX067205/c
LOCUS AX067205 20 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 57 from Patent WO0100669.
ACCESSION AX067205
VERSION AX067205.1 GI:12544870
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Barry,C., Bougueleret,L., Chumakov,I. and Cohen-Akenine,A.
TITLE A bap28 gene and protein
JOURNAL Patent: WO 0100669-A 57 04-JAN-2001;
GENSET (FR)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide BAP28polyTcour"

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1731 TTTACAAAAA...AAAAAAAAA 1750
Db 20 TATACAAAAA...AAAAAAAAA 1

RESULT 332
AX136903/c
LOCUS AX136903 20 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 5 from Patent EP1065278.
ACCESSION AX136903
VERSION AX136903.1 GI:14273252
KEYWORDS synthetic construct
SOURCE synthetic construct

```

ORGANISM      synthetic construct
REFERENCE      artificial sequences.
AUTHORS        1
               Makino,Y., Abe,Y., Ogawa,M., Takagi,M., Takenaka,S. and
               Yamashita,K.
TITLE          Detection of partly complementary nucleic acid fragment
JOURNAL        Patent: EP 1065278-A 5 03-JAN-2001;
               FUJI PHOTO FILM CO., LTD. (JP)
FEATURES       Location/Qualifiers
source         1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="sample nucleic acid fragment"

Query Match      1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAATAAAAAAAAAAA 1

RESULT 333
AR241831/c      21 bp DNA linear PAT 20-DEC-2002
LOCUS           Sequence 119 from patent US 6472154.
DEFINITION      AR241831
ACCESSION       AR241831
VERSION         AR241831.1 GI:27287643
KEYWORDS        Location/Qualifiers
SOURCE          1..21
               /organism="unknown"
               /mol_type="genomic DNA"

ORGANISM        Unclasseified.
REFERENCE        1 (bases 1 to 21)
AUTHORS          Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE            Polymorphic repeats in human genes
JOURNAL          Patent: US 6472154-A 119 29-OCT-2002;
FEATURES         Location/Qualifiers
source          1..21
               /organism="unknown"
               /mol_type="genomic DNA"

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAATAAAAAAAAAAA 2

RESULT 334
AX825104/c      21 bp DNA linear PAT 11-DEC-2003
LOCUS           Sequence 2 from Patent WO03072818.
DEFINITION      AX825104
ACCESSION       AX825104
VERSION         AX825104.1 GI:39750833
KEYWORDS        synthetic construct
SOURCE          artificial sequences.
ORGANISM        Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
REFERENCE        1
AUTHORS          Method for sorting single-stranded nucleic acids
TITLE            Patent: WO 03072818-A 2 04-SEP-2003;
JOURNAL          Degussa Bioactives GmbH (DE)
FEATURES         Location/Qualifiers
source          1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen

ORGANISM        Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
REFERENCE        1
AUTHORS          Method for sorting single-stranded nucleic acids
TITLE            Patent: WO 03072818-A 3 04-SEP-2003;
JOURNAL          Degussa Bioactives GmbH (DE)
FEATURES         Location/Qualifiers
source          1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen

```

```

Sequenz:Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAAAA 1751
Db 20 TTAATAAAAAAAAAAAAAAAAAAA 1

RESULT 335
AX825105/c      21 bp DNA linear PAT 11-DEC-2003
LOCUS           Sequence 3 from Patent WO03072818.
DEFINITION      AX825105
ACCESSION       AX825105
VERSION         AX825105.1 GI:39750834
KEYWORDS        synthetic construct
SOURCE          synthetic construct
ORGANISM        artificial sequences.
REFERENCE        1
AUTHORS          Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE            Method for sorting single-stranded nucleic acids
JOURNAL          Patent: WO 03072818-A 3 04-SEP-2003;
               Degussa Bioactives GmbH (DE)
FEATURES         Location/Qualifiers
source          1..21
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
1 /bound_moiety="Biotin"
3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

```

```
Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1751
Db 20 TTA 1

RESULT 336
AX825106/c      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION      Sequence 4 from Patent WO03072818.
ACCESSION      AX825106
VERSION      AX825106.1 GI:39750835
KEYWORDS      .
SOURCE      synthetic construct
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 4 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
              source
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
              misc_binding
                1
                /bound_moiety="Biotin"
              modified_base
                3
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                6
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                9
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                12
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                15
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                18
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                19
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1754
Db 20 CTA 1

RESULT 338
AX825108/c      21 bp      DNA      linear      PAT 11-DEC-2003
LOCUS      AX825108
DEFINITION      Sequence 6 from Patent WO03072818.
ACCESSION      AX825108
VERSION      AX825108.1 GI:39750837
KEYWORDS      .
SOURCE      synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE      Method for sorting single-stranded nucleic acids
JOURNAL      Patent: WO 03072818-A 6 04-SEP-2003;
              Degussa Bioactives GmbH (DE)
FEATURES      Location/Qualifiers
              source
                1..21
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Beschreibung der kuenstlichen
                Sequenz:Capture-Oligonukleotid"
              misc_binding
                1
                /bound_moiety="Biotin"
              modified_base
                3
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                6
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                9
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                12
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                15
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                18
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER
              modified_base
                19
                /note="LNA-T (Locked Nucleic Acid)"
                /mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1751
Db 20 TTA 1

RESULT 337
AX825107/c      21 bp      DNA      linear      PAT 11-DEC-2003
LOCUS      AX825107
DEFINITION      Sequence 5 from Patent WO03072818.
ACCESSION      AX825107
VERSION      AX825107.1 GI:39750836
KEYWORDS      .
SOURCE      synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE      1
```

```

/mod_base=OTHER
12
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
15
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
18
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CTAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 339
AX825109/c
LOCUS AX825109 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 7 from Patent WO03072818.
ACCESSION AX825109
VERSION AX825109.1 GI:39750838
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 7 04-SEP-2003;
DEGussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1753
Db 20 ATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 341
AX825118/c
LOCUS AX825118 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 16 from Patent WO03072818.
ACCESSION AX825118
VERSION AX825118.1 GI:39750847
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 16 04-SEP-2003;
DEGussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1
/bound_moiety="Biotin"
modified_base 3
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 6
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 9
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 12
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 15
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER
modified_base 18
/notes="LNA-T (Locked Nucleic Acid) "
/mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CTAATAAAAAAAAAAAAAAAAAAAAA 1

RESULT 340

```



```
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AATAAAAAAAAAAAAAAAAAAAAA 2

RESULT 342
AX825139/c
LOCUS AX825139 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 37 from Patent WO03072818.
ACCESSION AX825139
VERSION AX825139.1 GI:39750868
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 37 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 344
AX825141/c
LOCUS AX825141 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 39 from Patent WO03072818.
ACCESSION AX825141
VERSION AX825141.1 GI:39750870
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T. H. and Hoppe, H. U.
```

```

TITLE      Method for sorting single-stranded nucleic acids
JOURNAL    Patent: WO 03072818-A 39 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES   source
            1. .21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz:Capture-Oligonukleotid"
            1
            /bound_moiety="Biotin"
            3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            9
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            12
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            18
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            21
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1735 CAAAAA1754
Db      20 CGAAAAA1

RESULT 345
AX825149/c
LOCUS      AX825149      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 47 from Patent WO03072818.
ACCESSION  AX825149
VERSION     AX825149.1 GI:39750878
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE       Method for sorting single-stranded nucleic acids
JOURNAL     Patent: WO 03072818-A 47 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES    Location/Qualifiers
            1. .21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz:Capture-Oligonukleotid"
            1
            /bound_moiety="Biotin"
            3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            9
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            12
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            18
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            21
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 21

```

```

            12
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            18
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            21
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1734 ACAAAAA1753
Db      20 AGAAAAA1

RESULT 346
AX825150/c
LOCUS      AX825150      21 bp      DNA      linear      PAT 11-DEC-2003
DEFINITION Sequence 48 from Patent WO03072818.
ACCESSION  AX825150
VERSION     AX825150.1 GI:39750879
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Boekenkamp,D., Dieck,T.H. and Hoppe,H.U.
TITLE       Method for sorting single-stranded nucleic acids
JOURNAL     Patent: WO 03072818-A 48 04-SEP-2003;
            Degussa Bioactives GmbH (DE)
FEATURES    Location/Qualifiers
            1. .21
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Beschreibung der kuenstlichen
            Sequenz:Capture-Oligonukleotid"
            1
            /bound_moiety="Biotin"
            3
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            6
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            9
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            12
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            15
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            18
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER
            21
            /note="LNA-T (Locked Nucleic Acid)"
            /mod_base=OTHER

misc_binding 1
modified_base 3
modified_base 6
modified_base 9
modified_base 12
modified_base 15
modified_base 18
modified_base 21

```

```

Query Match      1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1736 AAAAAA1755
Db      21 AAGAAAAA1

RESULT 347
AX478523/c

```

```
LOCUS AX478523 22 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 27 from Patent WO0244209.
ACCESSION AX478523
VERSION AX478523.1 GI:22217295
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Preenell,S.R., Xu,W., Novak,J.E., Whitmore,T.E. and Grant,F.J.
TITLE Cytokine receptor zcytor19
JOURNAL Patent: WO 0244209-A 27 06-JUN-2002;
ZymoGenetics, Inc. (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer ZC37681"
Query Match 1.0%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 2.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 863 GAAGAGGAGGAGGAGCGAG 882
Db 21 GAGGAGGAAGAGGAGGCGAG 2
RESULT 348
BD244863/c
LOCUS BD244863 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double
strand formation unstable.
ACCESSION BD244863
VERSION BD244863.1 GI:33054633
KEYWORDS JP 2002532063-A/8.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double
strand formation unstable
JOURNAL Patent: JP 2002532063-A 8 02-OCT-2002;
MCGILL UNIVERSITY
COMMENT OS Artificial Sequence
PN JP 2002532063-A/8
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
CC N = 3-Nitropyrrole
CC N = 3-Nitropyrrole
FH Key Location/Qualifiers
FT modified base (8)
FT modified base (18).
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 23 AAAAAA 2
RESULT 350
AX053001/c
LOCUS AX053001 23 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 17 from Patent WO0071749.
ACCESSION AX053001
VERSION AX053001.1 GI:12227103
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Burtgatter,P., Konz,D., Woelk,U. and
Pignot,M.
TITLE Detection system for analyzing molecular interactions, production
and utilization thereof
JOURNAL Patent: WO 0071749-A 17 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Komponente (b)-4"
Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 349
BD244865/c
LOCUS BD244865 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Oligonucleotide primer capable of making the non-specific double
strand formation unstable.
ACCESSION BD244865
VERSION BD244865.1 GI:33054635
KEYWORDS JP 2002532063-A/10.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double
strand formation unstable
JOURNAL Patent: JP 2002532063-A 10 02-OCT-2002;
MCGILL UNIVERSITY
COMMENT OS Artificial Sequence
PN JP 2002532063-A/10
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
CC N = inosine
CC N = inosine
FH Key Location/Qualifiers
FT modified base (8)
FT modified base (18).
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1755
Db 23 AAAAAA 2
RESULT 350
AX053001/c
LOCUS AX053001 23 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 17 from Patent WO0071749.
ACCESSION AX053001
VERSION AX053001.1 GI:12227103
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Burtgatter,P., Konz,D., Woelk,U. and
Pignot,M.
TITLE Detection system for analyzing molecular interactions, production
and utilization thereof
JOURNAL Patent: WO 0071749-A 17 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Komponente (b)-4"
Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1734 ACAAAAAAAAAAAAAAAAAA 1753
Db 20 ACAAGAAAAAAAAAAAAAAAAA 1

RESULT 351
AR102020/c
LOCUS AR102020 19 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 18 from patent US 6083731.
ACCESSION AR102020
VERSION AR102020.1 GI:12812818
KEYWORDS
SOURCE
ORGANISM
Unidentified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
TITLE Recombinant materials and methods for the production of limonene hydroxylases
JOURNAL Patent: US 6083731-A 18 04-JUL-2000;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 DAAAAAAAAAAAAAAAAA 1

RESULT 352
AR134802/c
LOCUS AR134802 19 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 18 from patent US 6194185.
ACCESSION AR134802
VERSION AR134802.1 GI:14123707
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Croteau,R.Bruce., Lupien,S.Lee. and Karp,F.
TITLE Recombinant materials and methods for production of limonene hydroxylases
JOURNAL Patent: US 6194185-A 18 27-FEB-2001;
FEATURES
source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 DAAAAAAAAAAAAAAAAA 1

RESULT 353
E28098/c
LOCUS E28098 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for analyzing DNA fragment.
ACCESSION E28098
VERSION E28098.1 GI:13018323
KEYWORDS JP 1999196874-A/9.
SOURCE unidentified
ORGANISM unidentified

unclassified.
1 (bases 1 to 20)
AUTHORS Hideki, K. and Senshu, U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 9 27-JUL-1999;
HITACHI LTD
COMMENT
OS Unidentified
PN JP 1999196874-A/9
PD 27-JUL-1999
PF 14-JAN-1998 JP 1998005399
PR
PI HIDEKI KAMIBARA, SENSU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
/organism="Unidentified".
FEATURES
source
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 18.2; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.2e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 BAAAAAAAAAAAAAAAAA 1

RESULT 354
AR034896/c
LOCUS AR034896 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5869643.
ACCESSION AR034896
VERSION AR034896.1 GI:5950501
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed
JOURNAL Patent: US 5869643-A 12 09-FEB-1999;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 355
AR034899
LOCUS AR034899 18 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 18 from patent US 5869643.
ACCESSION AR034899
VERSION AR034899.1 GI:5950504
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE 1 (bases 1 to 18)

AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a tightly packed bed
JOURNAL Patent: US 5869643-A 18 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 356
AR058305 18 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 3 from patent US 5837820.
DEFINITION AR058305
ACCESSION AR058305
VERSION AR058305.1 GI:5983882
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS De Rose,R.; Douce,R.; Duval,M.; Job,C. and Job,D.
TITLE Seed specific biotinylated protein, SBP65, from leguminous plants
JOURNAL Patent: US 5837820-A 3 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 357
AR097579/c 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 9 from patent US 6071745.
DEFINITION AR097579
ACCESSION AR097579
VERSION AR097579.1 GI:12806309
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Lin,C.-I.Patsev., Wallace,R.Bruce., Cossman,J. and French,C.
TITLE Method and formulation for lyophilizing cultured human cells to preserve RNA and DNA contained in cells for use in molecular biology experiments
JOURNAL Patent: US 6071745-A 9 06-JUN-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 358
AR106506 18 bp DNA linear PAT 14-FEB-2001
LOCUS Sequence 30 from patent US 6107060.
DEFINITION AR106506
ACCESSION AR106506
VERSION AR106506.1 GI:12821036
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Keeling,P. and Guan,H.
TITLE Starch encapsulation
JOURNAL Patent: US 6107060-A 30 22-AUG-2000;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 359
E28535 18 bp DNA linear PAT 18-JUN-2001
LOCUS Method for labeling oligonucleotide and utilization thereof.
DEFINITION E28535
ACCESSION E28535
VERSION JP 1999075880-A/2.
KEYWORDS JP 1999075880-A 2 23-MAR-1999;
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE Method for labeling oligonucleotide and utilization thereof
JOURNAL Patent: JP 1999075880-A 2 23-MAR-1999;
COMMENT CHERO THERAPEUT RES INST
OS Unidentified
PN JP 1999075880-A/2
PD 23-MAR-1999
PF 10-JUL-1998 JP 1998195719
PR
PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
C12N15/09,C12Q1/68,G01N33/58,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..18
/organism="Unidentified".
FEATURES Location/Qualifiers
source 1..18
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

```
RESULT 360
E28536/c
LOCUS      18 bp      DNA      linear      PAT 18-JUN-2001
DEFINITION Method for labeling oligonucleotide and utilization thereof.
ACCESSION  E28536
VERSION    E28536
KEYWORDS   JP 199075880-A/3.
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kenichi,H., Hiroshi,Y. and Masahide,N.
TITLE     Method for labeling oligonucleotide and utilization thereof
JOURNAL   Patent: JP 199075880-A 3 23-MAR-1999;
          CHEMO SERO THERAPEUT RES INST
COMMENT   OS Unidentified
          PN JP 199075880-A/3
          PD 23-MAR-1999
          PF 10-JUL-1998 JP 1998195719
          PR
          PI KENICHI HANAKI,HIROSHI YOSHIKURA,MASAHIDE NOZAKI PC
          CL2N15/09,C12Q1/68,G01N33/58,C12N15/00
          CC Strandedness: Single;
          CC Topology: Linear;
          FH Key Location/Qualifiers
          FT source 1..18
          /organism='Unidentified'.
FEATURES
source
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 361
I79509/c
LOCUS      18 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 16 from patent US 5707807.
ACCESSION  I79509
VERSION    I79509
KEYWORDS   I79509.1 GI:3207799
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kato,K.
TITLE     Molecular indexing for expressed gene analysis
JOURNAL   Patent: US 5707807-A 16 13-JAN-1998;
          Location/Qualifiers
FEATURES
source
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 362
AR208426/c
LOCUS      18 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION  AR208426
VERSION    AR208426.1 GI:21509577
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE     Binary encoded sequence tags
JOURNAL   Patent: US 6383754-A 6 07-MAY-2002;
          Location/Qualifiers
FEATURES
source
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAA 1751
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 363
AR215435/c
LOCUS      18 bp      DNA      linear      PAT 25-SEP-2002
DEFINITION Sequence 9 from patent US 6410321.
ACCESSION  AR215435
VERSION    AR215435.1 GI:23313691
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Lin,C.-I.P., Wallace,R.B., Cossman,J. and French,C.
TITLE     Method and formulation for lyophilizing cultured human cells to
          preserve RNA and DNA contained in cells for use in molecular
          biology experiments
JOURNAL   Patent: US 6410321-A 9 25-JUN-2002;
          Location/Qualifiers
FEATURES
source
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 364
AR222464
LOCUS      18 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION Sequence 24 from patent US 6429300.
ACCESSION  AR222464
VERSION    AR222464.1 GI:23329995
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kurz,M., Lohse,P. and Wagner,R.
TITLE     Peptide acceptor ligation methods
JOURNAL   Patent: US 6429300-A 24 06-AUG-2002;
          Location/Qualifiers
FEATURES
source
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 365
AR208426/c
LOCUS      18 bp      DNA      linear      PAT 20-JUN-2002
DEFINITION Sequence 6 from patent US 6383754.
ACCESSION  AR208426
VERSION    AR208426.1 GI:21509577
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Kaufman,J.C., Roth,M.E., Lizardi,P.M., Feng,L. and Latimer,D.R.
TITLE     Binary encoded sequence tags
JOURNAL   Patent: US 6383754-A 6 07-MAY-2002;
          Location/Qualifiers
FEATURES
source
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAAAAAA 1751
Db 18 AAAAAAAAAAAAAAAAAA 1
```

```
Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 365
AX004875/c
LOCUS AX004875 18 bp DNA PAT 18-DEC-2003
DEFINITION Sequence 14 from patent US 6639062.
ACCESSION AR412363
VERSION AR412363
KEYWORDS
SOURCE
ORGANISM
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.18
/organism="unknown"
/mol_type="genomic DNA"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 366
AX004875/c
LOCUS AX004875 18 bp DNA PAT 24-AUG-2000
DEFINITION Sequence 4 from Patent WO9910527.
ACCESSION AX004875
VERSION AX004875.1 GI:9928275
KEYWORDS
SOURCE
ORGANISM
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="3' palmityl oligonucleotide"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 367
AX004879/c
LOCUS AX004879 18 bp RNA PAT 06-SEP-2000
DEFINITION Sequence 8 from Patent WO9910527.
ACCESSION AX004879
VERSION AX004879.1 GI:9928279
KEYWORDS
SOURCE
ORGANISM
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.18
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="2' methyl-modified oligonucleotide"
/mod_base=um

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 368
AX008117
LOCUS AX008117 18 bp DNA PAT 06-SEP-2000
DEFINITION Sequence 2 from Patent WO9967378.
ACCESSION AX008117
VERSION AX008117.1 GI:9995742
KEYWORDS
SOURCE
ORGANISM
AUTHORS
TITLE
JOURNAL
FEATURES
source
1.18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Use as an oligomer"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 369
AX008118/c
LOCUS AX008118 18 bp RNA PAT 06-SEP-2000
DEFINITION Sequence 3 from Patent WO9967378.
ACCESSION AX008118
VERSION AX008118.1 GI:9995743
```

```
KEYWORDS
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.

REFERENCE
1
AUTHORS     Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
TITLE       Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
JOURNAL     Patent: WO 9967378-A 3 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Use as an oligomer"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 370
AX008122/c
LOCUS      AX008122 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 7 from Patent WO9967378.
ACCESSION AX008122
VERSION    AX008122.1 GI:9995747
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE
1
AUTHORS     Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
TITLE       Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
JOURNAL     Patent: WO 9967378-A 7 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Use as an oligomer"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 371
AX008123
LOCUS      AX008123 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 8 from Patent WO9967378.
ACCESSION AX008123
VERSION    AX008123.1 GI:9995748
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE
1
AUTHORS     Damha,M.J., Parniak,M.A., Wilds,C., Arion,D., Noronha,A.M. and
            Borkow,G.
TITLE       Antisense oligonucleotide constructs based on beta -arabinofuranose
            and its analogues
JOURNAL     Patent: WO 9967378-A 8 29-DEC-1999;
            DAMHA MASSAD JOSE (CA); PARNIAK MICHAEL A (CA); WILDS CHRISTOPHER
            (CA); UNIV MCGILL (CA); ARION DOMINIQUE (CA); NORONHA ANNE M (CA);
            BORKOW GADI (IL)
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Use as an oligomer"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 372
AX028845/c
LOCUS      AX028845 18 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 29 from Patent WO9732023.
ACCESSION AX028845
VERSION    AX028845.1 GI:10189948
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE
1
AUTHORS     Brugliera,F., Holton,T.A. and Michael,M.Z.
TITLE       Genetic sequences encoding flavonoid pathway enzymes and uses
            therefor
JOURNAL     Patent: WO 9732023-A 29 04-SEP-1997;
            FLORIGENE LIMITED (AU); BRUGLIERA FILIPPA (AU); HOLTON TIMOTHY
            ALBERT (AU); MICHAEL MICHAEL ZENON (AU)
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 373
AX047271
LOCUS      AX047271 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 21 from Patent WO0068422.
ACCESSION AX047271
VERSION    AX047271.1 GI:11876551
KEYWORDS   synthetic construct
SOURCE     synthetic construct
ORGANISM   artificial sequences.

REFERENCE
1
AUTHORS     Muehleger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
            Gumbiowski,K. and Zulauf,M.
TITLE       High density labeling of dna with modified or chromophore carrying
            artificial sequences.
```



```

nucleotides and dna polymerases used
Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
    source
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="second fragment of SEQ ID NO: 6"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 374
AX047273/c
LOCUS AX047273 18 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 23 from Patent WO0068422.
ACCESSION AX047273
VERSION AX047273.1 GI:11876553
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE
    1
AUTHORS
    Muehlegger,K., Angerer,B., Seela,F., Ankenbauer,W., Augustin,M.,
    Gumbiowski,K. and Zulauf,M.
TITLE
    High density labeling of dna with modified or chromophore carrying
    nucleotides and dna polymerases used
JOURNAL
    Patent: WO 0068422-A 23 16-NOV-2000;
    Roche Diagnostics GmbH (DE)
FEATURES
    source
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="second fragment of SEQ ID NO: 6"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 375
AX085252/c
LOCUS AX085252 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 6 from Patent WO0112855.
ACCESSION AX085252
VERSION AX085252.1 GI:13275310
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE
    1
AUTHORS
    Kaufman,J.C., Roth,M.E., Lizardi,p.M., Feng,L. and Latimer,D.R.
TITLE
    Binary encoded sequence tags
JOURNAL
    Patent: WO 0112855-A 6 22-FEB-2001;
    YALE UNIVERSITY (US)
FEATURES
    source
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Primer"

nucleotides and dna polymerases used
Patent: WO 0068422-A 21 16-NOV-2000;
Roche Diagnostics GmbH (DE)
FEATURES
    source
        1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="second fragment of SEQ ID NO: 6"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAA 1751
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 376
AX104721/c
LOCUS AX104721 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 913 from Patent WO0122972.
ACCESSION AX104721
VERSION AX104721.1 GI:13920918
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE
    1
AUTHORS
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE
    Immunostimulatory nucleic acids
JOURNAL
    Patent: WO 0122972-A 913 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
    GmbH (DE)
FEATURES
    Location/Qualifiers
        source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 377
AX104747/c
LOCUS AX104747 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE
    1
AUTHORS
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE
    Immunostimulatory nucleic acids
JOURNAL
    Patent: WO 0122972-A 939 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
    GmbH (DE)
FEATURES
    Location/Qualifiers
        source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 378
AX104747/c
LOCUS AX104747 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE
    1
AUTHORS
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE
    Immunostimulatory nucleic acids
JOURNAL
    Patent: WO 0122972-A 939 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
    GmbH (DE)
FEATURES
    Location/Qualifiers
        source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 379
AX104747/c
LOCUS AX104747 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 939 from Patent WO0122972.
ACCESSION AX104747
VERSION AX104747.1 GI:13920944
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        synthetic construct
        artificial sequences.
REFERENCE
    1
AUTHORS
    Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE
    Immunostimulatory nucleic acids
JOURNAL
    Patent: WO 0122972-A 939 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
    GmbH (DE)
FEATURES
    Location/Qualifiers
        source
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"

```

```
AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 379
AX108642/c
LOCUS AX108642 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 379
AX108642/c
LOCUS AX108642 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123419.
ACCESSION AX108642
VERSION AX108642.1 GI:13923875
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Differentially expressed genes
JOURNAL Patent: WO 0123419-A 10 05-APR-2001;
SCIOS INC. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 380
AX268883/c
LOCUS AX268883 18 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 84 from Patent WO0174901.
ACCESSION AX268883
VERSION AX268883.1 GI:16541910
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and White,R.T.

AX105651/c
LOCUS AX105651 18 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 10 from Patent WO0123564.
ACCESSION AX105651
VERSION AX105651.1 GI:13921674
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stanton,L.W. and Kapoun,A.M.
TITLE Secreted factors
JOURNAL Patent: WO 0123564-A 10 05-APR-2001;
Scios Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 381
AX355809/c
LOCUS AX355809 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 837 from Patent WO0197843.
ACCESSION AX355809
VERSION AX355809.1 GI:18620477
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner,G. and Hartmann,G.
TITLE Methods for enhancing antibody-induced cell lysis and treating cancer
JOURNAL Patent: WO 0197843-A 837 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide-phosphorothioate backbone"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 382
AX547774/c
LOCUS AX547774 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 913 from Patent WO02053141.
ACCESSION AX547774
VERSION AX547774.1 GI:25812918
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 913 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
```

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 383
AX8147800/c
LOCUS AX8147800 18 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 939 from Patent WO02053141.
ACCESSION AX8147800
VERSION AX8147800.1 GI:25812944
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 939 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 384
AX814716/c
LOCUS AX814716 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 1 from Patent WO03064441.
ACCESSION AX814716
VERSION AX814716.1 GI:39103916
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 1 07-AUG-2003;
McGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 385
AX814725/c
LOCUS AX814725 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION AX814725
VERSION AX814725.1 GI:39103924
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 8 07-AUG-2003;
McGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"

AX814723/c
LOCUS AX814723 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 8 from Patent WO03064441.
ACCESSION AX814723
VERSION AX814723.1 GI:39103922
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 8 07-AUG-2003;
McGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
1..17
/notes="Residues 1, 3, 5, 7, 9, 11, 13, 15 and 17 are 2'-O-methyl-D-uridine"

misc_feature
1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 386
AX814724/c
LOCUS AX814724 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 9 from Patent WO03064441.
ACCESSION AX814724
VERSION AX814724.1 GI:39103923
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Damha,M.J. and Parniak,M.A.
TITLE Oligonucleotides comprising alternating segments and uses thereof
JOURNAL Patent: WO 03064441-A 9 07-AUG-2003;
McGILL UNIVERSITY (CA)
FEATURES
source Location/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide"
1..15
/notes="Residues 1-3, 7-9, and 13-15 are 2'-O-methyl-D-uridine"

misc_feature
1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 387
AX814725/c
LOCUS AX814725 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 10 from Patent WO03064441.
ACCESSION AX814725
VERSION AX814725.1 GI:39103924

```

KEYWORDS
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Damha,M.J. and Parniak,M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 10 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide"
misc_feature 1..18
            /note="Residues 1-6 and 13-18 are 2'-O-methyl-D-uridine"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 388
AX814736
LOCUS       AX814736                18 bp    RNA        linear        PAT 05-DEC-2003
DEFINITION   Sequence 21 from Patent WO03064441.
ACCESSION   AX814736
VERSION     AX814736.1   GI:39103935
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    artificial sequences.
REFERENCE   1
AUTHORS     Damha,M.J. and Parniak,M.A.
TITLE       Oligonucleotides comprising alternating segments and uses thereof
JOURNAL     Patent: WO 03064441-A 21 07-AUG-2003;
            MCGILL UNIVERSITY (CA)
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Target RNA oligonucleotide"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 18 AAAAAAAAAAAAAAAAAA 18

RESULT 389
BD085545/c
LOCUS       BD085545                18 bp    RNA        linear        PAT 27-AUG-2002
DEFINITION   Method of comparison and detection of RNA amount and DNA amount.
ACCESSION   BD085545
VERSION     BD085545.1   GI:22631155
KEYWORDS    JP 2001333800-A/2.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Shimada,K.
TITLE       Method of comparison and detection of RNA amount and DNA amount
JOURNAL     Patent: JP 2001333800-A 2 04-DEC-2001;

UNITECH CO LTD
OS Homo sapiens (human)
PN JP 2001333800-A/2
PD 04-DEC-2001
PF 30-MAY-2000 JP 2000160324
PI KAO RI SHIMADA
PC C12Q1/68,C12N15/09,G01N33/50,C12N15/00
CC Method of comparison and detection of RNA amount and DNA CC
amount
FH Key Location/Qualifiers
FT source 1..18
            /organism='Homo sapiens (human)'.
FEATURES
source      Location/Qualifiers
            1..18
            /organism="Homo sapiens"
            /mol_type="genomic RNA"
            /db_xref="taxon:9606"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 390
BD222596/c
LOCUS       BD222596                18 bp    DNA        linear        PAT 17-JUL-2003
DEFINITION   Aminoxy-modified nucleoside compound and oligomer compound
            produced therefrom.
ACCESSION   BD222596
VERSION     BD222596.1   GI:33032366
KEYWORDS    JP 2002522447-A/14.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Manoharan,M., Cook,P.D., Prakash,T.P. and Kawasaki,A.M.
TITLE       Aminoxy-modified nucleoside compound and oligomer compound
            produced therefrom
JOURNAL     Patent: JP 2002522447-A 14 23-JUL-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS Artificial Sequence
            PN JP 2002522447-A/14
            PD 23-JUL-2002
            PF 09-AUG-1999 JP 2000563675
            PR 07-AUG-1998 US 09/130973
            PI MUTHIAH MANOHARAN,PHILIP DAN COOK,THAZHA P PRAKASH,ANDREW M
            KAWASAKI
            PC C07H19/167,C07H19/067,C07H19/10,C07H19/20,C07H21/02,C12N15/00,
            C12N15/00
            CC Description of Artificial Sequence: antisense sequence FH
            Key Location/Qualifiers
            FT source 1..18
            /organism='Artificial Sequence'.
FEATURES
source      Location/Qualifiers
            1..18
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 391

```

AR432617/c
LOCUS AR432617 19 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6653458.
ACCESSION AR432617
VERSION AR432617.1 GI:40195150
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Manoharan,M., Cook,P.D. and Guinasso,C.J.
TITLE Modified oligonucleotides
JOURNAL Patent: US 6653458-A 7 25-NOV-2003;
FEATURES
source
1..19
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred.No. 2.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1
RESULT 392
BD234126
LOCUS BD234126 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Protein skeleton of antibody mimetics and other binding proteins.
ACCESSION BD234126
VERSION BD234126.1 GI:33043896
KEYWORDS JP 2002532072-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Lipovsek,D.
TITLE Protein skeleton of antibody mimetics and other binding proteins
JOURNAL Patent: JP 2002532072-A 14 02-OCT-2002;
COMMENT PHYLLOS INC
OS Artificial Sequence
PN JP 2002532072-A/14
PD 02-OCT-2002
PF 09-DEC-1999 JP 2000587187
PR 10-DEC-1998 US 60/111737
PI DASA LIPOVSEK
PC C12N15/09,C07K1/04,C07K14/78,C07K16/46,C07K17/00,C07K19/00, PC C12P21/02,
PC C12N15/00
CC Puromycin linker oligonucleotide
FH Key Location/Qualifiers
FT source 1..20
FT Location/Qualifiers
/organism="Artificial Sequence".
FEATURES
source
1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 2.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 393
AX095299
LOCUS AX095299 21 bp DNA linear PAT 30-MAR-2001

DEFINITION Sequence 477 from Patent WO0118250.
ACCESSION AX095299
VERSION AX095299.1 GI:13511502
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 477 15-MAR-2001;
FEATURES
source
1..21
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 90.0%; Pred.No. 2.4e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 831 AGAGGAAGCTGCTGGGTCT 850
Db 2 AGAGGAAGCTGCTGGGTCT 21
RESULT 394
AX095303/c
LOCUS AX095303 21 bp DNA linear PAT 30-MAR-2001
DEFINITION Sequence 481 from Patent WO0118250.
ACCESSION AX095303
VERSION AX095303.1 GI:13511506
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Lander,E.S., Gargill,M., Ireland,J.S., Bolk,S., Daley,G.Q. and McCarthy,J.J.
TITLE Single nucleotide polymorphisms in genes
JOURNAL Patent: WO 0118250-A 481 15-MAR-2001;
FEATURES
source
1..21
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 90.0%; Pred.No. 2.4e+02;
Matches 18; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 182 CCCGAGCAGCCGAGCCCC 201
Db 21 CCCGAGCAGCCGAGCCCC 2
RESULT 395
AX825111/c
LOCUS AX825111 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 9 from Patent WO03072818.
ACCESSION AX825111
VERSION AX825111.1 GI:39750840
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 9 04-SEP-2003;
 Degussa Bioactives GmbH (DE)

FEATURES
 source 1..21
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc_binding 1
 /bound_moiety="Biotin"
 modified_base 3
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 6
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 9
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 12
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 15
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 18
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 396
 AX825112/c
 LOCUS AX825112 21 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 10 from Patent WO03072818.
 ACCESSION AX825112
 VERSION AX825112.1 GI:39750841
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 10 04-SEP-2003;
 Degussa Bioactives GmbH (DE)

FEATURES
 source 1..21
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc_binding 1
 /bound_moiety="Biotin"
 modified_base 3
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 6
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 9
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER

/note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 12
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 15
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 18
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 397
 AX825113/c
 LOCUS AX825113 21 bp DNA linear PAT 11-DEC-2003
 DEFINITION Sequence 11 from Patent WO03072818.
 ACCESSION AX825113
 VERSION AX825113.1 GI:39750842
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.

REFERENCE 1
 AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
 TITLE Method for sorting single-stranded nucleic acids
 JOURNAL Patent: WO 03072818-A 11 04-SEP-2003;
 Degussa Bioactives GmbH (DE)
 FEATURES
 source 1..21
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Beschreibung der kuenstlichen Sequenz: Capture-Oligonukleotid"

misc_binding 1
 /bound_moiety="Biotin"
 modified_base 3
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 6
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 9
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 12
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 15
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER
 modified_base 18
 /note="LNA-T (Locked Nucleic Acid)"
 /mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
 |||||
 Db 18 AAAAAAAAAAAAAAAAAA 1

```

RESULT 398
AX825114/c
LOCUS AX825114 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 12 from Patent WO03072818.
ACCESSION AX825114
VERSION AX825114.1 GI:39750843
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 12 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 400
AX825136/c
LOCUS AX825136 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 34 from Patent WO03072818.
ACCESSION AX825136
VERSION AX825136.1 GI:39750865
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 34 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 399
AX825135/c
LOCUS AX825135 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 33 from Patent WO03072818.
ACCESSION AX825135
VERSION AX825135.1 GI:39750864
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 33 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz:Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
/modified_base=OTHER
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
|||||
Db 18 AAAAAAAAAAAAAAAAAA 1

```



```

/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 404
AX825144/c
LOCUS AX825144 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 42 from Patent WO03072818.
ACCESSION AX825144
VERSION AX825144.1 GI:39750873
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 42 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 405
AX825146/c
LOCUS AX825146 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 44 from Patent WO03072818.
ACCESSION AX825146
VERSION AX825146.1 GI:39750875
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 44 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

```

```

AX825145/c
LOCUS AX825145 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 43 from Patent WO03072818.
ACCESSION AX825145
VERSION AX825145.1 GI:39750874
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 43 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
6 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
9 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
12 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
15 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER
18 /note="LNA-T (Locked Nucleic Acid)"
/mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 406
AX825146/c
LOCUS AX825146 21 bp DNA linear PAT 11-DEC-2003
DEFINITION Sequence 44 from Patent WO03072818.
ACCESSION AX825146
VERSION AX825146.1 GI:39750875
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Boekenkamp, D., Dieck, T.H. and Hoppe, H.U.
TITLE Method for sorting single-stranded nucleic acids
JOURNAL Patent: WO 03072818-A 44 04-SEP-2003;
Degussa Bioactives GmbH (DE)
FEATURES
source
1. .21
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Beschreibung der kuenstlichen
Sequenz: Capture-Oligonukleotid"

```

```
misc_binding 1 /bound_moiety="Biotin"
modified_base 3 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 6 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 9 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 12 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 15 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER
modified_base 18 /note="LNA-T (Locked Nucleic Acid)"
               /mod_base=OTHER

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 407
AR164318/c
LOCUS AR164318 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 1 from patent US 6271369.
ACCESSION AR164318
VERSION AR164318.1 GI:16235432
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R.H., Maitra,R.K. and Lesiak,K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 1 07-AUG-2001;
FEATURES
source
    1..22
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 408
AR164319/c
LOCUS AR164319 22 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 2 from patent US 6271369.
ACCESSION AR164319
VERSION AR164319.1 GI:16235434
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R.H., Maitra,R.K. and Lesiak,K.
TITLE Chimeric molecules targeted to viral RNAs
JOURNAL Patent: US 6271369-A 2 07-AUG-2001;
FEATURES
source
    1..22
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 409
I31810/c
LOCUS I31810 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5583032.
ACCESSION I31810
VERSION I31810.1 GI:1822601
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 1 10-DEC-1996;
FEATURES
source
    1..22
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 410
I31811/c
LOCUS I31811 22 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 2 from patent US 5583032.
ACCESSION I31811
VERSION I31811.1 GI:1822602
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA
JOURNAL Patent: US 5583032-A 2 10-DEC-1996;
FEATURES
source
    1..22
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAA 5

RESULT 411
I69407/c
LOCUS I69407 22 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 1 from patent US 5677289.
```

```
ACCESSION I69407
VERSION I69407.1 GI:2831529
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA and medical treatments
thereby
JOURNAL Patent: US 5677289-A 1 14-OCT-1997;
FEATURES
source
Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAAAAAA 5
RESULT 412
LOCUS I69408 22 bp DNA linear PAT 04-FEB-1998
DEFINITION Sequence 2 from patent US 5677289.
ACCESSION I69408
VERSION I69408.1 GI:2831530
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Torrence,P., Silverman,R., Maitra,R. and Lesiak,K.
TITLE Method of cleaving specific strands of RNA and medical treatments
thereby
JOURNAL Patent: US 5677289-A 2 14-OCT-1997;
FEATURES
source
Location/Qualifiers
1..22
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1753
Db 22 AAAAAAAAAAAAAAAAAAAAAA 5
RESULT 413
LOCUS BD245238 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245238
VERSION BD245238.1 GI:33055008
KEYWORDS JP 2002532386-A/24.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 24 02-OCT-2002;
COMMENT FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/24
PD 02-OCT-2002
PF 19-NOV-1999 JP 2000583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
Location/Qualifiers
1..23
FT source
/organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1751
Db 6 AAAAAAAAAAAAAAAAAAAAAA 23
RESULT 414
LOCUS AX052993 23 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 9 from Patent WO0071749.
ACCESSION AX052993
VERSION AX052993.1 GI:12227095
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Bургstaller,P., Konz,D., Woelk,U. and
Pignot,M.
TITLE Detection system for analyzing molecular interactions, production
and utilization thereof
JOURNAL Patent: WO 0071749-A 9 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
source
Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/ncbi="komponente (b) -2"
Query Match 1.0%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1750
Db 18 TACAAAAAAAAAAAAAAAAAAAAA 1
RESULT 415
LOCUS AX053002 23 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 18 from Patent WO0071749.
ACCESSION AX053002
VERSION AX053002.1 GI:12227104
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U., Bургstaller,P., Konz,D., Woelk,U. and
Pignot,M.
TITLE Detection system for analyzing molecular interactions, production
```

```
and utilization thereof
Patent: WO 0071749-A 18 30-NOV-2000;
Aventis Research & Technology GmbH & Co. KG. (DE)
FEATURES
source
1. .23
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Komponente (b)-5"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 TACAAACAAAAA 1750
Db 18 TACAAACAAAAA 1

RESULT 416
AX394607
LOCUS AX394607 23 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 5 from Patent EP1186673.
ACCESSION AX394607
VERSION AX394607.1 GI:21065720
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 5 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
source
1. .23
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAACAAAAA 1753
Db 1 AAAAAACAAAAA 18

RESULT 417
AR168453/c
LOCUS AR168453 24 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 82 from patent US 6287854.
ACCESSION AR168453
VERSION AR168453.1 GI:17904379
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 24)
AUTHORS Spurr,N.K., Gray,I.C. and Stewart,L.M.
TITLE Diagnosis of susceptibility to cancer and treatment thereof
JOURNAL Patent: US 6287854-A 82 11-SEP-2001;
Agilent Technologies Inc (US)
FEATURES
source
1. .24
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAACAAAAA 1753
Db 19 CAAAAACAAAAA 1

RESULT 420
I28309/c
LOCUS I28309 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5569832.
ACCESSION I28309
VERSION I28309.1 GI:1819085
KEYWORDS
```

```
QY 1736 AAAAAACAAAAA 1753
Db 24 AAAAAACAAAAA 7

RESULT 418
AX394609
LOCUS AX394609 24 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 7 from Patent EP1186673.
ACCESSION AX394609
VERSION AX394609.1 GI:21065722
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Wobler,P.K. and Delenstarr,G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 7 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
source
1. .24
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"

Query Match
Best Local Similarity 100.0%; Score 18; DB 1; Length 24;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAACAAAAA 1753
Db 1 AAAAAACAAAAA 18

RESULT 419
AR030917/c
LOCUS AR030917 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5861487.
ACCESSION AR030917
VERSION AR030917.1 GI:5944131
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily., Kovacic,F., Tanaka,Y. and
Lester,D.Ruth.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: US 5861487-A 20 19-JAN-1999;
Agilent Technologies Inc (US)
FEATURES
source
1. .20
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 94.7%; Score 17.4; DB 1; Length 20;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAACAAAAA 1753
Db 19 CAAAAACAAAAA 1

RESULT 420
I28309/c
LOCUS I28309 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 20 from patent US 5569832.
ACCESSION I28309
VERSION I28309.1 GI:1819085
KEYWORDS
```

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL therefor: US 5569832-A 20 29-OCT-1996;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CTAATAAAAAAAAAAAAAAAAA 1

RESULT 421
LOCUS I47310/c 20 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 11 from patent US 5639870.
ACCESSION I47310
VERSION I47310.1 GI:2471275
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Holton,T.Albert., Cornish,E.Cecily, and Tanaka,Y.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
JOURNAL therefor: US 5639870-A 11 17-JUN-1997;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CTAATAAAAAAAAAAAAAAAAA 1

RESULT 422
LOCUS AR371268 20 bp DNA linear PAT 12-SEP-2003
DEFINITION Sequence 4 from patent US 6395474.
ACCESSION AR371268
VERSION AR371268.1 GI:34608200
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6395474-A 4 28-MAY-2002;
FEATURES
source Location/Qualifiers
1..20
/organism="unknown"
/mol_type="genomic DNA"
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 1 AAAAAAGAAAAAAAAAAAAA 19

RESULT 423
LOCUS BD245234 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245234
VERSION BD245234.1 GI:33055004
KEYWORDS JP 2002532386-A/20.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 20 02-OCT-2002;
COMMENT FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/20
PD 02-OCT-2002
PF 19-NOV-1999 JP 200583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC
G01N27/30,
PC
G01N27/416,G01N27/48,G01N33/483,G01N33/50,G01N33/566,C12N15/00, PC
G01N27/46
CC Method of electrochemically detecting nucleic acid FH Key
FT Location/Qualifiers
1..23
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 17.4; DB 1; Length 23;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 5 CAGAAAAAAAAAAAAAAAAA 23

RESULT 424
LOCUS BD245242 23 bp DNA linear PAT 17-JUL-2003
DEFINITION Method of electrochemically detecting nucleic acid.
ACCESSION BD245242
VERSION BD245242.1 GI:33055012
KEYWORDS JP 2002532386-A/28.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 23)
AUTHORS Hartwich,G. and Heller,A.
TITLE Method of electrochemically detecting nucleic acid
JOURNAL Patent: JP 2002532386-A 28 02-OCT-2002;
COMMENT FRIZ BIOCHEM GMBH
OS Artificial Sequence
PN JP 2002532386-A/28
PD 02-OCT-2002
PF 19-NOV-1999 JP 200583928
PR 23-NOV-1998 DE 198 53 957.6,29-APR-1999 DE 199 21 940.0 PI
GERHARD HARTWICH,ADAM HELLER
PC C07H21/00,C07H21/02,C07H21/04,C12N15/09,C12Q1/68,G01N27/12, PC

[illegible][illegible]

```
Imbach,J.Louis.
TITLE      Oligonucleotides having a conserved G4 core sequence
JOURNAL    Patent: US 5952490-A 110 14-SEP-1999;
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 435
AX032598
LOCUS      AX032598
DEFINITION Sequence 44 from Patent EP1016715.
ACCESSION AX032598
VERSION    AX032598.1 GI:10279536
KEYWORDS   .
SOURCE     unidentified
           unclassified
REFERENCE  1
AUTHORS    Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
TITLE      Oligonucleotides having a conserved g4 core sequence
JOURNAL    Patent: EP 1016715-A 44 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 1.0%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 436
AX032664
LOCUS      AX032664
DEFINITION Sequence 110 from Patent EP1016715.
ACCESSION AX032664
VERSION    AX032664.1 GI:10279602
KEYWORDS   .
SOURCE     unidentified
           unclassified
REFERENCE  1
AUTHORS    Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
TITLE      Oligonucleotides having a conserved g4 core sequence
JOURNAL    Patent: EP 1016715-A 110 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 1.0%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 437
AX032671
LOCUS      AX032671
```

```
Imbach,J.Louis.
TITLE      Oligonucleotides having a conserved G4 core sequence
JOURNAL    Patent: US 5952490-A 110 14-SEP-1999;
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 433
AR074309
LOCUS      AR074309
DEFINITION Sequence 117 from patent US 5952490.
ACCESSION AR074309
VERSION    AR074309.1 GI:10001064
KEYWORDS   .
SOURCE     Unknown.
           Unclassified.
REFERENCE  1 (bases 1 to 22)
AUTHORS    Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
            Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
            Imbach,J.Louis.
TITLE      Oligonucleotides having a conserved G4 core sequence
JOURNAL    Patent: US 5952490-A 117 14-SEP-1999;
            Location/Qualifiers
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 1.0%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22

RESULT 434
AX032590
LOCUS      AX032590
DEFINITION Sequence 36 from Patent EP1016715.
ACCESSION AX032590
VERSION    AX032590.1 GI:10279528
KEYWORDS   .
SOURCE     unidentified
           unclassified
REFERENCE  1
AUTHORS    Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
TITLE      Oligonucleotides having a conserved g4 core sequence
JOURNAL    Patent: EP 1016715-A 36 05-JUL-2000;
            ISIS PHARMACEUTICALS INC (US)
FEATURES   Location/Qualifiers
            source
            1..22
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match
Best Local Similarity 1.0%; Score 17.2; DB 1; Length 22;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGATGGGCTGGG 1036
Db 1 GGGGTTGGGTTGGGTTGGG 22
```


DEFINITION Sequence 117 from Patent EP1016715.
ACCESSION AX032671
VERSION AX032671.1 GI:10279609
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 117 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
1. .22
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1015 GTGGTTGGGGATGGGGCTGGGG 1036
Db 1 GGGGTTGGGGTTGGGGTTGGGG 22
RESULT 438
LOCUS AX103869
DEFINITION Sequence 61 from Patent WO0122972.
ACCESSION AX103869
VERSION AX103869.1 GI:13920066
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 61 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 22 AAAAAACAAAAAACAAAAAAA 1
RESULT 439
LOCUS AX457060
DEFINITION Sequence 21 from Patent WO0231186.
ACCESSION AX457060
VERSION AX457060.1 GI:21715842
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Berlin,K.
TITLE Method for the detection of cytosine methylations

JOURNAL Patent: WO 0231186-A 21 18-APR-2002;
Epigenomics AG (DE)
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 22 ATAATAAAAAATAAAAAAAA 1
RESULT 440
LOCUS AX546922/c
DEFINITION Sequence 61 from Patent WO02053141.
ACCESSION AX546922
VERSION AX546922.1 GI:25812066
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 61 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"
Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.3e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 22 AAAAAACAAAAAACAAAAAAA 1
RESULT 441
LOCUS A28997/c
DEFINITION Primer sequence 4 from patent EP0522880.
ACCESSION A28997
VERSION A28997.1 GI:1248848
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Holton,T.A., Cornish,E.C., Kovacic,F., Tanaka,Y. and Lester,D.R.
TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
therefor
JOURNAL Patent: EP 0522880-A 16 13-JAN-1993;
INTERNATIONAL FLOWER DEVELOPMENTS Pty. Ltd
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 442
LOCUS AR104585 17 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 132 from patent US 6093809.
ACCESSION AR104585
VERSION AR104585.1 GI:12817293
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 132 25-JUL-2000;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 443
LOCUS AR141074 17 bp DNA PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6207819.
ACCESSION AR141074
VERSION AR141074.1 GI:14483570
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6207819-A 5 27-MAR-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 444
LOCUS AR175846 17 bp DNA PAT 17-DEC-2001
DEFINITION Sequence 132 from patent US 6309867.
ACCESSION AR175846
VERSION AR175846.1 GI:17917145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 17)
AUTHORS Cech,T.R. and Nakamura,T.
TITLE Telomerase
JOURNAL Patent: US 6309867-A 132 30-OCT-2001;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 445
LOCUS AR222463 17 bp DNA PAT 26-SEP-2002
DEFINITION Sequence 23 from patent US 6429300.
ACCESSION AR222463
VERSION AR222463.1 GI:23329994
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 23 06-AUG-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 446
LOCUS AR236087 17 bp DNA PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6462184.
ACCESSION AR236087
VERSION AR236087.1 GI:27279786
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Manoharan,M. and Maier,M.A.
TITLE Compounds, processes and intermediates for synthesis of mixed backbone oligomeric compounds
JOURNAL Patent: US 6462184-A 5 08-OCT-2002;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 447
AX692526/c
LOCUS AX692526 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5258 from Patent EP1281758.
ACCESSION AX692526
VERSION AX692526.1 GI:29415484
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5258 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751
Db 17 CAAAAAAAAAAAAAAAAA 1

RESULT 448
AX728616
LOCUS AX728616 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 250 from Patent WO03025175.
ACCESSION AX728616
VERSION AX728616.1 GI:30507959
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 250 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751
Db 17 CAAAAAAAAAAAAAAAAA 1

RESULT 449
AX758974
LOCUS AX758974 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 2295 from Patent WO03040369.
ACCESSION AX758974

AX758974.1 GI:32253590
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 2295 15-MAY-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1644 GATCACTCTCCTGACA 1660
Db 1 GATCACTCTCCTGACA 17

RESULT 450
A14689
LOCUS A14689 18 bp DNA linear PAT 28-MAR-1994
DEFINITION Nucleotide sequence 9 from patent number WO8303623.
ACCESSION A14689
VERSION A14689.1 GI:513760
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS
TITLE CODING DNA FRAGMENTS FOR POLYPEPTIDES CONTAINING AT LEAST ONE ANTIGENIC DETERMINANT OF THE PAPILLOMAVIRUS PARTICULARLY OF THE 1a HPV TYPE AND CORRESPONDING POLYPEPTIDES
JOURNAL Patent: WO 8303623-A 9 27-OCT-1983;
FEATURES
source
1. .18
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751
Db 2 CAAAAAAAAAAAAAAAAA 18

RESULT 451
E32454/c
LOCUS E32454 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32454
VERSION E32454.1 GI:13018690
KEYWORDS JP 2000037190-A/14.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 14 08-FEB-2000;

JAPAN TOBACCO INC
 OS Artificial Sequence
 PN JP 2000037190-A/14
 PD 08-FEB-2000
 PF 23-JUL-1998 JP 1998225228
 PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N5/10, PC
 C12N15/02,
 PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
 PC C12N15/00,
 PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
 CC
 FH Key primer bind Location/Qualifiers
 FT (1)..(18).
 Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAA 1750
 Db 18 ACAAAAAAAAAAAAAA 2
 RESULT 452
 AR208425/c
 LOCUS
 DEFINITION Sequence 5 from patent US 6383754.
 ACCESSION AR208425
 VERSION AR208425.1 GI:21509576
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
 TITLE Binary encoded sequence tags
 JOURNAL Patent: US 6383754-A 5 07-MAY-2002;
 FEATURES
 Location/Qualifiers
 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAAAAAA 1751
 Db 17 CAAAAAAAAAAAAAAAAA 1
 RESULT 453
 AR208843/c
 LOCUS
 DEFINITION Sequence 27 from Patent WO9732023.
 ACCESSION AR208843
 VERSION AR208843.1 GI:10189946
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Brugliera, F., Holton, T.A. and Michael, M.Z.
 TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
 JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
 JAPAN TOBACCO INC
 OS Artificial Sequence
 PN JP 2000037190-A/14
 PD 08-FEB-2000
 PF 23-JUL-1998 JP 1998225228
 PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N5/10, PC
 C12N15/02,
 PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
 PC C12N15/00,
 PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
 CC
 FH Key primer bind Location/Qualifiers
 FT (1)..(18).
 Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAA 1750
 Db 18 ACAAAAAAAAAAAAAA 2
 RESULT 452
 AR208425/c
 LOCUS
 DEFINITION Sequence 5 from patent US 6383754.
 ACCESSION AR208425
 VERSION AR208425.1 GI:21509576
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
 TITLE Binary encoded sequence tags
 JOURNAL Patent: US 6383754-A 5 07-MAY-2002;
 FEATURES
 Location/Qualifiers
 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAAAAAA 1751
 Db 17 CAAAAAAAAAAAAAAAAA 1
 RESULT 453
 AR208843/c
 LOCUS
 DEFINITION Sequence 27 from Patent WO9732023.
 ACCESSION AR208843
 VERSION AR208843.1 GI:10189946
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Brugliera, F., Holton, T.A. and Michael, M.Z.
 TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
 JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
 JAPAN TOBACCO INC
 OS Artificial Sequence
 PN JP 2000037190-A/14
 PD 08-FEB-2000
 PF 23-JUL-1998 JP 1998225228
 PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N5/10, PC
 C12N15/02,
 PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
 PC C12N15/00,
 PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
 CC
 FH Key primer bind Location/Qualifiers
 FT (1)..(18).
 Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAA 1750
 Db 18 ACAAAAAAAAAAAAAA 2
 RESULT 452
 AR208425/c
 LOCUS
 DEFINITION Sequence 5 from patent US 6383754.
 ACCESSION AR208425
 VERSION AR208425.1 GI:21509576
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
 TITLE Binary encoded sequence tags
 JOURNAL Patent: US 6383754-A 5 07-MAY-2002;
 FEATURES
 Location/Qualifiers
 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAAAAAA 1751
 Db 17 CAAAAAAAAAAAAAAAAA 1
 RESULT 453
 AR208843/c
 LOCUS
 DEFINITION Sequence 27 from Patent WO9732023.
 ACCESSION AR208843
 VERSION AR208843.1 GI:10189946
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Brugliera, F., Holton, T.A. and Michael, M.Z.
 TITLE Genetic sequences encoding flavonoid pathway enzymes and uses
 JOURNAL Patent: WO 9732023-A 27 04-SEP-1997;
 JAPAN TOBACCO INC
 OS Artificial Sequence
 PN JP 2000037190-A/14
 PD 08-FEB-2000
 PF 23-JUL-1998 JP 1998225228
 PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N5/10, PC
 C12N15/02,
 PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
 PC C12N15/00,
 PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
 CC
 FH Key primer bind Location/Qualifiers
 FT (1)..(18).
 Location/Qualifiers
 1..18
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAA 1750
 Db 18 ACAAAAAAAAAAAAAA 2
 RESULT 452
 AR208425/c
 LOCUS
 DEFINITION Sequence 5 from patent US 6383754.
 ACCESSION AR208425
 VERSION AR208425.1 GI:21509576
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
 TITLE Binary encoded sequence tags
 JOURNAL Patent: US 6383754-A 5 07-MAY-2002;
 FEATURES
 Location/Qualifiers
 1..18
 /organism="unknown"
 /mol_type="unassigned DNA"
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.8e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAAAAAA 1751
 Db 17 CAAAAAAAAAAAAAAAAA 1
 RESULT 453
 AR208843/c

```
Query Match          1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751
    |||||
Db 17 CAAAAAAAAAAAAAAAAA 1

RESULT 456
BD190553
LOCUS BD190553 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Secretory proteins and polynucleotides encoding the same.
ACCESSION BD190553
VERSION BD190553.1 GI:33000292
KEYWORDS JP 2002515753-A/12.
SOURCE Rattus
ORGANISM Rattus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
1 (bases 1 to 18)
TITLE Jacobs, K., McCoy, J.M., Lavallie, E.R., Racie, L.A., Merberg, D.,
JOURNAL Tracy, M., Spaulding, V. and Agostino, M.J.
SECRETORY proteins and polynucleotides encoding the same
PATENT: JP 2002515753-A 12 28-MAY-2002;
GENETICS INSTITUTE INC
COMMENT PN JP 2002515753-A/12
PD 28-MAY-2002
PF 31-OCT-1997 JP 1998521609
PR 01-NOV-1996 US 08/724973
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
    source
        1..18
            /organism="Rattus"
            /mol_type="genomic DNA"
            /db_xref="taxon:10114"

Query Match          1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
    |||||
Db 2 AAAAAAAAAAAAAAAAAA 18

RESULT 457
A79657/c
LOCUS A79657 19 bp DNA linear PAT 20-OCT-1999
DEFINITION Sequence 6 from Patent WO9720069.
ACCESSION A79657
VERSION A79657.1 GI:6092611
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 19)
AUTHORS Enrich, T. and Leving, H.
TITLE METHOD OF DETECTING TELOMERASE ACTIVITY
JOURNAL Patent: WO 9720069-A 6 05-JUN-1997;
BOHRINGER MANNHEIM GMBH (DE); ENRICH THOMAS (DE)
FEATURES
    source
        1..19
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match          1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
    |||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 458
AR147331/c
LOCUS AR147331 19 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6221584.
ACCESSION AR147331
VERSION AR147331.1 GI:15111134
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 19)
TITLE Enrich, T., Leving, H., Hinzpeter, M. and Karl, G.
JOURNAL Method of detecting telomerase activity
PATENT: US 6221584-A 6 24-APR-2001;
FEATURES
    source
        1..19
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match          1.0%; Score 17; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
    |||||
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 459
BD161924/c
LOCUS BD161924 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for carrying out thermal cycle of PCR using DNA-immobilized
ACCESSION BD161924
VERSION BD161924.1 GI:27867682
KEYWORDS JP 2002191369-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Tanga, M., Okamura, H. and Takahashi, K.
TITLE Method for carrying out thermal cycle of PCR using DNA-immobilized
JOURNAL substrate
COMMENT Patent: JP 2002191369-A 1 09-JUL-2002;
TOYO KOHAN CO LTD, KOJIRO TAKAHASHI
OS Artificial Sequence
PN JP 2002191369-A/1
PD 09-JUL-2002
PF 27-DEC-2000 JP 2000399573
PI MICHIFUMI TANGA, HIROSHI OKAMURA, KOJIRO TAKAHASHI PC
C12N15/09, C12N15/09, C12Q1/68, C12N15/00, C12N15/00 CC Method for
carrying out thermal cycle of PCR using DNA- CC
immobilized
CC substrate
FH Key Location/Qualifiers
FT source
    1..20
        /organism="Artificial Sequence".
FEATURES
    source
        1..20
            /organism="synthetic construct"
            /mol_type="genomic DNA"
            /db_xref="taxon:32630"

Query Match          1.0%; Score 17; DB 1; Length 20;
```

```
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1752
Db 20 AAAAAAAAAAAAAA 4

RESULT 460
LOCUS AR074229 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 37 from patent US 5952490.
ACCESSION AR074229
VERSION AR074229.1 GI:10000984
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 37 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 463
LOCUS AR074310 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 118 from patent US 5952490.
ACCESSION AR074310
VERSION AR074310.1 GI:10001065
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 118 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 464
LOCUS AR126639/c 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 68 from patent US 6180353.
ACCESSION AR126639
VERSION AR126639.1 GI:14113232
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Cowsert,L.M.
TITLE Antisense modulation of daxx expression
JOURNAL Patent: US 6180353-A 68 30-JAN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"
```

```
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1752
Db 20 AAAAAAAAAAAAAA 4

RESULT 460
LOCUS AR074229 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 37 from patent US 5952490.
ACCESSION AR074229
VERSION AR074229.1 GI:10000984
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 37 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 463
LOCUS AR074310 20 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 118 from patent US 5952490.
ACCESSION AR074310
VERSION AR074310.1 GI:10001065
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 118 14-SEP-1999;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 464
LOCUS AR126639/c 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 68 from patent US 6180353.
ACCESSION AR126639
VERSION AR126639.1 GI:14113232
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 20)
AUTHORS Dean,N.M. and Cowsert,L.M.
TITLE Antisense modulation of daxx expression
JOURNAL Patent: US 6180353-A 68 30-JAN-2001;
FEATURES
source
Location/Qualifiers
1..20
/mol_type="unassigned DNA"
```

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 859 GCAGGAGGAGGAGGAGG 878
Db 20 GGAGGAGGAGGAGGAGG 1

RESULT 465
LOCUS ARI42677 20 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6203988.
ACCESSION ARI42677
VERSION ARI42677.1 GI:15103963
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kambara,H. and Uematsu,C.
TITLE DNA fragment preparation method for gene expression profiling
JOURNAL Patent: US 6203988-A 7 20-MAR-2001;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1750
Db 1 TCTCCAAAAA 20

RESULT 466
LOCUS E28096 20 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for analyzing DNA fragment.
ACCESSION E28096
VERSION E28096.1 GI:13018321
KEYWORDS JP 1999196874-A/7.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hideki,K. and Senshu,U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 7 27-JUL-1999;
COMMENT HITACHI LTD
OS Unidentified
PN JP 1999196874-A/7
PD 27-JUL-1999
PR 14-JAN-1998 JP 1998005399
PI HIDEKI KAMIBARA, SENSU UEMATSU
PC C12N15/09,C12Q1/68,G01N27/447,C12N15/00,G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..20
/organism="Unidentified".
FT Location/Qualifiers
1..20
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;

Qy 1731 TTTACAAAAA 1750
Db 1 TCTCCAAAAA 20

RESULT 467
LOCUS I20476 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 55 from patent US 5514577.
ACCESSION I20476
VERSION I20476.1 GI:1600831
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Draper,K.G., Crooke,S.T., Mirabelli,C.K., Ecker,D.J., Hanecak,R.C.,
Anderson,K.P., Brown-Driver,V.L. and Wyatt,J.R.
TITLE Oligonucleotide therapies for modulating the effects of herpes
viruses
JOURNAL Patent: US 5514577-A 55 07-MAY-1996;
FEATURES Location/Qualifiers
source
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGGGTT 1038
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 468
LOCUS AX032591 20 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 37 from Patent EP1016715.
ACCESSION AX032591
VERSION AX032591.1 GI:10279529
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 37 05-JUL-2000;
FEATURES Location/Qualifiers
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGGGTT 1038
Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 469
LOCUS AX032599 20 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 45 from Patent EP1016715.

```
ACCESSION AX032599
VERSION AX032599.1 GI:10279537
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 45 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
|||||
Db 1 TTGGGGTTGGGTTGGGGTT 20

RESULT 470
ACCESSION AX032668
LOCUS AX032668 20 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 114 from Patent EP1016715.
ACCESSION AX032668
VERSION AX032668.1 GI:10279506
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 114 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
|||||
Db 1 TTGGGGTTGGGTTGGGGTT 20

RESULT 471
ACCESSION AX032672
LOCUS AX032672 20 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 118 from Patent EP1016715.
ACCESSION AX032672
VERSION AX032672.1 GI:10279610
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 118 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
1..20
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGGTT 1038
|||||
Db 1 TTGGGGTTGGGTTGGGGTT 20

RESULT 472
ACCESSION AX032672
LOCUS AX032672 18 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 18 from Patent WO0208461.
ACCESSION AX032672
VERSION AX032672.1 GI:18694219
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Linnarsson,S.G., Ernforss,P.G. and Bauren,G.G.
TITLE A method and an algorithm for mrna expression analysis
JOURNAL Patent: WO 0208461-A 18 31-JAN-2002;
Global Genomics AB (SE)
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Double-stranded product DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;
```


Best Local Similarity 94.4%; Pred. No. 3.3e+02; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CGAAAAAAAAAAAAAAAAA 1

RESULT 474
AX814932/c
LOCUS AX814932 18 bp DNA linear PAT 05-DEC-2003
DEFINITION Sequence 18 from Patent WO03064691.
ACCESSION AX814932
VERSION AX814932.1 GI:39104070
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Linnarsson, S., Ernfor, P., Bauren, G., Metsis, A., Pihlak, A. and Montelius, A.
TITLE Methods and means for manipulating nucleic acid
JOURNAL Patent: WO 03064691-A 18 07-AUG-2003;
Global Genomics AB (SE)
FEATURES
source
1. .18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Double-stranded product DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CGAAAAAAAAAAAAAAAAA 1

RESULT 475
E59328
LOCUS E59328 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59328
VERSION E59328.1 GI:18622505
KEYWORDS JP 2000342265-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose, K. and Yoshida, T.
TITLE Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 9 12-DEC-2000;
TARGOSEI CHEM IND CO LTD
COMMENT OS Artificial Sequence
PN JP 2000342265-A/9
PD 12-DEC-2000
PP 02-JUN-1999 JP 1999154974
PR
PI KUNIHICO HIROSE, TADAO YOSHIDA
PC C12N15/09, B01D15/08, C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .20
Location/Qualifiers
1. .20
/organism="Artificial Sequence".
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CGAAAAAAAAAAAAAAAAA 1

RESULT 476
AX811603/c
LOCUS AX811603 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2140 from patent US 6559294.
ACCESSION AR311603
VERSION AR311603.1 GI:31705029
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais, R., Holseth, S.K., Zagursky, R.J., Metcalf, B.J., Peek, J.A., Sankaran, B. and Fletcher, L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2140 06-MAY-2003;
FEATURES
source
1. .20
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 137 TCTGGAGTCCCTTTCC 154
Db 18 TCTGGAGTCCCTTTCC 1

RESULT 477
A88115
LOCUS A88115 21 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 263 from Patent WO9833904.
ACCESSION A88115
VERSION A88115.1 GI:6736685
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Brysch, W. and Schlingensiepen, K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 263 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
source
1. .21
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 348 TCGGGGCGCGTGGTGGG 368
Db 1 TCGGGGCGCGTGGGCGG 21

RESULT 478
A90082
LOCUS A90082 21 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 263 from Patent EP0856579.
ACCESSION A90082

```
VERSION A90082.1 GI:6738596
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 21)
AUTHORS Brysch,W.D. and Schlingensiepen,K.D.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: EP 0856579-A 263 05-AUG-1998;
FEATURES
source
Location/Qualifiers
1..21
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 348 TCGGGGGCGGCGTGGTGGG 368
Db 1 TCGGGGGCTGGCGCGGCGGG 21

RESULT 479
LOCUS BD065628 21 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD065628
VERSION BD065628.1 GI:22611231
KEYWORDS JP 2001511000-A/263.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 263 07-AUG-2001;
COMMENT BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
OS Unknown
PN JP 2001511000-A/263
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101531.8
PI KARL HERMANN SCHLINGENSIEPEN WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
KEYWORDS Location/Qualifiers
1..21
Location/Qualifiers
1..21
/organism='Unknown'.
/db_xref="taxon:32644"

FEATURES
source
Location/Qualifiers
1..21
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 348 TCGGGGGCGGCGTGGTGGG 368
Db 1 TCGGGGGCTGGCGCGGCGGG 21

RESULT 480
LOCUS AR027678 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 15 from patent US 5856435.
ACCESSION AR027678
VERSION AR027678.1 GI:5938498
KEYWORDS
```

```
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Baziile,D., Emile,C., Helene,C. and Spenlehauer,G.
TITLE Nucleic acid-containing composition, its preparation and use
JOURNAL Patent: US 5856435-A 15 05-JAN-1999;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 481
LOCUS AR037355/C 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5801155.
ACCESSION AR037355
VERSION AR037355.1 GI:5955211
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 5801155-A 2 01-SEP-1998;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1

RESULT 482
LOCUS AR104584 16 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 131 from patent US 6093809.
ACCESSION AR104584
VERSION AR104584.1 GI:12817292
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Cech,T.R. and Lingner,J.
TITLE Telomerase
JOURNAL Patent: US 6093809-A 131 25-JUL-2000;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1751
```

```
Db      1 AAAAAAAAAAAAAAAAAA 16
|||||
RESULT 483
AR175845
LOCUS      16 bp      DNA
DEFINITION Sequence 131 from patent US 6309867.
ACCESSION  AR175845
VERSION     AR175845.1 GI:17917144
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Cech,T.R. and Nakamura,T.
TITLE      Telomerase
JOURNAL    Patent: US 6309867-A 131 30-OCT-2001;
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db      1 AAAAAAAAAAAAAAAAAA 16
|||||

RESULT 484
I38676/c
LOCUS      16 bp      DNA
DEFINITION Sequence 36 from patent US 5614617.
ACCESSION  I38676
VERSION     I38676.1 GI:2084730
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Cook,P.D. and Sanghvi,Y.S.
TITLE      Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
JOURNAL    Patent: US 5614617-A 36 25-MAR-1997;
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db      1 AAAAAAAAAAAAAAAAAA 16
|||||

RESULT 485
I38682/c
LOCUS      16 bp      DNA
DEFINITION Sequence 42 from patent US 5614617.
ACCESSION  I38682
VERSION     I38682.1 GI:2084736
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Cook,P.D. and Sanghvi,Y.S.

TITLE      Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
JOURNAL    Patent: US 5614617-A 42 25-MAR-1997;
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db      1 AAAAAAAAAAAAAAAAAA 16
|||||

TITLE      Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
JOURNAL    Patent: US 5614617-A 42 25-MAR-1997;
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db      16 AAAAAAAAAAAAAAAAAA 1
|||||

RESULT 486
I38700/c
LOCUS      16 bp      DNA
DEFINITION Sequence 60 from patent US 5614617.
ACCESSION  I38700
VERSION     I38700.1 GI:2084754
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Cook,P.D. and Sanghvi,Y.S.
TITLE      Nuclease resistant, pyrimidine modified oligonucleotides that
            detect and modulate gene expression
JOURNAL    Patent: US 5614617-A 60 25-MAR-1997;
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db      16 AAAAAAAAAAAAAAAAAA 1
|||||

RESULT 487
AR221692/c
LOCUS      16 bp      DNA
DEFINITION Sequence 2 from patent US 6426408.
ACCESSION  AR221692
VERSION     AR221692.1 GI:23328764
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS    Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B., Jr.
TITLE      Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL    Patent: US 6426408-A 2 30-JUL-2002;
FEATURES    Location/Qualifiers
            source
            1..16
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAAAAAA 1751
|||||
Db      16 AAAAAAAAAAAAAAAAAA 1
|||||
```

```
RESULT 488
AR222462
LOCUS AR222462 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 22 from patent US 6429300.
ACCESSION AR222462
VERSION AR222462.1 GI:23329993
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 22 06-AUG-2002;
FEATURES
Location/Qualifiers
source 1..16
/mol_type="genomic DNA"
/organism="unknown"
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAAA 16
|||||
RESULT 489
AR257437
LOCUS AR257437 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 2 from patent US 6486308.
ACCESSION AR257437
VERSION AR257437.1 GI:27307448
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 16)
AUTHORS Kutayavin,I.V., Lukhtanov,E.A., Gampert,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 2 26-NOV-2002;
FEATURES
Location/Qualifiers
source 1..16
/mol_type="genomic DNA"
/organism="unknown"
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAAA 16
|||||
RESULT 490
AX039049
LOCUS AX039049 16 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent WO0061594.
ACCESSION AX039049
VERSION AX039049.1 GI:11228345
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Beier,M. and Hoheisel,J.
TITLE Nucleoside derivatives with photo-unstable protective groups
JOURNAL Patent: WO 0061594-A 2 19-OCT-2000;
DEUTSCHES KREBSFORSCH (DE) ; BEIER MARKUS (DE) ; HOHEISEL JOERG (DE)
QY 1736 AAAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAAA 1
|||||
RESULT 491
AX235176
LOCUS AX235176 16 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 9 from Patent WO0163282.
ACCESSION AX235176
VERSION AX235176.1 GI:15593767
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Cuzin,M., Peltie,P., Fontecave,M., Decout,J.L. and Dueymes,C.
TITLE Analysis of biological targets using a biochip comprising a
JOURNAL Patent: WO 0163282-A 9 30-AUG-2001;
COMMISSARIAT A L'ENERGIE ATOMIQUE (FR)
FEATURES
Location/Qualifiers
source 1..16
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="sequence synthetique"
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAA 1
|||||
RESULT 492
BD167413
LOCUS BD167413 16 bp DNA linear PAT 17-JAN-2003
DEFINITION Surface-roughened slide glass and method of analyzing biological
substance using the same.
ACCESSION BD167413
VERSION BD167413.1 GI:27873225
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 16)
AUTHORS Okamura,H., Tanga,M., Oba,M., Yamakawa,K. and Takagi,K.
TITLE Surface-roughened slide glass and method of analyzing biological
substance using the same
JOURNAL Patent: JP 2002211954-A 1 31-JUL-2002;
TOYO KOHAN CO LTD
COMMENT OS Artificial Sequence
PN JP 2002211954-A/1
PD 31-JUL-2002
PF 30-OCT-2001 JP 2001332778
PI HIROSHI OKAMURA, MICHIFUMI TANGA, MITSUYOSHI OBA, KAORU YAMAKAWA,
PI KENICHI TAKAGI
PC C03C15/00, C03C17/245, C12M1/00, C12N11/14, C12N15/09, C12N15/09,
PC C12Q1/68,
```

RESULT 494	AR172076/c	LOCUS	AR172076	17 bp	DNA	linear	PAT 17-DEC-2001
		DEFINITION	Sequence 30 from patent US 6297425.				

PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,
PI NING NO,
PI KIORU OGAWA
PC C12N15/09, A61K31/00, A61K39/36, A61K45/00, C12Q1/68, C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
/organism='Artificial Sequence'.
1..17

FEATURES
source

/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1750

Db 17 CAAAAA 2

RESULT 497

E59657/c

LOCUS

DEFINITION E59657 17 bp DNA linear PAT 18-JUN-2001
Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same.

ACCESSION E59657.

VERSION E59657.1 GI:13019451

KEYWORDS JP 2000037193-A/3.

SOURCE unidentified

ORGANISM unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Takamichi M., Tsuyoshi F., Masaharu K., Takashi I. and Kazunori O.
TITLE Method for preparing nucleic acid sample for analyzing minor gene,
nucleic acid sample thus prepared and method for analyzing nucleic
acid sample by using the same, and reagent kit and analysis service
for using the same

JOURNAL Patent: JP 2000037193-A 3 08-FEB-2000;

HITACHI LTD

OS Unidentified

PN JP 2000037193-A/3

PD 08-FEB-2000

PF 19-MAY-1999 JP 1999138051

PR

PI TAKAMICHI MATSUMURA, TSUYOSHI FUJITA, MASAHARU KIYAMA, PI

TAKASHI IRIE,

PI KAZUNORI OKANO

PC C12N15/09, C12Q1/68, C12N15/00

CC Strandedness: Single;

CC Topology: Linear;

FH Key Location/Qualifiers

FT source 1..17

FT Location/Qualifiers
/organism='Unidentified'.
1..17

FEATURES
source

/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA 1750

Db 17 CAAAAA 2

RESULT 498

AR187062/c

LOCUS

DEFINITION AR187062 17 bp DNA linear PAT 20-APR-2002

ACCESSION Sequence 2550 from patent US 6346398.

VERSION AR187062

KEYWORDS AR187062.1 GI:20233027

SOURCE

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco P., McSwigen J., Stinchcomb D. and Escobedo J.

TITLE Method and reagent for the treatment of diseases or conditions

related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 2550 12-FEB-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.9%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1751

Db 17 AAAAAA 2

RESULT 499

AR187063/c

LOCUS

DEFINITION AR187063 17 bp DNA linear PAT 20-APR-2002

ACCESSION Sequence 2551 from patent US 6346398.

VERSION AR187063

KEYWORDS AR187063.1 GI:20233028

SOURCE

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco P., McSwigen J., Stinchcomb D. and Escobedo J.

TITLE Method and reagent for the treatment of diseases or conditions

related to levels of vascular endothelial growth factor receptor

JOURNAL Patent: US 6346398-A 2551 12-FEB-2002;

FEATURES Location/Qualifiers

source 1..17

/organism="unknown"

/mol_type="unassigned DNA"

Query Match 0.9%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1751

Db 16 AAAAAA 1

RESULT 500

AR256849/c

LOCUS

DEFINITION AR256849 17 bp DNA linear PAT 20-DEC-2002

ACCESSION Sequence 3 from patent US 6485916.

VERSION AR256849

KEYWORDS AR256849.1 GI:27306475

SOURCE

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 17)

AUTHORS Muramatsu T., Fujita T., Kiyama M., Irie T. and Okano K.

TITLE Preparation method of nucleic acid sample for rare expressed genes

and analyzing method using the prepared nucleic acid samples

```
thereby
Patent: US 6495916-A 3 26-NOV-2002;
LOCUS      17 bp      DNA
DEFINITION Sequence 64 from patent US 6495319.
ACCESSION  AR266626
VERSION     AR266626.1 GI:29695690
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS    McClelland,M., Welsh,J. and Trenkle,T.
TITLE      Reduced complexity nucleic acid targets and methods of using same
JOURNAL    Patent: US 6495319-A 64 17-DEC-2002;
FEATURES    Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1735 CAAAAA...AAAAA 1750
Db  17 CAAAAA...AAAAA 2

RESULT 501
LOCUS      AR266626      17 bp      DNA
DEFINITION Sequence 64 from patent US 6495319.
ACCESSION  AR266626
VERSION     AR266626.1 GI:29695690
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS    McClelland,M., Welsh,J. and Trenkle,T.
TITLE      Reduced complexity nucleic acid targets and methods of using same
JOURNAL    Patent: US 6495319-A 64 17-DEC-2002;
FEATURES    Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1735 CAAAAA...AAAAA 1750
Db  17 CAAAAA...AAAAA 2

RESULT 502
LOCUS      AR266626      17 bp      RNA
DEFINITION Sequence 1074 from patent US 6566127.
ACCESSION  AR323672
VERSION     AR323672.1 GI:33709480
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 1074 20-MAY-2003;
FEATURES    Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="unassigned RNA"

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1735 CAAAAA...AAAAA 1750
Db  17 CAAAAA...AAAAA 2

RESULT 503
LOCUS      AR323673      17 bp      RNA
DEFINITION Sequence 1075 from patent US 6566127.
ACCESSION  AR323673
VERSION     AR323673.1 GI:33709481
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 1075 20-MAY-2003;
FEATURES    Location/Qualifiers
             source
             1..17
             /organism="unknown"
             /mol_type="unassigned RNA"

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1736 AAAAAA...AAAAA 1751
Db  16 AAAAAA...AAAAA 1

RESULT 504
LOCUS      AX361606      17 bp      DNA
DEFINITION Sequence 24 from Patent WO0208461.
ACCESSION  AX361606
VERSION     AX361606.1 GI:18694225
KEYWORDS    .
SOURCE      synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM    Linnarsson,S.G., Ernfors,P.G. and Bauren,G.G.
REFERENCE   1
AUTHORS    A method and an algorithm for mrna expression analysis
TITLE      Patent: WO 0208461-A 24 31-JAN-2002;
JOURNAL    Global Genomics AB (SE)
FEATURES    Location/Qualifiers
             source
             1..17
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="Double-stranded product DNA"

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1736 AAAAAA...AAAAA 1751
Db  16 AAAAAA...AAAAA 1

RESULT 505
LOCUS      AX692525      17 bp      DNA
DEFINITION Sequence 5257 from Patent EP1281758.
ACCESSION  AX692525
VERSION     AX692525.1 GI:29415483
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
           Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS    Shannon,M., Gu,Y. and Nguyen,C.T.
```

TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

JOURNAL Patent: EP 1281758-A 5257 05-FEB-2003;

AEONICA, Inc. (US)

FEATURES Location/Qualifiers

source

1. .17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.9%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751

|||||

Db 17 AAAAAAAAAAAAAA 2

RESULT 506

AX692527/c

LOCUS AX692527 17 bp DNA linear PAT 31-MAR-2003

DEFINITION Sequence 5259 from Patent EP1281758.

ACCESSION AX692527

VERSION AX692527.1 GI:29415485

KEYWORDS Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12

Patent: EP 1281758-A 5259 05-FEB-2003;

AEONICA, Inc. (US)

FEATURES Location/Qualifiers

source

1. .17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.9%; Score 16; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750

|||||

Db 16 CAAAAAAAAAAAAA 1

RESULT 507

AX814938/c

LOCUS AX814938 17 bp DNA linear PAT 05-DEC-2003

DEFINITION Sequence 24 from Patent WO03064691.

ACCESSION AX814938

VERSION AX814938.1 GI:39104076

KEYWORDS synthetic construct

synthetic construct

artificial sequences.

ORGANISM

Linnarsson,S., Ernfors,P., Bauren,G., Metsis,A., Pihlak,A. and Montelius.A.

TITLE Methods and means for manipulating nucleic acid

Patent: WO 03064691-A 24 07-AUG-2003;

Global Genomics AB (SE)

FEATURES Location/Qualifiers

source

1. .17

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Description of Artificial Sequence: Double-stranded

product DNA"

Query Match

Best Local Similarity 0.9%; Score 16; DB 1; Length 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751

|||||

Db 16 AAAAAAAAAAAAAA 1

RESULT 508

BD011732/c

LOCUS BD011732 17 bp DNA linear PAT 02-AUG-2002

DEFINITION 795, a novel gene related to pollen allergy.

ACCESSION BD011732

VERSION BD011732.1 GI:22091921

KEYWORDS WO 0065050-A/4.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 17)

AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,

Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,

Takahashi,E. and Yokoi,A.

TITLE 795, a novel gene related to pollen allergy

JOURNAL Patent: WO 0065050-A 4 02-NOV-2000;

GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,

TADAHIRO OSHIDA,MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,

YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI

TAKAHASHI,AKIRA YOKOI

COMMENT OS Artificial Sequence

PN WO 0065050-A/4

PD 02-NOV-2000

PF 26-APR-2000 WO 2000JP002734

PR 27-APR-1999 JP 99P 120494

PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,

PI MASAYA ODAYASHI,SHIGEMICHI GUNJI,IZUMI ODAYASHI,YUKIHO IMAI,

PI NEI YOSHIDA,

PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC

C12N15/12,C07K14/47,C07K16/18,C12Q1/68,G01N33/50//A61K31/00, PC

A61P37/00

CC Description of Artificial Sequence:Artificially Synthesized CC

Primer Sequence

FH Key

Location/Qualifiers.

FEATURES

source

1. .17

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match

Best Local Similarity 0.9%; Score 16; DB 1; Length 17;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750

|||||

Db 17 CAAAAAAAAAAAAA 2

RESULT 509

BD091744/c

LOCUS BD091744 17 bp DNA linear PAT 27-AUG-2002

DEFINITION 441, a novel gene related to pollen allergy.

ACCESSION BD091744

VERSION BD091744.1 GI:22637355

KEYWORDS WO 0073435-A/4.

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 17)

AUTHORS Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,

Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.


```

TITLE
JOURNAL
441, a novel gene related to pollen allergy
Patent: WO 0073435-A 4 07-DEC-2000;
GENOX RESEARCH INC. TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAVASHI, SHIGEMICHI GUNJI, IZUMI OBAVASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI
OS Artificial Sequence
PN WO 0073435-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003190
PR 27-MAY-1999 JP 99P 148783
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAVASHI, SHIGEMICHI GUNJI, IZUMI OBAVASHI, YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI
PC C12N15/12, C12Q1/68, G01N33/15, G01N33/50
CC Description of Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match
Best Local Similarity 0.9%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2
RESULT 510
BD091752/c
LOCUS
BD091752
465, a novel gene related to pollen allergy.
DEFINITION
BD091752
ACCESSION
BD091752.1 GI:22637363
VERSION
BD091752.1 GI:22637363
KEYWORDS
WO 0073439-A/4.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 17)
Nagasu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,
Gunji, S., Obayashi, I., Imai, Y., Yoshida, N., Ogawa, K., Matsui, K.,
Takahashi, E. and Yokoi, A.
465, a novel gene related to pollen allergy
Patent: WO 0073439-A 4 07-DEC-2000;
GENOX RESEARCH INC. TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAVASHI, SHIGEMICHI GUNJI, IZUMI OBAVASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
OS Artificial Sequence
PN WO 0073439-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003191
PR 27-MAY-1999 JP 99P 148784
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAVASHI, SHIGEMICHI GUNJI, IZUMI OBAVASHI, YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, A61P37/08, A61K45/00 CC Description
of Artificially Synthesized CC Primer
Sequence
FH Key Location/Qualifiers
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match
0.9%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 17;
Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2
RESULT 512
BD097336/c
LOCUS
BD097336
Method for examination for allergosis.
DEFINITION
BD097336
ACCESSION
BD097336
VERSION
BD097336.1 GI:22642910
KEYWORDS
WO 0165259-A/7.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 17)
Nagasu, T., Oshida, T., Obayashi, I., Matsui, K. and Sait, H.
Method for examination for allergosis
Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAVASHI, KEIKO MATSUI, HIROHISA SAITO

```

```

Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2
RESULT 511
BD091775/c
LOCUS
BD091775
787, a novel gene related to pollen allergy.
DEFINITION
BD091775
ACCESSION
BD091775
VERSION
BD091775.1 GI:22637386
KEYWORDS
WO 0073440-A/4.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 17)
Nagasu, T., Sugita, Y., Kashiwabara, T., Oshida, T., Obayashi, M.,
Gunji, S., Obayashi, I., Imai, Y., Yoshida, N., Ogawa, K., Matsui, K.,
Takahashi, E. and Yokoi, A.
787, a novel gene related to pollen allergy
Patent: WO 0073440-A 4 07-DEC-2000;
GENOX RESEARCH INC. TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,
TADAHIRO OSHIDA, MASAYA OBAVASHI, SHIGEMICHI GUNJI, IZUMI OBAVASHI,
YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI
TAKAHASHI, AKIRA YOKOI
OS Artificial Sequence
PN WO 0073440-A/4
PD 07-DEC-2000
PF 18-MAY-2000 WO 2000JP003192
PR 27-MAY-1999 JP 99P 148785
PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,
PI MASAYA OBAVASHI, SHIGEMICHI GUNJI, IZUMI OBAVASHI, YUKIHO IMAI,
PI NEI YOSHIDA,
PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI PC
C12N15/12, C12Q1/68, C12N5/08, C12N5/06, C07K14/415 CC Description of
Artificially Synthesized CC Primer Sequence
FH Key Location/Qualifiers
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match
0.9%; Score 16; DB 1; Length 17;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2
RESULT 512
BD097336/c
LOCUS
BD097336
Method for examination for allergosis.
DEFINITION
BD097336
ACCESSION
BD097336
VERSION
BD097336.1 GI:22642910
KEYWORDS
WO 0165259-A/7.
SOURCE
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 17)
Nagasu, T., Oshida, T., Obayashi, I., Matsui, K. and Sait, H.
Method for examination for allergosis
Patent: WO 0165259-A 7 07-SEP-2001;
GENOX RESEARCH INC. JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI
OBAVASHI, KEIKO MATSUI, HIROHISA SAITO

```

```

COMMENT      OS Artificial Sequence
PN WO 0165259-A/7
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP 00P 61832
PI TAKESHI NAGASU,TADAHIRO OSHIDA,IZUMI OBAYASHI,KEIKO MATSUI, PI
    HIROHISA SAITO
PC G01N33/53,C12Q1/68,C12N15/12,G01N33/15,A01K67/027,A61K39/395,
A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
FEATURES
    source
        1..17 Location/Qualifiers
        /organism='Artificial Sequence'
        /mol_type='genomic DNA'
        /db_xref='taxon:32630'
Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAA1750
DB 17 CAAAAA1750
RESULT 513
BD142810/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD142810
VERSION BD142810.1 GI:23237755
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
    Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 4 28-MAR-2002;
    GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
    NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA,RYOICHI HASHIDA,KAORU
    OGAWA,TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO,EIKI
    TAKAHASHI
COMMENT      OS Artificial Sequence
PN WO 0224903-A/4
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI
    TAKESHI NAGASU,
    GOZO TSUJIMOTO,EIKI TAKAHASHI
PC C12N15/09,C12N5/10,C07K14/47,C07K16/18,C12P21/02,C12Q1/02, PC
    C12Q1/68,
    A01K67/027,A61K45/00,A61K48/00,A61P17/00,A61P37/08,
    PC G01N33/15,
    G01N33/50//C12P21/08,(C12N5/10,C12R1:91),(C12P21/02,C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized
    construct
CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
FEATURES
    source
        1..17 Location/Qualifiers
        /organism='synthetic construct'
        /mol_type='genomic DNA'
        /db_xref='taxon:32630'

```

```

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAA1750
DB 17 CAAAAA1750
RESULT 514
BD143836/c
LOCUS
DEFINITION Method of examining allergic disease.
ACCESSION BD143836
VERSION BD143836.1 GI:27849594
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
    Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 4 02-APR-2002;
    GENOX RESEARCH INC,THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
    OS Artificial Sequence
COMMENT PN JP 2002095500-A/4
    PD 02-APR-2002
    PF 25-SEP-2000 JP 2000291316
    PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
    TAKESHI NAGASU,
    PI KOZO TSUJIMOTO
    PC
    C12Q1/68,A01K67/027,A61K31/7088,A61K31/711,A61K45/00,A61P37/08, PC
    C07K14/47,
    PC C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
    C12N15/09,C12P21/02,
    PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
    C12N15/00
    CC Description of Artificial Sequence:an artificially synthesized
    construct
CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
FEATURES
    source
        1..17 Location/Qualifiers
        /organism='synthetic construct'
        /mol_type='genomic DNA'
        /db_xref='taxon:32630'
Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred.No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAA1750
DB 17 CAAAAA1750
RESULT 515
BD167837/c
LOCUS
DEFINITION Method for examination of allergosis.
ACCESSION BD167837
VERSION BD167837.1 GI:27873649
KEYWORDS WO 0233122-A/4.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)

```

AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 023122-A 4 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAIYASHI, TAKESHI NAGASU, HIROHISA SAITO,EIKI TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 023122-A/4
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAIYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO,EIKI TAKAHASHI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC A61K39/395
PC A01K67/027//C07K16/18, C12N5/10
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
FT source 1..17
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

RESULT 516
BD167909/c
LOCUS Method of examining allergic disease. 17 bp DNA linear PAT 17-JAN-2003
DEFINITION
ACCESSION BD167909
VERSION BD167909.1 GI:27873721
KEYWORDS WO 0226962-A/8.
SOURCE synthetic construct
ORGANISM synthetic sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 8 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0226962-A/8
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,TOMOKO FUJISHIMA, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC C12Q1/68.
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08, PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)

AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H. and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 023122-A 4 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAIYASHI, TAKESHI NAGASU, HIROHISA SAITO,EIKI TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 023122-A/4
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAIYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO,EIKI TAKAHASHI
PC C12Q1/68, C12N15/09, G01N33/53, G01N33/50, C12Q1/02, A61K48/00, PC A61K39/395
PC A01K67/027//C07K16/18, C12N5/10
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
FT source 1..17
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

RESULT 517
BD168113/c
LOCUS Method for examination for allergosis. 17 bp DNA linear PAT 17-JAN-2003
DEFINITION
ACCESSION BD168113
VERSION BD168113.1 GI:27873925
KEYWORDS WO 0233069-A/20.
SOURCE synthetic construct
ORGANISM synthetic sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 20 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAIYASHI, TAKESHI NAGASU, HIROHISA SAITO
COMMENT OS Artificial Sequence
PN WO 0233069-A/20
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAIYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key Location/Qualifiers
FT source 1..17
FEATURES Location/Qualifiers
source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

```
RESULT 518
BD171179/c
LOCUS          BD171179          17 bp      DNA          linear      PAT 17-JAN-2003
DEFINITION     Method of examining allergic disease.
ACCESSION      BD171179
VERSION        BD171179.1  GI:27876991
KEYWORDS       WO 0250269-A/4.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 17)
AUTHORS        Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and
                Tsujimoto,G.
TITLE          Method of examining allergic disease
JOURNAL        Patent: WO 0250269-A 4 27-JUN-2002;
                GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
                NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI,AKINORI OTA YOSHIKO
                MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, TAKESHI NAGASU,
                GOZO TSUJIMOTO
COMMENT        OS Artificial Sequence
                PN WO 0250269-A/4
                PD 27-JUN-2002
                PF 21-DEC-2001 WO 2001JP011286
                PR 21-DEC-2000 JP 00P 389476
                PI YOSHIKO MATSUMOTO,YUKIHO IMAI,TADAHIRO OSHIDA,YUJI SUGITA, PI
                TAKESHI NAGASU,
                PI GOZO TSUJIMOTO
                PC C12N15/11,C07K16/18,A61K67/027,A61K31/711,A61K45/00,A61K48/00,
                PC A61P37/08,
                PC C12Q1/68,G01N33/50
                CC Description of Artificial Sequence:'GT15G', an artificially
                CC synthesized
                CC primer sequence
                CC key sequence
                CC Location/Qualifiers
                FH Key
                FT source
                FT 1..17
                FT /organism='Artificial Sequence'.
                FT /location/Qualifiers
                FT 1..17
                FT /organism='synthetic construct'
                FT /mol_type='genomic DNA'
                FT /db_xref='taxon:32630'

Query Match          0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

RESULT 519
E32451/c
LOCUS          E32451          18 bp      DNA          linear      PAT 18-JUN-2001
DEFINITION     Mammal-derived tissue specific physiologically active protein.
ACCESSION      E32451
VERSION        E32451.1  GI:13018687
KEYWORDS       JP 2000037190-A/11.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Jun,N., Yuseke,N. and Toshihiro,T.
TITLE          Mammal-derived tissue specific physiologically active protein
JOURNAL        Patent: JP 2000037190-A 11 08-FEB-2000;
                JAPAN TOBACCO INC
COMMENT        OS Artificial Sequence
                PN JP 2000037190-A/11
                PD 08-FEB-2000
                PF 23-JUL-1998 JP 1998225228
                PR JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA

Query Match          0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

RESULT 521
E32460/c
LOCUS          E32460          18 bp      DNA          linear      PAT 18-JUN-2001
DEFINITION     Mammal-derived tissue specific physiologically active protein.
ACCESSION      E32460
VERSION        E32460.1  GI:13018696
KEYWORDS       JP 2000037190-A/11.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Jun,N., Yuseke,N. and Toshihiro,T.
TITLE          Mammal-derived tissue specific physiologically active protein
JOURNAL        Patent: JP 2000037190-A 11 08-FEB-2000;
                JAPAN TOBACCO INC
COMMENT        OS Artificial Sequence
                PN JP 2000037190-A/11
                PD 08-FEB-2000
                PF 23-JUL-1998 JP 1998225228
                PR JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
```

```
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02.
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
CC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
FH Key
FT primer_bind (1)..(18).
FEATURES
source
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match          0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

RESULT 520
E32457/c
LOCUS          E32457          18 bp      DNA          linear      PAT 18-JUN-2001
DEFINITION     Mammal-derived tissue specific physiologically active protein.
ACCESSION      E32457
VERSION        E32457.1  GI:13018693
KEYWORDS       JP 2000037190-A/17.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Jun,N., Yuseke,N. and Toshihiro,T.
TITLE          Mammal-derived tissue specific physiologically active protein
JOURNAL        Patent: JP 2000037190-A 17 08-FEB-2000;
                JAPAN TOBACCO INC
COMMENT        OS Artificial Sequence
                PN JP 2000037190-A/17
                PD 08-FEB-2000
                PF 23-JUL-1998 JP 1998225228
                PR JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA

Query Match          0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2

RESULT 521
E32460/c
LOCUS          E32460          18 bp      DNA          linear      PAT 18-JUN-2001
DEFINITION     Mammal-derived tissue specific physiologically active protein.
ACCESSION      E32460
VERSION        E32460.1  GI:13018696
KEYWORDS       JP 2000037190-A/11.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 18)
AUTHORS        Jun,N., Yuseke,N. and Toshihiro,T.
TITLE          Mammal-derived tissue specific physiologically active protein
JOURNAL        Patent: JP 2000037190-A 11 08-FEB-2000;
                JAPAN TOBACCO INC
COMMENT        OS Artificial Sequence
                PN JP 2000037190-A/11
                PD 08-FEB-2000
                PF 23-JUL-1998 JP 1998225228
                PR JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
```

KEYWORDS JP 2000037190-A/20.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun, N., Yusuke, N. and Toshihiro, T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 20 08-FEB-2000;
COMMENT JAPAN TOBACCO INC
OS Artificial Sequence
PN JP 2000037190-A/20
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT primer bind (1)..(18).
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAA AAAAAAAAAA 1750
Db 17 CAAAAA AAAAAAAAAA 2
RESULT 522
AR208427/c
LOCUS AR208427 18 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 7 from patent US 6383754.
ACCESSION AR208427
VERSION AR208427.1 GI:21509578
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: US 6383754-A 7 07-MAY-2002;
FEATURES
source
1..18
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAA AAAAAAAAAA 1751
Db 16 AAAAAA AAAAAAAAAA 1
RESULT 523
AX085253/c
LOCUS AX085253 18 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 7 from Patent WO0112855.
ACCESSION AX085253
VERSION AX085253.1 GI:13275311
KEYWORDS

synthetic construct
synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Kaufman, J.C., Roth, M.E., Lizardi, P.M., Feng, L. and Latimer, D.R.
TITLE Binary encoded sequence tags
JOURNAL Patent: WO 0112855-A 7 22-FEB-2001;
YALE UNIVERSITY (US)
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAA AAAAAAAAAA 1751
Db 16 AAAAAA AAAAAAAAAA 1
RESULT 524
AX394603
LOCUS AX394603 20 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1 from Patent EP1186673.
ACCESSION AX394603
VERSION AX394603.1 GI:21065716
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Wobler, P.K. and Delenstarr, G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 1 13-MAR-2002;
Agilent Technologies Inc (US)
FEATURES
source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="probes to target sequences"
Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAA AAAAAAAAAA 1751
Db 1 AAAAAA AAAAAAAAAA 16
RESULT 525
AR142678/c
LOCUS AR142678 21 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 8 from patent US 6203988.
ACCESSION AR142678
VERSION AR142678.1 GI:15103964
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
AUTHORS Kambara, H. and Uematsu, C.
TITLE DNA fragment preparation method for gene expression profiling
JOURNAL Patent: US 6203988-A 8 20-MAR-2001;
FEATURES
source
1..21
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

```

Query Match      0.9%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 21 AAAAAAAAAAAAAA 6

RESULT 526
E28097/c
LOCUS E28097 Method for analyzing DNA fragment. 21 bp DNA linear PAT 19-JUN-2001
DEFINITION E28097
ACCESSION E28097
VERSION E28097.1 GI:13018322
KEYWORDS JP 1999196874-A/8.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hideki K. and Senshu U.
TITLE Method for analyzing DNA fragment
JOURNAL Patent: JP 1999196874-A 8 27-JUL-1999;
HITACHI LTD
COMMENT OS Unidentified
PN JP 1999196874-A/8
PD 27-JUL-1999
PP 14-JAN-1998 JP 1998005399
PR HIDEKI KAWIBARA, SENSU UEMATSU
PC C12N15/09, C12Q1/68, G01N27/447, C12N15/00, G01N27/26 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..21
   Location/Qualifiers
   1..21
   /organism="Unidentified".
   /organism="unidentified"
   /mol_type="genomic DNA"
   /db_xref="taxon:32644"

Query Match      0.9%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 21 AAAAAAAAAAAAAA 6

RESULT 527
AX153987
LOCUS AX153987 21 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 85 from Patent WO0138576.
ACCESSION AX153987
VERSION AX153987.1 GI:14535601
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cargill, M., Ireland, J.S. and Lander, E.S.
TITLE Human single nucleotide polymorphisms
JOURNAL Patent: WO 0138576-A 85 31-MAY-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US)
   Location/Qualifiers
   1..21
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match      0.9%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 21 AAAAAAAAAAAAAA 6

RESULT 528
AX394604
LOCUS AX394604 21 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 2 from Patent EP1186673.
ACCESSION AX394604
VERSION AX394604.1 GI:21065717
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Wobler, P.K. and Delenstarr, G.C.
TITLE Calibration of molecular array data
JOURNAL Patent: EP 1186673-A 2 13-MAR-2002;
Agilent Technologies Inc (US)
   Location/Qualifiers
   1..21
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="probes to target sequences"

Query Match      0.9%; Score 16; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 1 AAAAAAAAAAAAAA 16

RESULT 529
AX130720
LOCUS AX130720 19 bp DNA linear PAT 15-MAY-2001
DEFINITION Sequence 1938 from Patent WO0130362.
ACCESSION AX130720
VERSION AX130720.1 GI:14137025
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases
JOURNAL Patent: WO 0130362-A 1938 03-MAY-2001;
IMMUSOL, INC. (US)
   Location/Qualifiers
   1..19
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"
   /note="Cyclin D2 ribozyme binding site"

Query Match      0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 4.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1515 TGGGCACATCTTGTGCAAG 1533
DB 1 TGAGCACATCTTGGCAAG 19

```

```
RESULT 530
AR062657/c
LOCUS AR062657 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 57 from patent US 5843738.
ACCESSION AR062657
VERSION AR062657.1 GI:5990348
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5843738-A 57 01-DEC-1998;
FEATURES
source
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 531
AR104760/c
LOCUS AR104760 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 57 from patent US 6093811.
ACCESSION AR104760
VERSION AR104760.1 GI:12817468
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 6093811-A 57 25-JUL-2000;
FEATURES
source
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 532
AR105582/c
LOCUS AR105582 20 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 57 from patent US 6096722.
ACCESSION AR105582
VERSION AR105582.1 GI:12819179
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett,C.Frank., Mirabelli,C.K. and Baker,B.
TITLE Antisense modulation of cell adhesion molecule expression and
JOURNAL treatment of cell adhesion molecule-associated diseases
Patent: US 6096722-A 57 01-AUG-2000;
FEATURES
Location/Qualifiers

source
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 533
AR123244/c
LOCUS AR123244 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 57 from patent US 6169079.
ACCESSION AR123244
VERSION AR123244.1 GI:14108210
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide inhibition of cell adhesion
JOURNAL Patent: US 6169079-A 57 02-JAN-2001;
FEATURES
Location/Qualifiers

source
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 534
AR12659/c
LOCUS AR12659 20 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 57 from patent US 5514788.
ACCESSION AR12659
VERSION AR12659.1 GI:1601014
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 20)
AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
TITLE Oligonucleotide modulation of cell adhesion
JOURNAL Patent: US 5514788-A 57 07-MAY-1996;
FEATURES
Location/Qualifiers

source
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 535
AR13352/c
LOCUS AR13352 20 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 57 from patent US 5591623.
Location/Qualifiers

source
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1
```

```
ACCESSION I33352
VERSION I33352.1 GI:1824143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES
  1 (bases 1 to 20)
  AUTHORS Bennett,C.Frank. and Mirabelli,C.K.
  TITLE Oligonucleotide modulation of cell adhesion
  JOURNAL Patent: US 5591623-A 57 07-JAN-1997;
  FEATURES Location/Qualifiers
    source
      1..20
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match      0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 536
LOCUS AR370582/c
DEFINITION Sequence 57 from patent US 5300491.
ACCESSION AR370582
VERSION AR370582.1 GI:34607335
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
  1 (bases 1 to 20)
  AUTHORS Bennett,C.F. and Mirabelli,C.K.
  TITLE Oligonucleotide inhibition of cell adhesion
  JOURNAL Patent: US 5300491-A 57 09-OCT-2001;
  FEATURES Location/Qualifiers
    source
      1..20
        /organism="unknown"
        /mol_type="genomic DNA"

Query Match      0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 537
LOCUS AX148814
DEFINITION Sequence 16 from Patent WO0136625.
ACCESSION AX148814
VERSION AX148814.1 GI:14347338
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1
  AUTHORS Wright,J.A., Young,A.H. and Dugourd,D.
  TITLE Antisense oligonucleotide sequences derived from groel and groes as inhibitors of microorganisms
  JOURNAL Patent: WO 0136625-A 16 25-MAY-2001;
  FEATURES Location/Qualifiers
    source
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"

/note="Antisense oligonucleotide"

Query Match      0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 25 GGGGGAAGAGGAAAAAAA 43
Db 1 GGGGGAAGAGGAAAAAAA 19

RESULT 538
LOCUS AX184029
DEFINITION Sequence 1782 from Patent WO0142511.
ACCESSION AX184029
VERSION AX184029.1 GI:15135365
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  AUTHORS Daly,M., Hudson,T.J., Lander,E.S., Rioux,J. and Siminovitch,K.
  TITLE Ibd-related polymorphisms
  JOURNAL Patent: WO 0142511-A 1782 14-JUN-2001;
  FEATURES Location/Qualifiers
    source
      1..20
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match      0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAGAAAAA 1755
Db 1 AAAAAAAGAAAAA 20

RESULT 539
LOCUS AX495922
DEFINITION Sequence 1687 from Patent WO02059256.
ACCESSION AX495922
VERSION AX495922.1 GI:23341532
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  AUTHORS Tuijnder,M., Telerman,A., Amson,R. and Susini,L.
  TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
  JOURNAL Patent: WO 02059256-A 1687 01-AUG-2002;
  FEATURES Location/Qualifiers
    source
      1..20
        /organism="Homo sapiens"
        /mol_type="unassigned DNA"
        /db_xref="taxon:9606"

Query Match      0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAGAAAAA 1755
Db 1 AAAAAAAGAAAAA 20
```



```

Db      1  AAACAAGAAAAAGAAAGAAA 20

RESULT 540
AR298736/c
LOCUS   AR298736          21 bp    DNA
DEFINITION Sequence 10471 from patent US 6537751.
ACCESSION AR298736
VERSION   AR298736.1  GI:31686020
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS  Cohen,D., Chumakov,I. and Blumenfeld,M.
TITLE    Biallelic markers for use in constructing a high density
          disequilibrium map of the human genome
JOURNAL  Patent: US 6537751-A 10471 25-MAR-2003;
FEATURES  Location/Qualifiers
           source
           1..21
           /organism="unknown"
           /mol_type="genomic DNA"
           0.9%; Score 15.8; DB 1; Length 21;
Query Match Best Local Similarity 89.5%; Pred. No. 4.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      289  GTCAATTTTGGCCCTTC 307
Db      19  GTCAATTTTGGCCCTTC 1

RESULT 541
AX038316
LOCUS   AX038316          21 bp    DNA
DEFINITION Sequence 73 from Patent WO0061795.
ACCESSION AX038316
VERSION   AX038316.1  GI:11227664
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS  De Canck,I.D., Rossau,R. and Rombout,A.
TITLE    Method for the amplification of bla class I alleles
JOURNAL  Patent: WO 0061795-A 73 19-OCT-2000;
          CANCK ILSE DE (BE); ROSSAU RUDI (BE); INNOGENETICS NV (BE);
          ROMBOUT ANNEELIES (BE)
FEATURES  Location/Qualifiers
           source
           1..21
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"
           0.9%; Score 15.8; DB 1; Length 21;
Query Match Best Local Similarity 81.0%; Pred. No. 4.7e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      182  CCCCGAAGCAGCGGAGCCG 202
Db      1  CCCCGAAGCAGCGGAGCACC 21

RESULT 542
BD217905/c
LOCUS   BD217905          17 bp    DNA
DEFINITION Gene family encoding apoptosis-associated peptides, peptides
          encoded thereby and method of using the same.
ACCESSION BD217905
VERSION   BD217905.1  GI:33027675
KEYWORDS  JP 2002516564-A/6.
          unidentified

ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS  Umansky,S. and Melkonian,H.
TITLE    Gene family encoding apoptosis-associated peptides, peptides
          encoded thereby and method of using the same
JOURNAL  Patent: JP 2002516564-A 6 04-JUN-2002;
          TANOX INC
COMMENT   OS Unidentified
          PN JP 2002516564-A/6
          PD 04-JUN-2002
          PR 24-SEP-1997 JP 1998515877
          PF 24-SEP-1996 US 60/026603,11-OCT-1996 US 60/028363 PI
          PC C12N15/12,C12N15/62,C07K14/47,C07K16/18,C12Q1/68,G01N33/53, PC
          G01N33/68,
          CC A61K38/17
          CC Strandedness: Single;
          CC Topology: linear;
          CC Gene family encoding apoptosis-associated peptides, peptides
          CC encoded
          CC thereby and method of using the same
          FH Key Location/Qualifiers
          FT source
          1..17
          /organism="Unidentified".
          Location/Qualifiers
           source
           1..17
           /organism="unidentified"
           /mol_type="genomic DNA"
           /db_xref="taxon:32644"
           0.9%; Score 15.6; DB 1; Length 17;
Query Match Best Local Similarity 88.2%; Pred. No. 4e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1735  CAAAAAAGAAAAAAGAAA 1751
Db      17  SNAAGAAAAAAGAAAAAAGAAA 1

RESULT 543
AX216922
LOCUS   AX216922          17 bp    RNA
DEFINITION Sequence 2364 from Patent WO0159103.
ACCESSION AX216922
VERSION   AX216922.1  GI:15526983
KEYWORDS
SOURCE    synthetic construct
          synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS  Blatt,L., McSwiggen,J. and Chowkira,B.M.
TITLE    Method and reagent for the modulation and diagnosis of cd20 and
          nogo gene expression
JOURNAL  Patent: WO 0159103-A 2364 16-AUG-2001;
          RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
          McSwiggen, James (US); Chowkira, Bharat M. (US)
FEATURES  Location/Qualifiers
           source
           1..17
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Nucleic Acid"
           0.9%; Score 15.4; DB 1; Length 17;
Query Match Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      861  AGGAAGAGGAGAGAGAGAG 877
Db      1  AGGAGAGAGAGAGAGAGAG 17

```

```
RESULT 544
AX423131
LOCUS AX423131 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1467 from Patent WO0188124.
ACCESSION AX423131
VERSION AX423131.1 GI:21526513
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1467 22-NOV-2001.
FEATURES
LOCATION/Qualifiers
SOURCE 1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 268 GCACCTCCAGCCACC 284
DB 1 GCCCTCCAGCCACC 17
RESULT 545
AX692523/C
LOCUS AX692523 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5255 from Patent EP1281758.
ACCESSION AX692523
VERSION AX692523.1 GI:29415481
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 5255 05-FEB-2003;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAGA 1
RESULT 546
AX692524/C
LOCUS AX692524 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5256 from Patent EP1281758.
ACCESSION AX692524
VERSION AX692524.1 GI:29415482
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 5255 05-FEB-2003;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAGA 1
RESULT 547
AX723348/C
LOCUS AX723348 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1035 from Patent WO03025176.
ACCESSION AX723348
VERSION AX723348.1 GI:30423849
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 1035 27-MAR-2003;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 4.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 102 GTGAGGCCAGAGGCTC 118
DB 17 GTGAGGCCAGAGGATC 1
RESULT 548
AR079076
LOCUS AR079076 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 7 from patent US 5965403.
ACCESSION AR079076
VERSION AR079076.1 GI:10005822
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 18)
Celeste,A.J. and Murray,B.I.
TITLE Nucleic acids encoding bone morphogenic protein-16 (BMP-16)
JOURNAL Patent: US 5965403-A 7 12-OCT-1999;
FEATURES
LOCATION/Qualifiers
SOURCE 1. .18
/organism="unknown"
```

```
/mol_type="unassigned DNA"

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1479 CTCTGAGGCGGAGTCTC 1495
Db 1 CTGTGAGGCGGAGTCTC 17

RESULT 549
E32450/c
LOCUS E32450 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32450
VERSION E32450.1 GI:13018686
KEYWORDS JP 2000037190-A/10.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 10 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/10
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08//(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC
CQ Key Location/Qualifiers
FT primer_bind (1)..(18).
   Location/Qualifiers
   source
   1..18
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1751
Db 18 CAAAAA..... 2

RESULT 551
E32453/c
LOCUS E32453 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32453
VERSION E32453.1 GI:13018689
KEYWORDS JP 2000037190-A/13.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 13 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/13
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHIU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08//(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00, (C12N5/00,C12R1:91)
CC
CQ Key Location/Qualifiers
FT primer_bind (1)..(18).
   Location/Qualifiers
   source
   1..18
   /organism="synthetic construct"
   /mol_type="genomic DNA"
   /db_xref="taxon:32630"

Query Match      0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA..... 1751
Db 18 CAAAAA..... 2

RESULT 550
E32452/c
LOCUS E32452 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32452
VERSION E32452.1 GI:13018688
KEYWORDS JP 2000037190-A/12.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 12 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/12
PD 08-FEB-2000
```

DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32455
VERSION E32455.1 GI:13018691
KEYWORDS JP 2000037190-A/15.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 15 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/15
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT primer bind (1)..(18).
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAA 1750
DB 18 AGAAAAAAAAAAAAAA 2
RESULT 553
E32456/c
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32456
VERSION E32456.1 GI:13018692
KEYWORDS JP 2000037190-A/16.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/16
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT primer bind (1)..(18).
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAA 1750
DB 18 AGAAAAAAAAAAAAAA 2
RESULT 553
E32456/c
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32456
VERSION E32456.1 GI:13018692
KEYWORDS JP 2000037190-A/16.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 16 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/16
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR
PI JUN NISHITU,YUSUKE NAKAMURA,TOSHIHIRO TANAKA
PC C12N15/09,C07K14/47,C07K16/18,C12N1/19,C12N1/21,C12N5/10, PC
C12N15/02,
PC C12P21/02,C12P21/08/(C12N5/10,C12R1:91), (C12P21/08,C12R1:91),
PC C12N15/00,
PC C12N5/00,C12N15/00,(C12N5/00,C12R1:91)
CC
FH Key Location/Qualifiers
FT primer bind (1)..(18).
FEATURES
source
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAA 1748
DB 18 TTAATAAAAAAAAAAAAA 2
RESULT 554
AR264176
LOCUS 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 7 from patent US 6331612.
ACCESSION AR264176
VERSION AR264176.1 GI:28076276
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Celeste,A.J. and Murray,B.L.
TITLE Bone morphogenetic protein-16 (BMP-16) compositions
JOURNAL Patent: US 6331612-A 7 18-DEC-2001;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTCTGAGGGCGAGTGTC 1495
DB 1 CTGTGAGGGCGAGTGTC 17
RESULT 555
AR401428
LOCUS 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6623934.
ACCESSION AR401428
VERSION AR401428.1 GI:40148748
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Celeste,A.J. and Murray,B.L.
TITLE Bone morphogenetic protein-16 (BMP-16) antibodies
JOURNAL Patent: US 6623934-A 7 23-SEP-2003;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTCTGAGGGCGAGTGTC 1495
DB 1 CTGTGAGGGCGAGTGTC 17
RESULT 556
AX039283
LOCUS 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 21 from Patent WO0063359.
ACCESSION AX039283

/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1732 TTACAAAAAAAAAAAA 1748
DB 18 TTAATAAAAAAAAAAAAA 2
RESULT 554
AR264176
LOCUS 18 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 7 from patent US 6331612.
ACCESSION AR264176
VERSION AR264176.1 GI:28076276
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Celeste,A.J. and Murray,B.L.
TITLE Bone morphogenetic protein-16 (BMP-16) compositions
JOURNAL Patent: US 6331612-A 7 18-DEC-2001;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTCTGAGGGCGAGTGTC 1495
DB 1 CTGTGAGGGCGAGTGTC 17
RESULT 555
AR401428
LOCUS 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 7 from patent US 6623934.
ACCESSION AR401428
VERSION AR401428.1 GI:40148748
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Celeste,A.J. and Murray,B.L.
TITLE Bone morphogenetic protein-16 (BMP-16) antibodies
JOURNAL Patent: US 6623934-A 7 23-SEP-2003;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1479 CTCTGAGGGCGAGTGTC 1495
DB 1 CTGTGAGGGCGAGTGTC 17
RESULT 556
AX039283
LOCUS 19 bp DNA linear PAT 18-NOV-2000
DEFINITION Sequence 21 from Patent WO0063359.
ACCESSION AX039283

```
VERSION AX039283.1 GI:11229388
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Roes,J.T.
TITLE Gene expression in eukaryotic cells
JOURNAL Patent: WO 0063359-A 21 26-OCT-2000;
University College London (GB)
FEATURES
    source
        1..19
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="PCR PRIMER"
Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 19;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 765 CCCAGCGCGAGGTGAAG 781
Db 3 CCCGCGCGCGAGGTGAAG 19
RESULT 557
AR086109/c
LOCUS AR086109 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 3 from patent US 5985556.
ACCESSION AR086109
VERSION AR086109.1 GI:10012875
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kambara,H. and Okano,K.
TITLE DNA sequencing method and DNA sample preparation method
JOURNAL Patent: US 5985556-A 3 16-NOV-1999;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1749
Db 17 TGCAAAAA 1
RESULT 558
AR086110/c
LOCUS AR086110 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 4 from patent US 5985556.
ACCESSION AR086110
VERSION AR086110.1 GI:10012876
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kambara,H. and Okano,K.
TITLE DNA sequencing method and DNA sample preparation method
JOURNAL Patent: US 5985556-A 4 16-NOV-1999;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1749
Db 17 TGCAAAAA 1
RESULT 559
AR086111/c
LOCUS AR086111 20 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5985556.
ACCESSION AR086111
VERSION AR086111.1 GI:10012877
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kambara,H. and Okano,K.
TITLE DNA sequencing method and DNA sample preparation method
JOURNAL Patent: US 5985556-A 5 16-NOV-1999;
FEATURES
    source
        1..20
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 0.9%; Score 15.4; DB 1; Length 20;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAA 1751
Db 17 CGAAAAA 1
RESULT 560
E13187/c
LOCUS E13187 20 bp DNA linear PAT 27-APR-1998
DEFINITION Oligonucleotide.
ACCESSION E13187
VERSION E13187.1 GI:3251992
KEYWORDS JP 1997140400-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 20)
AUTHORS Okano,K. and Kambara,H.
TITLE DETERMINATION OF BASE SEQUENCE
JOURNAL Patent: JP 1997140400-A 1 03-JUN-1997;
COMMENT HITACHI LTD
OS None
OC Artificial sequences.
PN JP 1997140400-A/1
PD 03-JUN-1997
PF 13-SEP-1996 JP 1996242929
PR 18-SEP-1995 JP 95P 238141
PI OKANO KAZUNOBU, KANBARA HIDEKI
PC C12Q1/68,G01N27/447,G01N33/58//C12N15/09;
CC strandedness: Single;
CC topology: Linear;
FH Key
FT Location/Qualifiers
FT source 1..20
FT /organism='Artificial sequences'.
FEATURES
    source
        1..20
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"
```

Best Local Similarity 94.1%; Pred. No. 5.1e+02; Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	1733	TACAAAAA	1749		
DB	17	TGCAAAAA	1		
RESULT 561 E13188/c					
LOCUS	E13188	20 bp	DNA	linear	PAT 27-APR-1998
DEFINITION	Oligonucleotide.				
ACCESSION	E13188				
VERSION	E13188.1 GI:3251993				
KEYWORDS	JP 1997140400-A/2.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Okano,K. and Kanbara,H.				
TITLE	DETERMINATION OF BASE SEQUENCE				
JOURNAL	Patent: JP 1997140400-A 2 03-JUN-1997;				
HITACHI LTD					
COMMENT	OS None				
OC Artificial sequences.					
PN JP 1997140400-A/2					
PD 03-JUN-1997					
PF 13-SEP-1996 JP 1996242929					
PR 18-SEP-1995 JP 95P 238141					
PI OKANO KAZUNOBU, KANBARA HIDEKI					
PC C12Q1/68,G01N27/447,G01N33/58/C12N15/09;					
CC strandedness: Single;					
CC topology: Linear;					
FH Key Location/Qualifiers					
FT source 1..20 /organism='Artificial sequences'.					
Query Match	0.9%; Score 15.4; DB 1; Length 20;				
Best Local Similarity	94.1%; Pred. No. 5.1e+02;				
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY	1735	CAAAAAAAAA	1751		
DB	17	CGAAAAAAAA	1		
RESULT 563 E40060					
LOCUS	E40060	20 bp	DNA	linear	PAT 31-JAN-2002
DEFINITION	Drug containing anti-Pas antibody.				
ACCESSION	E40060				
VERSION	E40060.1 GI:18627176				
KEYWORDS	JP 2000169393-A/57.				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Serizawa,N., Haruyama,H., Takahashi,W., Yoshida,H., Ichikawa,K., Okuma,J., Otsuki,M., Shiraishi,A. and Yonehara,S.				
TITLE	Drug containing anti-Pas antibody				
JOURNAL	Patent: JP 2000169393-A 57 20-JUN-2000;				
SANKYO CO LTD					
COMMENT	OS Artificial Sequence				
PN JP 2000169393-A/57					
PD 20-JUN-2000					
PF 30-SEP-1999 JP 1999278301					
PR NOBUKI SERIZAWA,HIDEYUKI HARUYAMA,WATARU TAKAHASHI, PI HIROKO YOSHIDA, JUN OKUMA, MASAHIKO OTSUKI, AKTO SHIRAISHI, PI KIMIHISA ICHIKAWA,					
SHIN YONEHARA					
PC A61K39/395,A61K39/00,A61P1/16,A61P7/06,A61P9/00, PC A61P9/10,					
PC A61P13/12,A61P31/18,A61P37/06,C12N5/10,C12N15/02,C12N15/09, PC C12P21/08//					
CC C07K16/28,C12N5/00,C12N15/00,C12N15/00					
CC Ligonucleotide.					
FH Key Location/Qualifiers					
FT source 1..20 /organism='Artificial Sequence'.					
Query Match	0.9%; Score 15.4; DB 1; Length 20;				
Best Local Similarity	94.1%; Pred. No. 5.1e+02;				
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY	1733	TACAAAAA	1749		
DB	17	TGCAAAAA	1		
RESULT 562 E13189/c					
LOCUS	E13189	20 bp	DNA	linear	PAT 27-APR-1998
DEFINITION	Oligonucleotide.				
ACCESSION	E13189				
VERSION	E13189.1 GI:3251994				
KEYWORDS	JP 1997140400-A/3.				
SOURCE	unidentified				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Okano,K. and Kanbara,H.				
TITLE	DETERMINATION OF BASE SEQUENCE				
JOURNAL	Patent: JP 1997140400-A 3 03-JUN-1997;				
HITACHI LTD					
COMMENT	OS None				
OC Artificial sequences.					
PN JP 1997140400-A/3					
PD 03-JUN-1997					
PF 13-SEP-1996 JP 1996242929					
PR 18-SEP-1995 JP 95P 238141					
PI OKANO KAZUNOBU, KANBARA HIDEKI					
PC C12Q1/68,G01N27/447,G01N33/58/C12N15/09;					
CC strandedness: Single;					
CC topology: Linear;					
FH Key Location/Qualifiers					
FT source 1..20 /organism='Artificial sequences'.					
Query Match	0.9%; Score 15.4; DB 1; Length 20;				
Best Local Similarity	94.1%; Pred. No. 5.1e+02;				
Matches 16; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY					

CC		Key	Location/Qualifiers	
PH		source	1..20	
FT			/organism='Artificial Sequence'	
FT		Location/Qualifiers		
		1..20	/organism="synthetic construct"	
			/mol_type="genomic DNA"	
			/db_xref="taxon:32630"	
FEATURES				
source				
		Query Match	0.9%; Score 15.4; DB 1; Length 20;	
		Best Local Similarity	94.1%; Pred.No.5.1e+02;	
		Matches 16;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	21	TTAGGGGGGAAGAGGAA 37		
DB	3	TTTGGGGGGAAGAGGAA 19		
RESULT 566				
E40872/c				
LOCUS		20 bp	DNA	linear PAT 31-JAN-2002
DEFINITION		Humanized anti-Fas antibody.		
ACCESSION	E40872			
VERSION	E40872.1	GI:18627449		
KEYWORDS	JP 2000166574-A/61.			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			
REFERENCE	1 (bases 1 to 20)			
AUTHORS	Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.			
TITLE	Humanized anti-Fas antibody			
JOURNAL	Patent: JP 2000166574-A 61 20-JUN-2000;			
COMMENT	SANKYO CO LTD			
	OS Artificial Sequence			
	PN JP 2000166574-A/61			
	PD 20-JUN-2000			
	PF 29-SEP-1999 JP 1999275441			
	PR			
	PI NORUKI SERIZAWA, HIDEYUKI HARUYAMA, KAORI NAKAHARA, IKUKO TAMAKI			
	PC C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,			
	PC C07K16/18,			
	PC C12N1/21.C12N5/10,C12P21/08//(C12N1/21.C12R1:19).C12N15/00, PC			
	C12N5/00			
CC		Key	Location/Qualifiers	
PH		source	1..20	
FT			/organism='Artificial Sequence'	
FT		Location/Qualifiers		
		1..20	/organism="synthetic construct"	
			/mol_type="genomic DNA"	
			/db_xref="taxon:32630"	
FEATURES				
source				
		Query Match	0.9%; Score 15.4; DB 1; Length 20;	
		Best Local Similarity	94.1%; Pred.No.5.1e+02;	
		Matches 16;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	21	TTAGGGGGGAAGAGGAA 37		
DB	18	TTTTGGGGGGAAGAGGAA 2		
RESULT 567				
E43414				
LOCUS		20 bp	DNA	linear PAT 31-JAN-2002
DEFINITION		Humanized anti-Fas antibody.		
ACCESSION	E43414			
VERSION	E43414.1	GI:18627680		
KEYWORDS	JP 2000166573-A/57.			
SOURCE	synthetic construct			
ORGANISM	artificial sequences.			

```

REFERENCE 1 (bases 1 to 20)
AUTHORS Takahashi,W., Haruyama,H. and Serizawa,N.
TITLE Humanized anti-Fas antibody
JOURNAL Patent: JP 2000166573-A 57 20-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000166573-A/57
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275440
PR
PI WATARU TAKAHASHI,HIDEYUKI HARUYAMA,NOBUKI SERIZAWA PC
C12N15/09,A61K38/00,A61K39/00,A61K39/395,A61K39/00, PC
A61P43/00,
PC C07K16/28,C12N1/21,C12N5/10,C12N15/02,C12P21/08,
PC C12R1.91),
PC C12N15/00,A61K37/02,C12N5/00,C12N15/00
CC
CC
FH Key 1 Location/Qualifiers
FT source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 TTAGGGGGAGAGGAA 37
||| ||||| |||||
DB 3 TTGGGGGAGAGGAA 19
||| ||||| |||||

RESULT 568
E43418/c
LOCUS Humanized anti-Fas antibody. 20 bp DNA linear PAT 31-JAN-2002
DEFINITION
ACCESSION E43418
VERSION JP 2000166573-A/61.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Takahashi,W., Haruyama,H. and Serizawa,N.
TITLE Humanized anti-Fas antibody
JOURNAL Patent: JP 2000166573-A 61 20-JUN-2000;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2000166573-A/61
PD 20-JUN-2000
PF 29-SEP-1999 JP 1999275440
PR
PI WATARU TAKAHASHI,HIDEYUKI HARUYAMA,NOBUKI SERIZAWA PC
C12N15/09,A61K38/00,A61K39/00,A61K39/395,A61K39/00, PC
A61P43/00,
PC C07K16/28,C12N1/21,C12N5/10,C12N15/02,C12P21/08,
PC C12R1.91),
PC C12N15/00,A61K37/02,C12N5/00,C12N15/00
CC
CC
FH Key 1 Location/Qualifiers
FT source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 TTAGGGGGAGAGGAA 37
||| ||||| |||||
DB 3 TTGGGGGAGAGGAA 19
||| ||||| |||||

RESULT 569
E43418/c
LOCUS Humanized anti-Fas antibody. 20 bp DNA linear PAT 20-DEC-2002
DEFINITION
ACCESSION E43418
VERSION JP 2000166573-A/61.
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Takahashi,W., Haruyama,H., Nakahara,K. and Tamaki,I.
TITLE Drug containing humanized anti-Fas antibody
JOURNAL Patent: JP 2001342148-A 57 11-DEC-2001;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2001342148-A/57
PD 11-DEC-2001
PF 28-MAR-2001 JP 2001093106
PI NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO PI
TAMAKI
PC A61K39/395,A61K38/00,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
A61P13/12,
PC A61P19/02,A61P29/00,A61P37/00,A61P37/06,A61P37/08,A61P43/00,
PC C12N15/09,
PC A61K37/02,C12N15/00
CC Description of Artificial Sequence: Sequencing primer for a
CC DNA encoding
CC the heavy chain of a humanized anti-Fas antibody FH Key
CC Location/Qualifiers
FT source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 88.9%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
||||| ||||| |||||
DB 19 AAAAAAAAAAGAGAGAA 2
||||| ||||| |||||

RESULT 570
BD090597
LOCUS Drug containing humanized anti-Fas antibody. 20 bp DNA linear PAT 27-AUG-2002
DEFINITION
ACCESSION BD090597
VERSION BD090597.1 GI:22636207
KEYWORDS JP 2001342148-A/57.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 20)
AUTHORS Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
TITLE Drug containing humanized anti-Fas antibody
JOURNAL Patent: JP 2001342148-A 57 11-DEC-2001;
SANKYO CO LTD
COMMENT OS Artificial Sequence
PN JP 2001342148-A/57
PD 11-DEC-2001
PF 28-MAR-2001 JP 2001093106
PI NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO PI
TAMAKI
PC A61K39/395,A61K38/00,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
A61P13/12,
PC A61P19/02,A61P29/00,A61P37/00,A61P37/06,A61P37/08,A61P43/00,
PC C12N15/09,
PC A61K37/02,C12N15/00
CC Description of Artificial Sequence: Sequencing primer for a
CC DNA encoding
CC the heavy chain of a humanized anti-Fas antibody FH Key
CC Location/Qualifiers
FT source 1..20
/organism="synthetic construct"
/db_xref="taxon:32630"

```



```
Query Match          0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 TTAGGGGGGAGAGGAA 37
DB 3 TTTGGGGGAGAGGAA 19

RESULT 571
BD090601/c
LOCUS          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Drug containing humanized anti-Fas antibody.
ACCESSION    BD090601
VERSION      BD090601.1 GI:22636211
KEYWORDS     JP 2001342148-A/61.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Serizawa,N., Haruyama,H., Nakahara,K. and Tamaki,I.
TITLE       Drug containing humanized anti-Fas antibody
JOURNAL     Patent: JP 2001342148-A 61 11-DEC-2001;
           SANKYO CO LTD

COMMENT      OS Artificial Sequence
           PN JP 2001342148-A/61
           PD 11-DEC-2001
           PF 28-MAR-2001 JP 2001093106
           PI NOBUFUSA SERIZAWA,HIDEYUKI HARUYAMA,KAORI NAKAHARA,IKUKO PI
           TAMAKI
           PC A61K39/395,A61K38/00,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
           A61P13/12,
           PC A61P19/02,A61P29/00,A61P37/00,A61P37/06,A61P37/08,A61P43/00//
           PC C12N15/09,
           PC A61K37/02,C12N15/00
           CC Description of Artificial Sequence: Sequencing primer for a
           CC DNA encoding
           CC the heavy chain of a humanized anti-Fas antibody FH Key
           Location/Qualifiers
           FT source 1..20
           FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match          0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 TTAGGGGGGAGAGGAA 37
DB 3 TTTGGGGGAGAGGAA 19

RESULT 573
BD090710/c
LOCUS          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Drug containing humanized anti-Fas antibody.
ACCESSION    BD090710
VERSION      BD090710.1 GI:22636320
KEYWORDS     JP 2001342149-A/61.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Takahashi,W., Haruyama,H. and Serizawa,N.
TITLE       Drug containing humanized anti-Fas antibody
JOURNAL     Patent: JP 2001342149-A 61 11-DEC-2001;
           SANKYO CO LTD

COMMENT      OS Artificial Sequence
           PN JP 2001342149-A/61
           PD 11-DEC-2001
           PF 28-MAR-2001 JP 2001093243
           PI WATARU TAKAHASHI,HIDEYUKI HARUYAMA,NOBUFUSA SERIZAWA PC
           A61K39/395,A61K39/395,A61P1/16,A61P7/06,A61P9/00,A61P9/10, PC
           A61P13/12,
           PC A61P17/00,A61P31/14,A61P31/18,A61P31/20,A61P37/00,A61P37/06,
           PC A61P37/08,
           PC A61P43/00//C12N15/02,C12N15/00
           CC Description of Artificial Sequence: Sequencing primer for a
           CC DNA encoding
           CC the heavy chain of a humanized anti-Fas antibody FH Key
           Location/Qualifiers
           FT source 1..20
           FT /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..20
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match          0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 TTAGGGGGGAGAGGAA 37
DB 18 TTTGGGGGAGAGGAA 2

RESULT 572
BD090706
LOCUS          20 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION    Drug containing humanized anti-Fas antibody.
ACCESSION    BD090706
VERSION      BD090706.1 GI:22636316
KEYWORDS     JP 2001342149-A/57.
SOURCE       synthetic construct
ORGANISM     artificial sequences.
REFERENCE    1 (bases 1 to 20)
AUTHORS     Takahashi,W., Haruyama,H. and Serizawa,N.
TITLE       Drug containing humanized anti-Fas antibody
JOURNAL     Patent: JP 2001342149-A 57 11-DEC-2001;
           SANKYO CO LTD

COMMENT      OS Artificial Sequence
```

```
Db      18 TTGGGGGGAAGAGGAA 2
RESULT 574
AR183909/c
LOCUS      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION      Sequence 2 from patent US 6342376.
ACCESSION      AR183909
VERSION      AR183909.1 GI:20227878
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Kozian,D. and Reuner,B.
TITLE      Two-color differential display as a method for detecting regulated
genes
JOURNAL      Patent: US 6342376-A 2 29-JAN-2002;
FEATURES
source      Location/Qualifiers
1..17
/mol_type="unassigned DNA"

Query Match      0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAA
Db      16 BAAAAA

RESULT 575
AR429726/c
LOCUS      17 bp      DNA      linear      PAT 18-DEC-2003
DEFINITION      Sequence 2 from patent US 6645741.
ACCESSION      AR429726
VERSION      AR429726.1 GI:40190064
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 17)
AUTHORS      Kozian,D. and Reuner,B.
TITLE      Two-color differential display as a method for detecting regulated
genes
JOURNAL      Patent: US 6645741-A 2 11-NOV-2003;
FEATURES
source      Location/Qualifiers
1..17
/mol_type="genomic DNA"

Query Match      0.9%; Score 15.2; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAA
Db      16 BAAAAA

RESULT 576
AR066905/c
LOCUS      20 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 253 from patent US 5851760.
ACCESSION      AR066905
VERSION      AR066905.1 GI:5998127
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Evans,G.A. and Smith,M.W.

TITLE      Method for generation of sequence sampled maps of complex genomes
JOURNAL      Patent: US 5851760-A 253 22-DEC-1998;
FEATURES
source      Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      914 CAGAGTCAGCTGCATAGG 933
Db      20 CAGAAGGTGAGCTGGAAGG 1

RESULT 577
AR118884
LOCUS      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION      Sequence 10 from patent US 6150092.
ACCESSION      AR118884
VERSION      AR118884.1 GI:14100794
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
TITLE      Antisense nucleic acid compound targeted to VEGF
JOURNAL      Patent: US 6150092-A 10 21-NOV-2000;
FEATURES
source      Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1736 AAAAAA
Db      1 AAAAAA

RESULT 578
AR123336
LOCUS      20 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION      Sequence 2 from patent US 6169176.
ACCESSION      AR123336
VERSION      AR123336.1 GI:14108302
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 20)
AUTHORS      Bruice,T.C. and Dev,A.P.
TITLE      Deoxynucleic alkyl thiourea compounds and uses thereof
JOURNAL      Patent: US 6169176-A 2 02-JAN-2001;
FEATURES
source      Location/Qualifiers
1..20
/mol_type="unassigned DNA"

Query Match      0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1735 CAAAAA
Db      1 CAAAAA

RESULT 579
```

AR125322/c
LOCUS AR125322 20 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 22 from patent US 6177249.
ACCESSION AR125322
VERSION AR125322.1 GI:14111384
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 20)
TITLES Kwok,P.-Y. and Chen,X.
JOURNAL Method for nucleic acid analysis using fluorescence resonance
FEATURES energy transfer
Patent: US 6177249-A 22 23-JAN-2001;
Location/Qualifiers
1..20
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1729 AGTTTACAAAAA 1748
Db 20 ATTTTACAAAAA 1

RESULT 580
LOCUS BD267704 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Extracellular protease of Acremonium chrysogenum having CPC
acetylhydrolase activity, and use thereof in gene inactivation for
synthesizing deacetylated cepharosporin C and elevating
cepharosporin yield.
ACCESSION BD267704
VERSION BD267704.1 GI:33077472
KEYWORDS JP 2002541812-A/4.
SOURCE Acremonium chrysogenum
ORGANISM Acremonium chrysogenum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreales; Hypocreaceae; mitosporic
Hypocreaceae; Acremonium.
1 (bases 1 to 20)
Alvarez,J.V., Martin,S.G., Blanco,F.J.C., Garcia,S.C., Fierro,F.,
Fuente,J.L.B., Garcia,B.D. and Martin,J.F.M.
Extracellular protease of Acremonium chrysogenum having CPC
acetylhydrolase activity, and use thereof in gene inactivation for
synthesizing deacetylated cepharosporin C and elevating
cepharosporin yield
Patent: JP 2002541812-A 4 10-DEC-2002;
JOURNAL ANTIBIOTICS SAU
COMMENT OS Acremonium chrysogenum
PN JP 2002541812-A/4
PD 10-DEC-2002
PF 07-APR-2000 JP 2000611690
PR 09-APR-1999 ES P 9900731
PI JAVIER VELASCO ALVAREZ, SANTIAGO GUTIERREZ MARTIN, PI
FRANCISCO JAVIER CASQUEIRO BLANCO, SONIA CAMPOY GARCIA, PI
FRANCISCO FIERRO FIERRO, JOSE LUIS BARREDO FUENTE, BRUNO DIEZ PI
GARCIA,
PI JUAN FRANCISCO MARTIN MARTIN
PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12P35/06, PC
C12R1:645,
PC C12N15/00
CC Synthetic oligonucleotide corresponding to the 5' end of the
cshB gene of
CC Acremonium chrysogenum
CC Key Location/Qualifiers
FH Key 1..20
FT source /organism='Acremonium chrysogenum'.
FT Location/Qualifiers
1..20

FEATURES source

/organism="Acremonium chrysogenum"
/mol_type="genomic DNA"
/db_xref="taxon:5044"

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1462 TGTGGCTGCTGCTCTCTC 1481
Db 1 TGCCTGCTGCTACTCTCTC 20

RESULT 581
LOCUS E06099 20 bp DNA linear PAT 29-SEP-1997
DEFINITION Oligonucleotide specific to subtype Tr of Hepatitis C virus.
ACCESSION E06099
VERSION E06099.1 GI:2174286
KEYWORDS JP 1993337000-A/23.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Chayama,K. and Kumada,H.
TITLES METHOD FOR EXAMINING C TYPE HEPATITIS VIRUS AND PRIMER SET USED FOR
THE SAME
JOURNAL CHAYAMA KAZUAKI
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
OS Hepatitis C virus
PN JP 1993337000-A/23
PD 21-DEC-1993
PF 04-JUN-1992 JP 1992168226
PI CHAYAMA KAZUAKI, KUMADA HIROMITSU
PC C12Q1/68, C12N15/10, C12N15/11, C12Q1/70;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No.
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1000 GGCTGCGGAGAGATGTGGT 1019
Db 1 GTCTGCGGAGATGATTGGT 20

RESULT 582
LOCUS E59334/c 20 bp DNA linear PAT 31-JAN-2002
DEFINITION Method for purifying oligonucleotide.
ACCESSION E59334
VERSION E59334.1 GI:18622511
KEYWORDS JP 2000342265-A/15.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 20)
AUTHORS Hirose,K. and Yoshida,T.
TITLES Method for purifying oligonucleotide
JOURNAL Patent: JP 2000342265-A 15 12-DEC-2000;
TOAGOSEI CHEM IND CO LTD
COMMENT OS Artificial Sequence
PN JP 2000342265-A/15

```
PD 12-DEC-2000
PF 02-JUN-1999 JP 1999154974
PR
PI KUNIHICO HIROSE,TADAO YOSHIDA
PC C12N15/09,B01D15/08,C12N15/00
CC
CH
FT Key Location/Qualifiers
FT source 1..20
FT /organism='Artificial Sequence'.
FEATURES
    source
        1..20
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 583
AR232303
LOCUS AR232303 20 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 93 from patent US 6455307.
ACCESSION AR232303
VERSION AR232303.1 GI:27274295
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 20)
    McKay,R., Freier,S.M. and Wyatt,J.
    TITLE Antisense modulation of casein kinase 2-alpha prime expression
    JOURNAL Patent: US 6455307-A 93 24-SEP-2002;
    FEATURES
        source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 857 CTGCAGGAAGAGGAGGAGGA 876
Db 1 CTGCAGGAGGAGGAGGAGGA 20
RESULT 584
AR294828
LOCUS AR294828 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 6563 from patent US 6537751.
ACCESSION AR294828
VERSION AR294828.1 GI:31682112
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 20)
    Cohen,D., Chumakov,I. and Blumenfeld,M.
    AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
    TITLE Biallelic markers for use in constructing a high density
    disequilibrium map of the human genome
    JOURNAL Patent: US 6537751-A 6563 25-MAR-2003;
    FEATURES
        source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1014 TGTGTTGGGATGGGGCTG 1033
Db 1 TCTGATTTGGGATGGGGCTG 20
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1014 TGTGTTGGGATGGGGCTG 1033
Db 1 TCTGATTTGGGATGGGGCTG 20
RESULT 585
AR298452
LOCUS AR298452 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 10187 from patent US 6537751.
ACCESSION AR298452
VERSION AR298452.1 GI:31685736
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 20)
    Cohen,D., Chumakov,I. and Blumenfeld,M.
    AUTHORS Cohen,D., Chumakov,I. and Blumenfeld,M.
    TITLE Biallelic markers for use in constructing a high density
    disequilibrium map of the human genome
    JOURNAL Patent: US 6537751-A 10187 25-MAR-2003;
    FEATURES
        source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 564 CCTGAAGCCAAATCCAGCCT 583
Db 20 CCTGAAGCCAAACACACCCCT 1
RESULT 586
AR360403
LOCUS AR360403 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 18 from patent US 6596489.
ACCESSION AR360403
VERSION AR360403.1 GI:33767433
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 20)
    Dattagupta,N. and Tseng,T.-C.
    AUTHORS Dattagupta,N. and Tseng,T.-C.
    TITLE Methods and compositions for analyzing nucleotide sequence
    mismatches using RNase H
    JOURNAL Patent: US 6596489-A 18 22-JUL-2003;
    FEATURES
        source
            1..20
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.9%; Score 15.2; DB 1; Length 20;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAATTATAAAAAA 20
RESULT 587
AR360430
LOCUS AR360430 20 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 18 from patent US 6596490.
ACCESSION AR360430
VERSION AR360430.1 GI:33767460
KEYWORDS
```



```
AX591245
LOCUS AX591245 20 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 6 from Patent WO02085940.
ACCESSION AX591245
VERSION AX591245.1 GI:27949717
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Escary,J.L.
TITLE New polynucleotides and polypeptides of the erythropoietin gene
JOURNAL Patent: WO 02085940-A 6 31-OCT-2002;
GenOdysee (FR)
FEATURES
source
1..20 Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1644 GATCACTCTCCCTGACATCC 1663
DB 1 GATCATTCTCCCTTCATCC 20
RESULT 593
BD102552/c
LOCUS BD102552 20 bp DNA linear PAT 27-AUG-2002
DEFINITION TLR/CD14 binding inhibitor.
ACCESSION BD102552
VERSION BD102552.1 GI:22648126
KEYWORDS WO 0172993-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Furusako,S., Mori,S., Shirakawa,K. and Takahashi,T.
TITLE TLR/CD14 binding inhibitor
JOURNAL Patent: WO 0172993-A 5 04-OCT-2001;
MOCHIDA PHARMACEUTICAL CO LTD,SHOJI FURUSAKO, SADA0 MORI, KAMON
SHIRAKAWA, TOMOHIRO TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0172993-A/5
PD 04-OCT-2001
PF 02-APR-2001 WO 2001JP002869
PR 31-MAR-2000 JP 00P 99617,22-NOV-2000 JP 00P 356719 PR
28-MAR-2001 US 09/806158
PI SHOJI FURUSAKO, SADA0 MORI, KAMON SHIRAKAWA, TOMOHIRO TAKAHASHI
PC CL2N15/00, C07K14/705, C07K16/28, A61K45/00, A61P31/04,
A61P38/02,
PC A61P39/395, A61P43/00, G01N33/15, G01N33/50, G01N33/53, G01N33/577
CC TLR/CD14 binding inhibitor
FH Key Location/Qualifiers
FT source 1..20
/organism="Artificial Sequence".
FEATURES
source
1..20 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1687 TCGTGTCTTCTCTTCTTCTCA 1706
DB 20 TGGTGTCTTCTCTTCTTCTCGA 1
RESULT 594
BD196041
LOCUS BD196041 20 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense oligonucleotide sequences as inhibitors of
microorganisms.
ACCESSION BD196041
VERSION BD196041.1 GI:33005811
KEYWORDS JP 2002514093-A/72.
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
REFERENCE
1 (bases 1 to 20)
AUTHORS Wright,J.A., Young,A.H. and Dugourd,D.
TITLE Antisense oligonucleotide sequences as inhibitors of microorganisms
JOURNAL Patent: JP 2002514093-A 72 14-MAY-2002;
GENESENSE TECHNOLOGIES INC
COMMENT OS Escherichia coli
PN JP 2002514093-A/72
PD 14-MAY-2002
PF 10-JUL-1998 JP 1999507930
PR 10-JUL-1997 US 60/052160
PI JIM A WRIGHT, AIPING H YOUNG, DOMINIQUE DUGOURD PC
C12N15/11, C12N15/31
CC Antisense oligonucleotide sequences as inhibitors of CC
microorganisms
FH Key Location/Qualifiers
FT source 1..20
/organism="Escherichia coli".
FEATURES
source
1..20 Location/Qualifiers
/organism="Escherichia coli"
/mol_type="genomic DNA"
/db_xref="taxon:562"
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1204 CGGATCCTGCGGCTATGGG 1223
DB 1 CGGATCAAACGGCTATGGG 20
RESULT 595
AR029402/c
LOCUS AR029402 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5859233.
ACCESSION AR029402
VERSION AR029402.1 GI:5941375
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
Nelson,J.S. and Schultz,R.G.
TITLE Synthesis for synthesis of oligonucleotide N3-P5 phosphoramidates
JOURNAL Patent: US 5859233-A 3 12-JAN-1999;
FEATURES
source
1..15 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1
```

RESULT 596
LOCUS AR029403 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5859233.
ACCESSION AR029403
VERSION AR029403.1 GI:5941376
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
Nelson,J.S. and Schultz,R.G.
TITLE Synthesis for synthesis of oligonucleotide N3-P5 phosphoramidates
JOURNAL Patent: US 5859233-A 4 12-JAN-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 597
LOCUS AR034895 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 10 from patent US 5869643.
ACCESSION AR034895
VERSION AR034895.1 GI:5950500
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a
tightly packed bed
JOURNAL Patent: US 5869643-A 10 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 598
LOCUS AR034898 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5869643.
ACCESSION AR034898
VERSION AR034898.1 GI:5950503
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Chatelain,F. and Kumarev,V.
TITLE Process for preparing polynucleotides on a solid support in a

tightly packed bed
JOURNAL Patent: US 5869643-A 16 09-FEB-1999;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 599
LOCUS AR048768 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 2 from patent US 5821354.
ACCESSION AR048768
VERSION AR048768.1 GI:5971111
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Leclerc,G. and Martel,R.
TITLE Radiolabeled DNA oligonucleotide and method of preparation
JOURNAL Patent: US 5821354-A 2 13-OCT-1998;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 600
LOCUS AR049970 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5824793.
ACCESSION AR049970
VERSION AR049970.1 GI:5971962
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
Nelson,J.S. and Schultz,R.G.
TITLE Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
JOURNAL Patent: US 5824793-A 3 20-OCT-1998;
FEATURES Location/Qualifiers
source 1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

```
RESULT 601
LOCUS AR049971 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5824793.
ACCESSION AR049971
VERSION AR049971.1 GI:5971963
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Hirschbein,B.L., Fearon,K.L., Gryaznov,S.M., McCurdy,S.N.,
Nelson,J.S. and Schultz,R.G.
TITLE Solid phase synthesis of oligonucleotide N3'-P5' phosphoramidates
JOURNAL Patent: US 5824793-A 4 20-OCT-1998;
FEATURES
Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15
RESULT 602
LOCUS AR056157 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 361 from patent US 5837542.
ACCESSION AR056157
VERSION AR056157.1 GI:5981734
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 361 17-NOV-1998;
FEATURES
Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15
RESULT 603
LOCUS AR056158 15 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 362 from patent US 5837542.
ACCESSION AR056158
VERSION AR056158.1 GI:5981735
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 362 17-NOV-1998;
FEATURES
Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15
RESULT 604
LOCUS AR080676 15 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 5 from patent US 5968822.
ACCESSION AR080676
VERSION AR080676.1 GI:10007406
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Pecker,I., Vlodevsky,I. and Feinstein,E.
TITLE Polynucleotide encoding a polypeptide having heparanase activity
and expression of same in transduced cells
JOURNAL Patent: US 5968822-A 5 19-OCT-1999;
FEATURES
Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15
RESULT 605
LOCUS AR084516 15 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 5 from patent US 5981185.
ACCESSION AR084516
VERSION AR084516.1 GI:10011287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 5 09-NOV-1999;
FEATURES
Location/Qualifiers
source 1..15
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15
RESULT 606
LOCUS AR084518
```


Query Match	0.9%; Score 15; DB 1; Length 15;	
Best Local Similarity	100.0%; Pred. No. 4.1e+02;	
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1736 AAAAAAAAAAAAAA 1750	
Db	15 AAAAAAAAAAAAAA 1	
RESULT 609		
ARL13915/c		
LOCUS	ARL13915 15 bp DNA linear PAT 16-MAY-2001	
DEFINITION	Sequence 361 from patent US 6132967.	
ACCESSION	ARL13915	
VERSION	ARL13915.1 GI:14094237	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)	
JOURNAL	Patent: US 6132967-A 361 17-OCT-2000;	
FEATURES	Location/Qualifiers	
source	1..15 /organism="unknown" /mol_type="unassigned DNA"	
Query Match	0.9%; Score 15; DB 1; Length 15;	
Best Local Similarity	100.0%; Pred. No. 4.1e+02;	
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1736 AAAAAAAAAAAAAA 1750	
Db	15 AAAAAAAAAAAAAA 1	
RESULT 610		
ARL13916/c		
LOCUS	ARL13916 15 bp DNA linear PAT 16-MAY-2001	
DEFINITION	Sequence 362 from patent US 6132967.	
ACCESSION	ARL13916	
VERSION	ARL13916.1 GI:14094238	
KEYWORDS		
SOURCE	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 15) Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.	
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)	
JOURNAL	Patent: US 6132967-A 362 17-OCT-2000;	
FEATURES	Location/Qualifiers	
source	1..15 /organism="unknown" /mol_type="unassigned DNA"	
Query Match	0.9%; Score 15; DB 1; Length 15;	
Best Local Similarity	100.0%; Pred. No. 4.1e+02;	
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1736 AAAAAAAAAAAAAA 1750	
Db	15 AAAAAAAAAAAAAA 1	
RESULT 611		
ARL170375		
LOCUS	ARL170375 15 bp DNA linear PAT 17-DEC-2001	
DEFINITION	Sequence 1 from patent US 6291438.	

```
ACCESSION   AR170375.1  GI:17908334
VERSION     AR170375.1
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Wang,J.H.
TITLE       Antiviral anticancer poly-substituted phenyl derivatized
            oligoribonucleotides and methods for their use
JOURNAL     Patent: US 6291438-A 1 18-SEP-2001;
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 612
E08522/c
LOCUS       E08522
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
TITLE       S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
JOURNAL     Patent: JP 1994335389-A 7 06-DEC-1994;
COMMENT     KAGOME CO LTD
            OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993  JP 1993126286
            PI   TEI ITSURU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key
            FT   Location/Qualifiers
            FT   source
            1..15
            /organism='Artificial sequences'.

LOCUS       E08522
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
TITLE       S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
JOURNAL     Patent: JP 1994335389-A 7 06-DEC-1994;
COMMENT     KAGOME CO LTD
            OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993  JP 1993126286
            PI   TEI ITSURU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key
            FT   Location/Qualifiers
            FT   source
            1..15
            /organism='Artificial sequences'.

LOCUS       E12591/c
DEFINITION  PRIMER.
ACCESSION   E12591
VERSION     E12591.1  GI:3251423
KEYWORDS    JP 1997028381-A/8.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Tei,I., Minami,K. and Takagi,M.
TITLE       S-RIBONUCLEASE GENE AND PROMOTER SEQUENCE
JOURNAL     Patent: JP 1997028381-A 8 04-FEB-1997;
COMMENT     TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
            OS   None
            OC   Artificial sequences.
            PN   JP 1997028381-A/8
            PD   04-FEB-1997
            PF   24-JUL-1995  JP 1995187557
            PI   TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key
            FT   Location/Qualifiers
            FT   source
            1..15
            /organism='Artificial sequences'.

FEATURES    source
            1..15
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 614
I29068
LOCUS       I29068
DEFINITION  Sequence 6 from patent US 5576427.
ACCESSION   I29068
VERSION     I29068.1  GI:1819859
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Cook,P.D., Delecki,D.J. and Guinasso,C.
TITLE       Acyclic nucleoside analogs and oligonucleotide sequences containing
            them
JOURNAL     Patent: US 5576427-A 6 19-NOV-1996;
FEATURES    Location/Qualifiers
            source
            1..15
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 613
E08522/c
LOCUS       E08522
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
TITLE       S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
JOURNAL     Patent: JP 1994335389-A 7 06-DEC-1994;
COMMENT     KAGOME CO LTD
            OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993  JP 1993126286
            PI   TEI ITSURU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key
            FT   Location/Qualifiers
            FT   source
            1..15
            /organism='Artificial sequences'.

LOCUS       E08522
DEFINITION  PCR primer.
ACCESSION   E08522
VERSION     E08522.1  GI:2176637
KEYWORDS    JP 1994335389-A/7.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Tei,I., Nakada,K., Ito,T., Horiuchi,H., Ota,A., Takagi,M.,
            Tsubura,H., Tanaka,H. and Ishiguro,Y.
TITLE       S-RIBONUCLEASE SPECIFIC TO STYLE AND DNA SEQUENCE CODING THEREFOR
JOURNAL     Patent: JP 1994335389-A 7 06-DEC-1994;
COMMENT     KAGOME CO LTD
            OS   None
            OC   Artificial sequences.
            PN   JP 1994335389-A/7
            PD   06-DEC-1994
            PF   27-MAY-1993  JP 1993126286
            PI   TEI ITSURU, NAKADA KENGO, ITO TORU, HORIUCHI HIROYUKI, PI
            OTA AKINORI,
            PI   TAKAGI MASAMICHI, TSUBURA HIROKAZU, TANAKA HIROSHI, PI
            ISHIGURO YUKIO
            PC   C12N9/22,C12N15/52;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key
            FT   Location/Qualifiers
            FT   source
            1..15
            /organism='Artificial sequences'.

LOCUS       E12591/c
DEFINITION  PRIMER.
ACCESSION   E12591
VERSION     E12591.1  GI:3251423
KEYWORDS    JP 1997028381-A/8.
SOURCE      unidentified
ORGANISM    unclassified.
REFERENCE   1 (bases 1 to 15)
AUTHORS     Tei,I., Minami,K. and Takagi,M.
TITLE       S-RIBONUCLEASE GENE AND PROMOTER SEQUENCE
JOURNAL     Patent: JP 1997028381-A 8 04-FEB-1997;
COMMENT     TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI
            OS   None
            OC   Artificial sequences.
            PN   JP 1997028381-A/8
            PD   04-FEB-1997
            PF   24-JUL-1995  JP 1995187557
            PI   TEI ITSUKIYON, MINAMI KOUKICHI, TAKAGI MASAMICHI PC
            C12N15/09,C07H21/04,C12N1/21//A01H1/00,C12N5/10,C12N9/22, PC
            (C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Single;
            CC   topology: Linear;
            CC   hypothetical: No;
            FH   Key
            FT   Location/Qualifiers
            FT   source
            1..15
            /organism='Artificial sequences'.

FEATURES    source
            1..15
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 15

RESULT 613
```

```
RESULT 615
I38641/c
LOCUS I38641 15 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 1 from patent US 5614617.
ACCESSION I38641
VERSION I38641.1 GI:2084695
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook,P.D. and Sanghvi,Y.S.
TITLE Nuclease resistant, pyrimidine modified oligonucleotides that
detect and modulate gene expression
JOURNAL Patent: US 5614617-A 1 25-MAR-1997;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 616
AR200476/c
LOCUS AR200476 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 19 from patent US 6357163.
ACCESSION AR200476
VERSION AR200476.1 GI:20251364
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical
procedures
JOURNAL Patent: US 6357163-A 19 19-MAR-2002;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 617
AR200477/c
LOCUS AR200477 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 20 from patent US 6357163.
ACCESSION AR200477
VERSION AR200477.1 GI:20251365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical
procedures
JOURNAL Patent: US 6357163-A 20 19-MAR-2002;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 618
AR222461/c
LOCUS AR222461 15 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 21 from patent US 6429300.
ACCESSION AR222461
VERSION AR222461.1 GI:23329992
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Kurz,M., Lohse,P. and Wagner,R.
TITLE Peptide acceptor ligation methods
JOURNAL Patent: US 6429300-A 21 06-AUG-2002;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 619
AR266630/c
LOCUS AR266630 15 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 68 from patent US 6495319.
ACCESSION AR266630
VERSION AR266630.1 GI:29695694
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 68 17-DEC-2002;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 620
AR371280/c
LOCUS AR371280 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 20 from patent US 6357163.
ACCESSION AR371280
VERSION AR371280.1 GI:20251365
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE Use of nucleic acid analogues in diagnostics and analytical
procedures
JOURNAL Patent: US 6357163-A 20 19-MAR-2002;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
```

```
LOCUS       AR371280               15 bp      DNA              linear      PAT 12-SEP-2003
DEFINITION   Sequence 17 from patent US 6395474.
ACCESSION    AR371280
VERSION      AR371280.1  GI:34608212
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE       Peptide nucleic acids
JOURNAL     Patent: US 6395474-A 17 28-MAY-2002;
            Location/Qualifiers
FEATURES             1..15
                     /organism="unknown"
                     /mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 621
LOCUS       AR371281               15 bp      DNA              linear      PAT 12-SEP-2003
DEFINITION   Sequence 18 from patent US 6395474.
ACCESSION    AR371281
VERSION      AR371281.1  GI:34608213
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Buchardt,O., Egholm,M., Nielsen,P.E. and Berg,R.H.
TITLE       Peptide nucleic acids
JOURNAL     Patent: US 6395474-A 18 28-MAY-2002;
            Location/Qualifiers
FEATURES             1..15
                     /organism="unknown"
                     /mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 622
LOCUS       AR410213               15 bp      DNA              linear      PAT 18-DEC-2003
DEFINITION   Sequence 9 from patent US 6635452.
ACCESSION    AR410213
VERSION      AR410213.1  GI:40161460
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS     Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE       Releasable nonvolatile mass label molecules
JOURNAL     Patent: US 6635452-A 9 21-OCT-2003;
            Location/Qualifiers
FEATURES             1..15
                     /organism="unknown"
                     /mol_type="genomic DNA"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 15

RESULT 623
LOCUS       AR410213/c             15 bp      DNA              linear      PAT 16-SEP-2000
DEFINITION   Sequence 4 from Patent WO0028046.
ACCESSION    AR410213/c
VERSION      AR410213/c.1  GI:10187502
KEYWORDS     .
SOURCE       synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE    1
AUTHORS     Marraccini,P. and Rogers,J.
TITLE       Coffea arabica mannanase
JOURNAL     Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
            Location/Qualifiers
FEATURES             1..15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHÈSE"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 624
LOCUS       AX026066/c             15 bp      DNA              linear      PAT 16-SEP-2000
DEFINITION   Sequence 4 from Patent WO0028046.
ACCESSION    AX026066
VERSION      AX026066.1  GI:10187502
KEYWORDS     .
SOURCE       synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE    1
AUTHORS     Marraccini,P. and Rogers,J.
TITLE       Coffea arabica mannanase
JOURNAL     Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
            Location/Qualifiers
FEATURES             1..15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHÈSE"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 625
LOCUS       AX026066/c             15 bp      DNA              linear      PAT 16-SEP-2000
DEFINITION   Sequence 4 from Patent WO0028046.
ACCESSION    AX026066
VERSION      AX026066.1  GI:10187502
KEYWORDS     .
SOURCE       synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE    1
AUTHORS     Marraccini,P. and Rogers,J.
TITLE       Coffea arabica mannanase
JOURNAL     Patent: WO 0028046-A 4 18-MAY-2000;
            NESTLE SA (CH) ; MARRACCINI PIERRE (FR) ; ROGERS JOHN (FR)
            Location/Qualifiers
FEATURES             1..15
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="OLIGONUCLEOTIDE DE SYNTHÈSE"

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 625
```

AX048407/c
LOCUS AX048407 15 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 6 from Patent WO0071747.
ACCESSION AX048407
VERSION AX048407.1 GI:12222571
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and production and use of the same
JOURNAL Patent: WO 0071747-A 6 30-NOV-2000;
Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
source 1. .15
misc_structure 1 /organism="synthetic construct"
misc_feature 15 /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Region A"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 626
AX106973
LOCUS AX106973 15 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 26 from Patent WO0125442.
ACCESSION AX106973
VERSION AX106973.1 GI:13922522
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Blanco,D.L., bernad Miana,A., dominguez Lopez,O. and garcia Diaz,M.
TITLE Dna polymerase lambda and uses thereof
JOURNAL Patent: WO 0125442-A 26 12-APR-2001;
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS (ES)
FEATURES
source 1. .15
misc_structure 1 /organism="synthetic construct"
misc_feature 15 /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligo dA"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 627
AX127272/c
LOCUS AX127272 15 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 3 from Patent EP111068.
ACCESSION AX127272
VERSION AX127272.1 GI:14133346
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1

AUTHORS Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
TITLE Branched compound for use in nucleic acid detection and analysis reactions
JOURNAL Patent: EP 1111068-A 3 27-JUN-2001;
LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES
source 1. .15
misc_structure 1 /organism="synthetic construct"
misc_feature 15 /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="(NH2-C6-ttt)2-branch-"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 628
AX127273/c
LOCUS AX127273 15 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 4 from Patent EP1111068.
ACCESSION AX127273
VERSION AX127273.1 GI:14133347
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Schmidt,W., Hiller,R., Huber,M. and Mueller,M.
TITLE Branched compound for use in nucleic acid detection and analysis reactions
JOURNAL Patent: EP 1111068-A 4 27-JUN-2001;
LION Bioscience AG (DE) ; VBC Genomics GmbH (AT)
FEATURES
source 1. .15
misc_structure 1 /organism="synthetic construct"
misc_feature 15 /mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="(dt-COOH)2-branch-"
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 629
AX180140/c
LOCUS AX180140 15 bp DNA linear PAT 06-AUG-2001
DEFINITION Sequence 3 from Patent WO0146464.
ACCESSION AX180140
VERSION AX180140.1 GI:15132181
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Huber,M., Schmidt,W., Mueller,M. and Hiller,R.

TITLE Branched compound for use in nucleic acid detection and analysis
reactions

JOURNAL Patent: WO 0146464-A 3 28-JUN-2001;
LION Bioscience AG (DE)

FEATURES Location/Qualifiers
source

1. .15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="stem of branched oligonucleotide - base 1
modified-Modification is (NH2-C6-TTT)2-branch-"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 630

AX180141/c 15 bp DNA linear PAT 06-AUG-2001

LOCUS Sequence 4 from Patent WO0146464.

DEFINITION AX180141

ACCESSION AX180141

VERSION AX180141.1 GI:15132182

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Huber, M., Schmidt, W., Mueller, M. and Hiller, R.

TITLE Branched compound for use in nucleic acid detection and analysis

reactions

JOURNAL Patent: WO 0146464-A 4 28-JUN-2001;
LION Bioscience AG (DE)

FEATURES Location/Qualifiers
source

1. .15
/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="stem of branched oligonucleotide - base 1
modified-Modification is (dT-COOH)2-branch-"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 631

AX429224/c 15 bp DNA linear PAT 21-JUN-2002

LOCUS Sequence 1 from Patent EP1201765.

DEFINITION AX429224

ACCESSION AX429224

VERSION AX429224.1 GI:21540537

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Schubart, D., Habenberger, P., Stein-Gerlach, M. and Bevec, D.

TITLE Cellular kinases involved in cytomegalovirus infection and their

inhibition

JOURNAL Patent: EP 1201765-A 1 02-MAY-2002;

Axxima Pharmaceuticals Aktiengesellschaft (DE)

FEATURES Location/Qualifiers
source

1. .15
/organism="synthetic construct"

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="N/A"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 632

AX525141 15 bp DNA linear PAT 21-NOV-2002

LOCUS Sequence 1 from Patent WO02066675.

DEFINITION AX525141

ACCESSION AX525141

VERSION AX525141.1 GI:25170126

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Kahmann, S. and Mueller, O.

TITLE Methods for detecting mutations

JOURNAL Patent: WO 02066675-A 1 29-AUG-2002;

Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)

FEATURES Location/Qualifiers
source

1. .15
/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="lys-Biotin"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 633

AX525143 15 bp DNA linear PAT 21-NOV-2002

LOCUS Sequence 3 from Patent WO02066675.

DEFINITION AX525143

ACCESSION AX525143

VERSION AX525143.1 GI:25170128

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Kahmann, S. and Mueller, O.

TITLE Methods for detecting mutations

JOURNAL Patent: WO 02066675-A 3 29-AUG-2002;

Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)

FEATURES Location/Qualifiers
source

1. .15
/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="lys-Digoxigenin"

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

```

RESULT 634
AX633197/c
LOCUS
DEFINITION Sequence 336 from Patent EP1260586.
ACCESSION AX633197
VERSION AX633197.1 GI:28468811
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match
    Best Local Similarity 100.0%; Score 15; DB 1; Length 15;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 635
AX633199/c
LOCUS
DEFINITION Sequence 338 from Patent EP1260586.
ACCESSION AX633199
VERSION AX633199.1 GI:28468813
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match
    Best Local Similarity 100.0%; Score 15; DB 1; Length 15;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 636
AX633197/c
LOCUS
DEFINITION Sequence 336 from Patent EP1260586.
ACCESSION AX633197
VERSION AX633197.1 GI:28468811
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match
    Best Local Similarity 100.0%; Score 15; DB 1; Length 15;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 637
AX711176
LOCUS
DEFINITION Sequence 476 from Patent EP1288296.
ACCESSION AX711176
VERSION AX711176.1 GI:29787557
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
    Query Match
    Best Local Similarity 100.0%; Score 15; DB 1; Length 15;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 638
BD074424/c
LOCUS
DEFINITION Polynucleotide encoding polypeptide having heparanase activity and
ACCESSION BD074424
VERSION BD074424.1 GI:22620027
KEYWORDS
SOURCE
ORGANISM

```

```
unclassified.
1 (bases 1 to 15)
Pecker,I., Vlodavsky,I. and Elena,F.
Polynucleotide encoding polypeptide having heparanase activity and
expression of the polypeptide in induced cell
Patent: JP 2001514855-A 5 18-SEP-2001;
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
& DEVELOPMENT LTD
OS Nucleic acid
PN JP 2001514855-A/5
PD 18-SEP-2001
PF 31-AUG-1998 JP 2000508806
PR 02-SEP-1997 US 08/922170, 02-JUL-1998 US 09/109386 PI
IRIS PECKER, ISRAEL VLODAVSKY, FEINSTEIN ELENA
PC C12N15/09, A61K38/00, A61P9/10, A61P17/00, A61P29/00, A61P35/00, PC
A61P37/00,
PC A61P43/00, C12N5/10, C12N9/24, C12Q1/68, G01N33/15, G01N33/50// PC
A61K39/395,
PC A61K39/395, C12N15/00, A61K37/02, C12N5/00
CC Polynucleotide encoding polypeptide having
heparanase activity
CC and
CC expression of the polypeptide in induced cell FH Key
FT Location/Qualifiers
FT 1. .15
/organism='Nucleic acid'.
FEATURES
source
1. .15
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 639
BD084687/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 15)
AUTHORS
Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE
Releasable nonvolatile mass-label molecules
JOURNAL
GENTRACE SYSTEMS INC
COMMENT
OS Artificial Sequence
PN JP 2001524808-A/5
PD 04-DEC-2001
PF 10-DEC-1997 JP 1998526924
PR 10-DEC-1996 US 60/033037, 16-MAY-1997 US 60/046719 PI
JOSEPH A MONFORTE, CHRISTOPHER H BECKER, DANIEL J POLLART, PI
THOMAS A SHALER
PC C12Q1/68, G01N15/06, G01N33/53, G01N33/542, C12P19/34, C12M1/00, PC
B01D59/44,
PC H01J49/00, C07H21/04, C07K15/26, C07K15/28
CC Description of Artificial Sequence: oligo dt15 primer FH Key
FT source
FT 1. .15
/organism='Artificial Sequence'.
FEATURES
source
1. .15
/organism='synthetic construct'

unclassified.
1 (bases 1 to 15)
Pecker,I., Vlodavsky,I. and Elena,F.
Polynucleotide encoding polypeptide having heparanase activity and
expression of the polypeptide in induced cell
Patent: JP 2001514855-A 5 18-SEP-2001;
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
& DEVELOPMENT LTD
OS Nucleic acid
PN JP 2001514855-A/5
PD 18-SEP-2001
PF 31-AUG-1998 JP 2000508806
PR 02-SEP-1997 US 08/922170, 02-JUL-1998 US 09/109386 PI
IRIS PECKER, ISRAEL VLODAVSKY, FEINSTEIN ELENA
PC C12N15/09, A61K38/00, A61P9/10, A61P17/00, A61P29/00, A61P35/00, PC
A61P37/00,
PC A61P43/00, C12N5/10, C12N9/24, C12Q1/68, G01N33/15, G01N33/50// PC
A61K39/395,
PC A61K39/395, C12N15/00, A61K37/02, C12N5/00
CC Polynucleotide encoding polypeptide having
heparanase activity
CC and
CC expression of the polypeptide in induced cell FH Key
FT Location/Qualifiers
FT 1. .15
/organism='Nucleic acid'.
FEATURES
source
1. .15
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 639
BD084687/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 15)
AUTHORS
Monforte,J.A., Becker,C.H., Pollart,D.J. and Shaler,T.A.
TITLE
Releasable nonvolatile mass-label molecules
JOURNAL
GENTRACE SYSTEMS INC
COMMENT
OS Artificial Sequence
PN JP 2001524808-A/5
PD 04-DEC-2001
PF 10-DEC-1997 JP 1998526924
PR 10-DEC-1996 US 60/033037, 16-MAY-1997 US 60/046719 PI
JOSEPH A MONFORTE, CHRISTOPHER H BECKER, DANIEL J POLLART, PI
THOMAS A SHALER
PC C12Q1/68, G01N15/06, G01N33/53, G01N33/542, C12P19/34, C12M1/00, PC
B01D59/44,
PC H01J49/00, C07H21/04, C07K15/26, C07K15/28
CC Description of Artificial Sequence: oligo dt15 primer FH Key
FT source
FT 1. .15
/organism='Artificial Sequence'.
FEATURES
source
1. .15
/organism='synthetic construct'

unclassified.
1 (bases 1 to 15)
Pecker,I., Vlodavsky,I. and Elena,F.
Polynucleotide encoding polypeptide having heparanase activity and
expression of the polypeptide in induced cell
Patent: JP 2001514855-A 5 18-SEP-2001;
INSIGHT STRATEGY & MARKETING LTD, HADASIT MEDICAL RESEARCH SERVICES
& DEVELOPMENT LTD
OS Nucleic acid
PN JP 2001514855-A/5
PD 18-SEP-2001
PF 31-AUG-1998 JP 2000508806
PR 02-SEP-1997 US 08/922170, 02-JUL-1998 US 09/109386 PI
IRIS PECKER, ISRAEL VLODAVSKY, FEINSTEIN ELENA
PC C12N15/09, A61K38/00, A61P9/10, A61P17/00, A61P29/00, A61P35/00, PC
A61P37/00,
PC A61P43/00, C12N5/10, C12N9/24, C12Q1/68, G01N33/15, G01N33/50// PC
A61K39/395,
PC A61K39/395, C12N15/00, A61K37/02, C12N5/00
CC Polynucleotide encoding polypeptide having
heparanase activity
CC and
CC expression of the polypeptide in induced cell FH Key
FT Location/Qualifiers
FT 1. .15
/organism='Nucleic acid'.
FEATURES
source
1. .15
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 640
BD184668/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 15)
AUTHORS
Ling,C., Lin,R., Yoo,Z., Huang,X., Lee,B., Lee,S., Lin,Y.,
Huang,C., Hsu,H., Shi,C., Yeh,C., Cao,Y. and Pan,C.
TITLE
Method and detector for identifying subtypes of human papiloma
JOURNAL
Patent: JP 2002360271-A 647 17-DEC-2002;
COMMENT
KING CAR FOOD INDUSTRIAL CO LTD
OS Artificial Sequence
PN JP 2002360271-A/647
PD 17-DEC-2002
PF 28-NOV-2001 JP 2001362595
PR 04-MAY-2001 TW 90110785
PI CHING-YEE LING, RUEY-WEN LIN, ZHOU-MENG YOO, XIN-HSIUAN HUANG, BOW-
HAENG LEE,
PI SHENG-HSIUNG LEE, YI-JU LIN, CI-CHUNG HUANG, HAN-CHANG HSU, CHA-
WEN SHI,
PI CHIH-XIN YEH, YI-FENG CAO, CHIH-LONG PAN
PC C12N15/09, C12N15/09, C12M1/34, C12Q1/04, C12Q1/42, C12Q1/68 PC
C12Q1/70, G01N21/64,
PC G01N33/53, G01N33/574, G01N33/58, G01N37/00// (C12M1/34, C12R1:93),
PC (C12Q1/70, C12R1:93), C12N15/00, C12N15/00
CC Added sequence for 3' end labeling of oligonucleic acid. FH
Key
FT source
FT 1. .15
/organism='Artificial Sequence'.
FEATURES
source
1. .15
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 641
BD206432/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 15)
AUTHORS
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
TITLE
Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection.
JOURNAL
BD206432
COMMENT
BD206432.1 GI:33016202
KEYWORDS
JP 2002512791-A/22.
SOURCE
unidentified
ORGANISM
unclassified.
```


REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 22 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/22
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)'.
FEATURES
source Location/Qualifiers
1..15
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 642
BD209488/c
LOCUS BD209488 15 bp RNA linear PAT 17-JUL-2003
DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection.
ACCESSION BD209488
VERSION BD209488.1 GI:33019258
KEYWORDS JP 2002512791-A/3078.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Blatt,L., Mcswiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 3078 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/3078
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT,JAMES A MCSWIGGEN,ELISABETH ROBERTS,PAMELA A PI
PAVCO,
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00,
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers

FT source 1..15
FT /organism='Hepatitis virus (hepatitis C FT
virus)'.
FEATURES
source Location/Qualifiers
1..15
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 643
AR221693/c
LOCUS AR221693 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6426408.
ACCESSION AR221693
VERSION AR221693.1 GI:23328765
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 3 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 644
AR221694/c
LOCUS AR221694 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 4 from patent US 6426408.
ACCESSION AR221694
VERSION AR221694.1 GI:23328766
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 4 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 645
AR221694/c
LOCUS AR221694 16 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 4 from patent US 6426408.
ACCESSION AR221694
VERSION AR221694.1 GI:23328766
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutuyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6426408-A 4 30-JUL-2002;
FEATURES
source Location/Qualifiers
1..16
/organism='unknown'
/mol_type='genomic DNA'

```
RESULT 645
AR221695/c
LOCUS           AR221695           16 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION      Sequence 5 from patent US 6426408.
ACCESSION       AR221695
VERSION         AR221695.1 GI:23328767
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 16)
AUTHORS         Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE           Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL         Patent: US 6426408-A 5 30-JUL-2002;
FEATURES        Location/Qualifiers
source          1..16
                1736 AAAAAAAAAAAAAA 1750
                |||||
                15 AAAAAAAAAAAAAA 1

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
    15 AAAAAAAAAAAAAA 1

Db 15 AAAAAAAAAAAAAA 1

RESULT 646
AR221696/c
LOCUS           AR221696           16 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION      Sequence 6 from patent US 6426408.
ACCESSION       AR221696
VERSION         AR221696.1 GI:23328768
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 16)
AUTHORS         Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE           Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL         Patent: US 6426408-A 6 30-JUL-2002;
FEATURES        Location/Qualifiers
source          1..16
                1736 AAAAAAAAAAAAAA 1750
                |||||
                15 AAAAAAAAAAAAAA 1

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
    15 AAAAAAAAAAAAAA 1

Db 15 AAAAAAAAAAAAAA 1

RESULT 647
AR221697/c
LOCUS           AR221697           16 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION      Sequence 7 from patent US 6426408.
ACCESSION       AR221697
VERSION         AR221697.1 GI:23328769
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 16)
AUTHORS         Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE           Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL         Patent: US 6426408-A 7 30-JUL-2002;
FEATURES        Location/Qualifiers
source          1..16
                1736 AAAAAAAAAAAAAA 1750
                |||||
                15 AAAAAAAAAAAAAA 1

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
    15 AAAAAAAAAAAAAA 1

Db 15 AAAAAAAAAAAAAA 1

RESULT 648
AR221698/c
LOCUS           AR221698           16 bp      DNA      linear      PAT 26-SEP-2002
DEFINITION      Sequence 8 from patent US 6426408.
ACCESSION       AR221698
VERSION         AR221698.1 GI:23328770
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 16)
AUTHORS         Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE           Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL         Patent: US 6426408-A 8 30-JUL-2002;
FEATURES        Location/Qualifiers
source          1..16
                1736 AAAAAAAAAAAAAA 1750
                |||||
                15 AAAAAAAAAAAAAA 1

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
    15 AAAAAAAAAAAAAA 1

Db 15 AAAAAAAAAAAAAA 1

RESULT 649
AR257438/c
LOCUS           AR257438           16 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION      Sequence 3 from patent US 6486308.
ACCESSION       AR257438
VERSION         AR257438.1 GI:27307449
KEYWORDS        .
SOURCE          Unknown.
ORGANISM        Unclassified.
REFERENCE       1 (bases 1 to 16)
AUTHORS         Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE           Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL         Patent: US 6486308-A 3 26-NOV-2002;
FEATURES        Location/Qualifiers
source          1..16
                1736 AAAAAAAAAAAAAA 1750
                |||||
                15 AAAAAAAAAAAAAA 1

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
    |||||
    15 AAAAAAAAAAAAAA 1

Db 15 AAAAAAAAAAAAAA 1

RESULT 650
AR257439/c
LOCUS           AR257439           16 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION      Sequence 4 from patent US 6486308.
ACCESSION       AR257439
```

```
VERSION AR257439.1 GI:27307450
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 4 26-NOV-2002;
FEATURES
    source
        Location/Qualifiers
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 651
AR257440/c
LOCUS AR257440 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 5 from patent US 6486308.
ACCESSION AR257440
VERSION AR257440.1 GI:27307451
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 5 26-NOV-2002;
FEATURES
    source
        Location/Qualifiers
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 652
AR257441/c
LOCUS AR257441 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6 from patent US 6486308.
ACCESSION AR257441
VERSION AR257441.1 GI:27307452
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 6 26-NOV-2002;
FEATURES
    source
        Location/Qualifiers
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 653
AR257442/c
LOCUS AR257442 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 7 from patent US 6486308.
ACCESSION AR257442
VERSION AR257442.1 GI:27307453
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 7 26-NOV-2002;
FEATURES
    source
        Location/Qualifiers
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 654
AR257443/c
LOCUS AR257443 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 8 from patent US 6486308.
ACCESSION AR257443
VERSION AR257443.1 GI:27307454
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Kutyavin,I.V., Lukhtanov,E.A., Gamper,H.B. and Meyer,R.B. Jr.
TITLE Covalently linked oligonucleotide minor groove binder conjugates
JOURNAL Patent: US 6486308-A 8 26-NOV-2002;
FEATURES
    source
        Location/Qualifiers
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 655
AR257478/c
LOCUS AR257478 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1682 from patent US 5837542.
ACCESSION AR257478
VERSION AR257478.1 GI:5983055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
```

```

AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL      Patent: US 5837542-A 1682 17-NOV-1998;
FEATURES     Location/Qualifiers
             1..17
             /mol_type="unassigned DNA"
             /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCAC 271
Db 15 CCCACGGAGCAGCAC 1

RESULT 656
E34258/c
LOCUS      ARI15236      17 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 1682 from patent US 6132967.
ACCESSION  ARI15236
VERSION     ARI15236.1 GI:14095558
KEYWORDS   Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE       Ribozyme treatment of diseases or conditions related to levels of
              intercellular adhesion molecule-1 (ICAM-1)
JOURNAL     Patent: US 6132967-A 1682 17-OCT-2000;
FEATURES     Location/Qualifiers
             1..17
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCAC 271
Db 15 CCCACGGAGCAGCAC 1

RESULT 657
BD233654/c
LOCUS      BD233654      17 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Two-color differential display as a method for detecting regulated
              genes.
ACCESSION  BD233654
VERSION     BD233654.1 GI:33043424
KEYWORDS   JP 2002524088-A/2.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 17)
AUTHORS     Kozian,D. and Reuner,B.
TITLE       Two-color differential display as a method for detecting regulated
              genes.
JOURNAL     Patent: JP 2002524088-A 2 06-AUG-2002;
              AVENTIS PHARMA DEUTSCHLAND GMBH
COMMENT     OS Unidentified
             PN JP 2002524088-A/2
             PD 06-AUG-2002
             PF 26-AUG-1999 JP 2000569015
             PR 07-SEP-1998 DE 198 40 731.9
             PI DETLEF KOZIAN,BIRGIT REUNER
             PC C12Q1/68,G01N33/58//A61K45/00,C12N15/09,C12N15/00,C12N15/00,
             CC C12N15/00
             CC Strandedness: Single;

AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL      Patent: US 5837542-A 1682 17-NOV-1998;
FEATURES     Location/Qualifiers
             1..17
             /mol_type="unassigned DNA"
             /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCAC 271
Db 15 CCCACGGAGCAGCAC 1

RESULT 658
E34258/c
LOCUS      E34258      17 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION  E34258
VERSION     E34258.1 GI:18624263
KEYWORDS   JP 2000106879-A/2.
SOURCE      synthetic construct
             synthetic construct
             artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
              Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE       Pollinosis-associated gene
JOURNAL     Patent: JP 2000106879-A 2 18-APR-2000;
              GENOX RESEARCH INC
FEATURES     Location/Qualifiers
             1..17
             /organism="artificial Sequence"

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 659
E34259/c
LOCUS      E34259      17 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION  E34259
VERSION     E34259.1 GI:18624264
KEYWORDS   JP 2000106879-A/3.
SOURCE      synthetic construct
             synthetic construct

AUTHORS      Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
              Draper,K.G.
TITLE        Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL      Patent: US 5837542-A 1682 17-NOV-1998;
FEATURES     Location/Qualifiers
             1..17
             /mol_type="unassigned DNA"
             /mol_type="unassigned DNA"

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 659
E34259/c
LOCUS      E34259      17 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Pollinosis-associated gene.
ACCESSION  E34259
VERSION     E34259.1 GI:18624264
KEYWORDS   JP 2000106879-A/3.
SOURCE      synthetic construct
             synthetic construct
```

```
artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE
Pollinosis-associated gene
JOURNAL
Patent: JP 2000106879-A 3 18-APR-2000;
GENOX RESEARCH INC
COMMENT
OS Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NING NO,
PI KAOJU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 16 AAAAAAAAAAAAAA 2

RESULT 660
AR187061/c
LOCUS
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 17)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
AUTHORS
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 17 AAAAAAAAAAAAAA 3

RESULT 661
AR187064/c
LOCUS
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS
SOURCE
Unknown.

artificial sequences.
1 (bases 1 to 17)
Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
Gunji,S., Obayashi,I., Imai,Y., No,N. and Ogawa,K.
TITLE
Pollinosis-associated gene
JOURNAL
Patent: JP 2000106879-A 3 18-APR-2000;
GENOX RESEARCH INC
COMMENT
OS Artificial Sequence
PN JP 2000106879-A/3
PD 18-APR-2000
PF 06-OCT-1998 JP 1998284610
PR
PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
PI NING NO,
PI KAOJU OGAWA
PC C12N15/09,A61K31/00,A61K39/36,A61K45/00,C12Q1/68,C12N15/00 CC

FH Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence'.
FEATURES
source
Location/Qualifiers
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 16 AAAAAAAAAAAAAA 2

RESULT 660
AR187061/c
LOCUS
DEFINITION Sequence 2549 from patent US 6346398.
ACCESSION AR187061
VERSION AR187061.1 GI:20233026
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 17)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
AUTHORS
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6346398-A 2549 12-FEB-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 17 AAAAAAAAAAAAAA 3

RESULT 661
AR187064/c
LOCUS
DEFINITION Sequence 2552 from patent US 6346398.
ACCESSION AR187064
VERSION AR187064.1 GI:20233029
KEYWORDS
SOURCE
Unknown.

ORGANISM Unknown.
REFERENCE
1 (bases 1 to 17)
Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
AUTHORS
Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL
Patent: US 6346398-A 2552 12-FEB-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 662
AR241830/c
LOCUS
DEFINITION Sequence 118 from patent US 6472154.
ACCESSION AR241830
VERSION AR241830.1 GI:27287642
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 17)
Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
AUTHORS
Polymorphic repeats in human genes
JOURNAL
Patent: US 6472154-A 118 29-OCT-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 663
AR266625/c
LOCUS
DEFINITION Sequence 63 from patent US 6495319.
ACCESSION AR266625
VERSION AR266625.1 GI:29695689
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 17)
McClelland,M., Welsh,J. and Trenkle,T.
AUTHORS
Reduced complexity nucleic acid targets and methods of using same
JOURNAL
Patent: US 6495319-A 63 17-DEC-2002;
FEATURES
source
Location/Qualifiers
1..17
/organism='unknown'
/mol_type='genomic DNA'
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
```

Db 16 AAAAAAAAAAAAAA 2
|||||
RESULT 664
AR323671/C
LOCUS AR323671 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1073 from patent US 6566127.
ACCESSION AR323671
VERSION AR323671.1 GI:33709479
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1073 20-MAY-2003;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 17 AAAAAAAAAAAAAA 3
|||||
RESULT 665
AR323674/C
LOCUS AR323674 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1076 from patent US 6566127.
ACCESSION AR323674
VERSION AR323674.1 GI:33709482
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1076 20-MAY-2003;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="unassigned RNA"
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1
|||||
RESULT 666
AR401695
LOCUS AR401695 17 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 35 from patent US 6623962.
ACCESSION AR401695
VERSION AR401695.1 GI:40149145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)

AUTHORS Akhtar, S., Fell, P. and McSwiggen, J.A.
TITLE Enzymatic nucleic acid treatment of diseases of conditions related to levels of epidermal growth factor receptors
JOURNAL Patent: US 6623962-A 35 23-SEP-2003;
FEATURES
source Location/Qualifiers
1. .17
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 907 CAGCCTCCAGAGGAT 921
|||||
Db 3 CAGCCTCCAGAGGAT 17
|||||
RESULT 667
AX422500
LOCUS AX422500 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 836 from Patent WO0188124.
ACCESSION AX422500
VERSION AX422500.1 GI:21525882
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 836 22-NOV-2001;
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 271 CTCACGCCACCC 285
|||||
Db 2 CTCACGCCACCC 16
|||||
RESULT 668
AX422501
LOCUS AX422501 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 837 from Patent WO0188124.
ACCESSION AX422501
VERSION AX422501.1 GI:21525883
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 837 22-NOV-2001;
FEATURES
source Location/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 271 CTCACGCCACCC 285
DB 1 CTCACGCCACCC 15

RESULT 669
AX531994/c

LOCUS AX531994 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1503 from Patent EP1239051.
ACCESSION AX531994
VERSION AX531994.1 GI:25255754
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1503 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 897 GCCCTGAGCCAGCC 911
DB 17 GCCCTGAGCCAGCC 3

RESULT 670
AX531995/c

LOCUS AX531995 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1504 from Patent EP1239051.
ACCESSION AX531995
VERSION AX531995.1 GI:25255756
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1504 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 897 GCCCTGAGCCAGCC 911
DB 16 GCCCTGAGCCAGCC 2

RESULT 671
AX531996/c

LOCUS AX531996 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1505 from Patent EP1239051.
ACCESSION AX531996
VERSION AX531996.1 GI:25255758
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon,M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1505 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 897 GCCCTGAGCCAGCC 911
DB 15 GCCCTGAGCCAGCC 1

RESULT 672
AX634505/c

LOCUS AX634505 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1644 from Patent EP1260586.
ACCESSION AX634505
VERSION AX634505.1 GI:28470119
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Dizenzo,A., Karpelsky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., Meswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related genes
JOURNAL Patent: EP 1260586-A 1644 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 257 CCCACGGAGCAGCAC 271
DB 15 CCCACGGAGCAGCAC 1

RESULT 673
AX692528/c

LOCUS AX692528 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5260 from Patent EP1281758.
ACCESSION AX692528
VERSION AX692528.1 GI:29415486
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 Shannon.M., Gu.Y. and Nguyen.C.T.

AUTHORS

Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

TITLE

mdz12

JOURNAL

Patent: EP 1281758-A 5260 05-FEB-2003;

FEATURES

Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

source

Query Match 0.9%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1749

Db 15 CAAAAAAAAAAAAA 1

RESULT 674

BD011730/c

LOCUS

BD011730 17 bp DNA linear PAT 02-AUG-2002

DEFINITION

795, a novel gene related to pollen allergy.

ACCESSION

BD011730

VERSION

BD011730.1 GI:22091919

KEYWORDS

WO 0065050-A/2.

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1 (bases 1 to 17)

AUTHORS

Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,

Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,

Takahashi,E. and Yokoi,A.

795, a novel gene related to pollen allergy

Patent: WO 0065050-A 2 02-NOV-2000;

GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,

TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,

YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI

TAKAHASHI, AKIRA YOKOI

OS Artificial Sequence

PN WO 0065050-A/2

PD 02-NOV-2000

PF 26-APR-2000 WO 2000JP002734

PR 27-APR-1999 JP 99P 120494

PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,

PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,

PI NEI YOSHIDA,

PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI

PC

CL2N15/12, C07K14/47, C07K16/18, C12Q1/68, G01N33/50//A61K31/00, PC

A61P37/00

CC Description of Artificial Sequence:Artificially Synthesized CC

Primer Sequence

FH Key Location/Qualifiers.

1..17

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 16 AAAAAAAAAAAAAA 2

RESULT 675

BD011731/c

LOCUS

BD011731 17 bp DNA linear PAT 02-AUG-2002

DEFINITION

795, a novel gene related to pollen allergy.

ACCESSION

BD011731

VERSION

BD011731.1 GI:22091920

KEYWORDS

WO 0065050-A/3.

SOURCE

synthetic construct

ORGANISM

artificial sequences.

REFERENCE

1 (bases 1 to 17)

AUTHORS

Nagasu,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,

Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K., Matsui,K.,

Takahashi,E. and Yokoi,A.

795, a novel gene related to pollen allergy

Patent: WO 0065050-A 3 02-NOV-2000;

GENOX RESEARCH INC, TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA,

TADAHIRO OSHIDA, MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI,

YUKIHO IMAI, NEI YOSHIDA, KAORU OGAWA, KEIKO MATSUI, EIKI

TAKAHASHI, AKIRA YOKOI

OS Artificial Sequence

PN WO 0065050-A/3

PD 02-NOV-2000

PF 26-APR-2000 WO 2000JP002734

PR 27-APR-1999 JP 99P 120494

PI TAKESHI NAGASU, YUJI SUGITA, TOMOKO KASHIWABARA, TADAHIRO OSHIDA,

PI MASAYA OBAYASHI, SHIGEMICHI GUNJI, IZUMI OBAYASHI, YUKIHO IMAI,

PI NEI YOSHIDA,

PI KAORU OGAWA, KEIKO MATSUI, EIKI TAKAHASHI, AKIRA YOKOI

PC

CL2N15/12, C07K14/47, C07K16/18, C12Q1/68, G01N33/50//A61K31/00, PC

A61P37/00

CC Description of Artificial Sequence:Artificially Synthesized CC

Primer Sequence

FH Key Location/Qualifiers.

1..17

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 16 AAAAAAAAAAAAAA 2

RESULT 676

BD067195

LOCUS

BD067195 17 bp RNA linear PAT 27-AUG-2002

DEFINITION

Enzymatic nucleic acid treatment of diseases or conditions related

to levels of epidermal growth factor receptors.

ACCESSION

BD067195

VERSION

BD067195.1 GI:22612798

KEYWORDS

JP 2001511003-A/35.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 17)

AUTHORS

Akhtar,S., Fell,P. and Mcswiggen,J.A.

Enzymatic nucleic acid treatment of diseases or

conditions related

to levels of epidermal growth factor receptors

Patent: JP 2001511003-A 35 07-AUG-2001;

RIBOZYME PHARMACEUTICALS INC, ASTON UNIV

OS Unidentified

PN JP 2001511003-A/35

PD 07-AUG-2001

PF 14-JAN-1998 JP 1998532913

PR 31-JAN-1997 US 60/036476.04-DEC-1997 US

SAGHIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC

CC Strandedness: Single;


```

CC      Topology: Linear;
CC      Enzymatic nucleic acid treatment of diseases or conditions CC
SOURCE  related to
CC      levels of epidermal growth factor receptors
FH      Key      Location/Qualifiers
FT      source    1..17
FT      source    /organism='Unidentified'.
FEATURES
source
1..17
Location/Qualifiers
/organism='Unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      907 CAGCCTCCAGAGGAT 921
        |||||||
DB      3 CAGCCTCCAGAGGAT 17

RESULT 677
BD091742/c
LOCUS      BD091742      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION  BD091742
VERSION     BD091742.1 GI:22637353
KEYWORDS   WO 0073435-A/2.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagaau,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE      441, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073435-A 2 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS Artificial Sequence
            PN WO 0073435-A/2
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003190
            PR 27-MAY-1999 JP 99P 148783
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI
            PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC Description of Artificial Sequence:Artificially Synthesized CC
            Primer Sequence
            FH Key      Location/Qualifiers.
            source
            1..17
            Location/Qualifiers
            /organism='synthetic construct'
            /mol_type='genomic DNA'
            /db_xref='taxon:32630'

FEATURES
source
1..17
Location/Qualifiers
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
        |||||||
DB      16 AAAAAAAAAAAAAA 2

RESULT 678
BD091743/c
LOCUS      BD091743      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 441, a novel gene related to pollen allergy.
ACCESSION  BD091743
VERSION     BD091743.1 GI:22637361
KEYWORDS   WO 0073439-A/2.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagaau,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Takahashi,E. and Yokoi,A.
TITLE      465, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073439-A 2 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS Artificial Sequence
            PN WO 0073439-A/2
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003191
            PR 27-MAY-1999 JP 99P 148784
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K45/00 CC Description
            of Artificial Sequence:Artificially Synthesized CC
            Primer
            Sequence

```

```

BD091743.1 GI:22637354
WO 0073435-A/3.
synthetic construct
synthetic construct
artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagaau,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Gunji,S., Obayashi,I., Imai,Y., Yoshida,N., Ogawa,K. and Matsui,K.
TITLE      441, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073435-A 3 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI
COMMENT     OS Artificial Sequence
            PN WO 0073435-A/3
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003190
            PR 27-MAY-1999 JP 99P 148783
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI
            PC C12N15/10,C12Q1/68,G01N33/15,G01N33/50
            CC Description of Artificial Sequence:Artificially Synthesized CC
            Primer Sequence
            FH Key      Location/Qualifiers.
            source
            1..17
            Location/Qualifiers
            /organism='synthetic construct'
            /mol_type='genomic DNA'
            /db_xref='taxon:32630'

Query Match      0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAA 1750
        |||||||
DB      16 AAAAAAAAAAAAAA 2

RESULT 679
BD091750/c
LOCUS      BD091750      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION 465, a novel gene related to pollen allergy.
ACCESSION  BD091750
VERSION     BD091750.1 GI:22637361
KEYWORDS   WO 0073439-A/2.
SOURCE     synthetic construct
ORGANISM   artificial sequences.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Nagaau,T., Sugita,Y., Kashiwabara,T., Oshida,T., Obayashi,M.,
            Takahashi,E. and Yokoi,A.
TITLE      465, a novel gene related to pollen allergy
JOURNAL    Patent: WO 0073439-A 2 07-DEC-2000;
            GENOX RESEARCH INC.TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,
            TADAHIRO OSHIDA,MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,
            YUKIHO IMAI,NEI YOSHIDA,KAORU OGAWA,KEIKO MATSUI,EIKI
            TAKAHASHI,AKIRA YOKOI
COMMENT     OS Artificial Sequence
            PN WO 0073439-A/2
            PD 07-DEC-2000
            PF 18-MAY-2000 WO 2000JP003191
            PR 27-MAY-1999 JP 99P 148784
            PI TAKESHI NAGASU,YUJI SUGITA,TOMOKO KASHIWABARA,TADAHIRO OSHIDA,
            PI MASAYA OBAYASHI,SHIGEMICHI GUNJI,IZUMI OBAYASHI,YUKIHO IMAI,
            PI NEI YOSHIDA,
            PI KAORU OGAWA,KEIKO MATSUI,EIKI TAKAHASHI,AKIRA YOKOI PC
            C12N15/12,C12Q1/68,A61P37/08,A61K45/00 CC Description
            of Artificial Sequence:Artificially Synthesized CC
            Primer
            Sequence

```



```

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.9%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 683
BD097334/c
LOCUS BD097334 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097334
VERSION BD097334.1 GI:22642908
KEYWORDS WO 0165259-A/5
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagaau, T., Oshida, T., Obayashi, I., Matsui, K. and Sait, H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 5 07-SEP-2001;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, HIROMITSU NAKAUCHI, YUTAKA
FUJIKI, KAZUO FUKAWA, OSAMU KUDO TAKESHI NAKAGUCHI, YUTAKA
OBAYASHI, KEIKO MATSUI, HIROHISA SAITO
OS Artificial Sequence
PN WO 0165259-A/5
PD 07-SEP-2001
PF 23-FEB-2001 WO 2001JP001372
PR 02-MAR-2000 JP OOP 61832
PI TAKESHI NAGASU, TADAHIRO OSHIDA, IZUMI OBAYASHI, KEIKO MATSUI, PI
HIROHISA SAITO
PC G01N33/53, C12Q1/68, C12N15/12, G01N33/15, A01K67/027, A61K39/395,
A61P37/08
CC Description of Artificial Sequence:Artificially Synthesized CC
Primer Sequence
FH Key Location/Qualifiers
FT source 1..17
/organism="Artificial Sequence".

FEATURES
source
1..17 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 685
BD142808/c
LOCUS BD142808 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142808
VERSION BD142808.1 GI:23237753
KEYWORDS WO 0224903-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita, Y., Hashida, R., Ogawa, K., Fujishima, T., Nagaau, T.,
Tsujimoto, G. and Takahashi, E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 2 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
OS Artificial Sequence
PN WO 0224903-A/2
PD 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP OOP 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU.
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
G01N33/15,
PC G01N33/50//C12P21/08 (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized
CC sequence primer
FH Key Location/Qualifiers
FT source 1..17
/organism="Artificial Sequence".

FEATURES
source
1..17 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 684
BD097335/c
LOCUS BD097335 17 bp DNA linear PAT 27-AUG-2002
DEFINITION Method for examination for allergosis.
ACCESSION BD097335
VERSION BD097335.1 GI:22642909
KEYWORDS WO 0165259-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Nagaau, T., Oshida, T., Obayashi, I., Matsui, K. and Sait, H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0165259-A 6 07-SEP-2001;

```

```

source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 686
BD142809/c
LOCUS BD142809 17 bp DNA linear PAT 18-SEP-2002
DEFINITION Method of examining allergic disease.
ACCESSION BD142809
VERSION BD142809.1 GI:23237754
KEYWORDS WO 0224903-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T.,
Tsujimoto,G. and Takahashi,E.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0224903-A 3 28-MAR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, TOMOKO FUJISHIMA, TAKESHI NAGASU, GOZO TSUJIMOTO, EIKI
TAKAHASHI
OS Artificial Sequence
PN WO 0224903-A/3
PD 28-MAR-2002
PF 21-SEP-2001 WO 2001JP008246
PR 25-SEP-2000 JP 00P 291318
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU
PI GOZO TSUJIMOTO, EIKI TAKAHASHI
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C13Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

FEATURES
source
CC sequence primer
FH key Location/Qualifiers
FT source 1..17
/organism="synthetic construct"
/organism="Artificial Sequence".

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 687
BD143834/c
LOCUS BD143834 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD143834
VERSION BD143834.1 GI:27849593
KEYWORDS JP 2002095500-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 3 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PN JP 2002095500-A/3
PD 02-APR-2002
PF 25-SEP-2000 JP 2002091316
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJIMOTO
PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
C07K14/47,
PC C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10 PC
C12N15/09, C12P21/02,
PC C12Q1/02, G01N33/15, G01N33/50//C12P21/08, C12N5/00, C12N5/00, PC
C12N15/00
CC Description of Artificial Sequence:an artificially synthesized

FEATURES
source
CC sequence primer
FH key Location/Qualifiers
FT source 1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Score 15; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 688
BD143835/c
LOCUS BD143835 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD143835
VERSION BD143835.1 GI:27849593
KEYWORDS JP 2002095500-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Tsujimoto,K.
TITLE Method of examining allergic disease
JOURNAL Patent: JP 2002095500-A 3 02-APR-2002;
GENOX RESEARCH INC, THE DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL
OS Artificial Sequence
PN JP 2002095500-A/3
PD 02-APR-2002
PF 25-SEP-2000 JP 2002091316
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAAYASHI, PI
TAKESHI NAGASU,
PI KOZO TSUJIMOTO
PC C12Q1/68, A01K67/027, A61K31/7088, A61K31/711, A61K45/00, A61P37/08, PC
C07K14/47,

```

```

PC  C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/10 PC
,C12N15/09,C12P21/02,
PC C12Q1/02,G01N33/15,G01N33/50//C12P21/08,C12N5/00,C12N5/00, PC
C12N15/00
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC sequence Location/Qualifiers
FH Key 1..17
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers
FEATURES
source
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 689
LOCUS BD167835/c 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination of allergosis.
ACCESSION BD167835
VERSION BD167836.1 GI:27873647
KEYWORDS WO 0233122-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T., Saito,H.
and Takahashi,E.
TITLE Method for examination of allergosis
JOURNAL Patent: WO 0233122-A 3 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, RINAKO NAKAGAWA YUJI SUGITA,RYOICHI
HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA
SAITO,EIKI TAKAHASHI
COMMENT OS Artificial Sequence
PN WO 0233122-A/3
PD 25-APR-2002
PF 11-OCT-2001 WO 2001JP008937
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA,RYOICHI HASHIDA,KAORU OGAWA,MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO,EIKI TAKAHASHI
PC C12Q1/68,C12N15/09,G01N33/53,G01N33/50,C12Q1/02,A61K48/00, PC
A61K39/395,
PC A01K67/027//C07K16/18,C12N5/10
CC Description of Artificial Sequence:an artificially synthesized

CC anchor
CC primer sequence
FH Key 1..17 Location/Qualifiers
FT source /organism='Artificial Sequence'.
FT Location/Qualifiers
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | | | |
Db 16 AAAAAAAAAAAAAA 2

RESULT 691
LOCUS BD167907/c 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167907
VERSION BD167907.1 GI:27873719
KEYWORDS WO 0226962-A/6.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 6 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF

```

```

NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/6
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC key Location/Qualifiers
FH key 1..17
FT source /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2

RESULT 692
BD167908/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD167908
VERSION BD167908.1 GI:27873720
KEYWORDS WO 0226962-A/7.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Fujishima,T., Nagasu,T. and
Saito,H.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0226962-A 7 04-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, MASAKAZU ADACHI, KAZUO MIYANAGA YUJI
SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, TAKESHI
NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0226962-A/7
PD 04-APR-2002
PF 21-SEP-2001 WO 2001JP008247
PR 26-SEP-2000 JP 00P 293021
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, TOMOKO FUJISHIMA, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N5/10, C07K14/47, C07K16/18, C12P21/02, C12Q1/02, PC
C12Q1/68,
PC A01K67/027, A61K31/713, A61K45/00, A61K48/00, A61P17/00, A61P37/08,
PC G01N33/15,
PC G01N33/50//C12P21/08, (C12N5/10, C12R1:91), (C12P21/02, C12R1:91)
CC Description of Artificial Sequence:an artificially synthesized

CC sequence primer
CC key Location/Qualifiers
FH key 1..17
FT source /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2

RESULT 694
BD168112/c
LOCUS 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergosis.
ACCESSION BD168111
VERSION BD168111.1 GI:27873923
KEYWORDS WO 0233069-A/18.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and
Saito,H.
TITLE Method for examination for allergosis
JOURNAL Patent: WO 0233069-A 18 25-APR-2002;
GENOX RESEARCH INC, JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF
NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO
MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU
OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0233069-A/18
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI
TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC
A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence:an artificially synthesized

CC sequence anchor
CC key Location/Qualifiers
FH key 1..17
FT source /organism='Artificial Sequence'.

FEATURES
source
Location/Qualifiers
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2

RESULT 694
BD168112/c
```

LOCUS BD168112 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method for examination for allergic disease.
ACCESSION BD168112
VERSION BD168112.1 GI:27873924
KEYWORDS WO 0233069-A/19.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Sugita,Y., Hashida,R., Ogawa,K., Obayashi,M., Nagasu,T. and Saito,H.
TITLE Method for examination for allergic disease
JOURNAL Patent: WO 0233069-A 19 25-APR-2002;
GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, TOMOYUKI FUKASAWA, CHUHEI NOJIRI, NOBUO MATSUHASHI, KOJI NISHIZAWA, YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, TAKESHI NAGASU, HIROHISA SAITO
OS Artificial Sequence
PN WO 0233069-A/19
PD 25-APR-2002
PF 28-SEP-2001 WO 2001JP008574
PR 13-OCT-2000 JP 00P 314093
PI YUJI SUGITA, RYOICHI HASHIDA, KAORU OGAWA, MASAYA OBAYASHI, PI TAKESHI NAGASU,
PI HIROHISA SAITO
PC C12N15/09, C12N15/63, C12Q1/68, C12Q1/02, G01N33/53, C12N5/10, PC A61K39/395,
PC C07K14/47, C07K16/18//C12P21/02, C12P21/08
CC Description of Artificial Sequence: an artificially synthesized

CC anchor
CC primer sequence
FH Key
FT source
FT Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 695
BD171177/c
LOCUS BD171177 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171177
VERSION BD171177.1 GI:27876989
KEYWORDS WO 0250269-A/3.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 3 27-JUN-2002;
GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 0250269-A/3
PD 27-JUN-2002
PF 21-DEC-2001 WO 2001JP011286
PR 21-DEC-2000 JP 00P 389476
PI YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU,
PI GOZO TSUJIMOTO
PC C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00, PC A61P37/08,
PC C12Q1/68, G01N33/50
CC Description of Artificial Sequence: 'Grl5C', an artificially synthesized
CC primer sequence
FH Key
FT source
FT Location/Qualifiers
1. .17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

FEATURES
source
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 695
BD171177/c
LOCUS BD171177 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Method of examining allergic disease.
ACCESSION BD171177
VERSION BD171177.1 GI:27876989
KEYWORDS WO 0250269-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 17)
AUTHORS Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagasu,T. and Tsujimoto,G.
TITLE Method of examining allergic disease
JOURNAL Patent: WO 0250269-A 2 27-JUN-2002;
GENOX RESEARCH INC., JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF NATIONAL CHILDREN'S HOSPITAL, MASAMICHI TAKAGI, AKINORI OTA YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, TAKESHI NAGASU,
GOZO TSUJIMOTO
OS Artificial Sequence
PN WO 0250269-A/2
PD 21-JUN-2002
PF 21-DEC-2001 WO 2001JP011286

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 697
E32458/c
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32458
VERSION E32458.1 GI:13018694
KEYWORDS JP 2000037190-A/18.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 18 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/18
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
LOCATION/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 698
E32459/c
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32459
VERSION E32459.1 GI:13018695
KEYWORDS JP 2000037190-A/19.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 19 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/19
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,

PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
LOCATION/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 699
E32461/c
LOCUS 18 bp DNA linear PAT 18-JUN-2001
DEFINITION Mammal-derived tissue specific physiologically active protein.
ACCESSION E32461
VERSION E32461.1 GI:13018697
KEYWORDS JP 2000037190-A/21.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 18)
AUTHORS Jun,N., Yusuke,N. and Toshihiro,T.
TITLE Mammal-derived tissue specific physiologically active protein
JOURNAL Patent: JP 2000037190-A 21 08-FEB-2000;
JAPAN TOBACCO INC
COMMENT OS Artificial Sequence
PN JP 2000037190-A/21
PD 08-FEB-2000
PF 23-JUL-1998 JP 1998225228
PR JUN NISHIU, YUSUKE NAKAMURA, TOSHIHIRO TANAKA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
C12N15/02,
PC C12P21/02, C12P21/08// (C12N5/10, C12R1:91), (C12P21/08, C12R1:91),
PC C12N15/00,
PC C12N5/00, C12N15/00, (C12N5/00, C12R1:91)
CC
FH Key Location/Qualifiers
FT primer_bind (1)..(18).
LOCATION/Qualifiers
1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 700
BD140103/c
LOCUS 19 bp DNA linear PAT 18-SEP-2002
DEFINITION Enzyme-specific cleavable polynucleotide substrate and assay
method
ACCESSION BD140103
VERSION BD140103.1 GI:23235048
KEYWORDS JP 2002508935-A/3.

Query Match	0.9%	Score 15;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 5.7e+02;		

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 19 AAAAAAAAAAAAAA 5

RESULT 705
AX404077/c
LOCUS 20 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 4 from Patent EP1195382.
ACCESSION AX404077
VERSION AX404077.1 GI:21437393
KEYWORDS
ORGANISM
SOURCE
REFERENCE 1
AUTHORS Aizawa, A., Kawakami, A. and Kondo, T.
TITLE Testis-specific gene
JOURNAL Patent: EP 1195382-A 4 10-APR-2002;
Of Gunma Livestock Improvement Association of Japan, Inc. (JP); President
Of Gunma University (JP)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 19 AAAAAAAAAAAAAA 5

RESULT 706
AX498246
LOCUS 20 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 2 from Patent WO0218951.
ACCESSION AX498246
VERSION AX498246.1 GI:23343165
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Dubertret, B., Calame, M. and Libchaber, A.
TITLE Methods employing fluorescence quenching by metal surfaces
JOURNAL Patent: WO 0218951-A 2 07-MAR-2002;
THE ROCKEFELLER UNIVERSITY (US)
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15

RESULT 707
BD143136/c
LOCUS 20 bp DNA linear PAT 17-JAN-2003
DEFINITION Novel testis-specific gene.
ACCESSION BD143136

BD143136.1 GI:27848894
JP 2002112777-A/3.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 20)
Aizawa, A., Kawakami, A. and Kondo, T.
Novel testis-specific gene
Patent: JP 2002112777-A 3 16-APR-2002;
KACHIKU KAIRYO JIGYODAN, PRESIDENT OF GUNMA UNIVERSITY
OS Artificial Sequence
PN JP 2002112777-A/3
PD 16-APR-2002
PF 03-OCT-2000 JP 2000303994
PI AKIRA AIZAWA, AKIKO KAWAKAMI, TOSHIHIKO KONDO
PC C12N15/09, C07K14/47, C12N15/00
CC Novel testis-specific gene
FH Key Location/Qualifiers
FT source 1. .20
/organism="Artificial Sequence".
FEATURES
source
1. .20
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 19 AAAAAAAAAAAAAA 5

RESULT 708
AR016068/c
LOCUS 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 36 from patent US 5776679.
ACCESSION AR016068
VERSION AR016068.1 GI:3972345
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 36 07-JUL-1998;
FEATURES
source
1. .18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
Db 18 TTGGGGTGGGGTTGGG 1

RESULT 709
AR016069/c
LOCUS 18 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 37 from patent US 5776679.
ACCESSION AR016069
VERSION AR016069.1 GI:3972346
KEYWORDS
SOURCE
ORGANISM
Unclassified.

```
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Assays for the DNA component of human telomerase
JOURNAL Patent: US 5776679-A 37 07-JUL-1998;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1017 GTTGGGATGGGCTGGG 1034
Db 18 GGTGGGTTGGGTTGGG 1

RESULT 710
LOCUS AR074230 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 38 from patent US 5952490.
ACCESSION AR074230
VERSION AR074230.1 GI:10000985
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 38 14-SEP-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
Db 1 TTGGGTTGGGTTGGG 18

RESULT 711
LOCUS AR074246 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 54 from patent US 5952490.
ACCESSION AR074246
VERSION AR074246.1 GI:10001001
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 54 14-SEP-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
Db 1 TTGGGTTGGGTTGGG 18

RESULT 712
LOCUS AR074303 18 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 111 from patent US 5952490.
ACCESSION AR074303
VERSION AR074303.1 GI:10001058
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 111 14-SEP-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
Db 1 TTGGGTTGGGTTGGG 18

RESULT 713
LOCUS AR075538 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 35 from patent US 5958680.
ACCESSION AR075538
VERSION AR075538.1 GI:10002284
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 35 28-SEP-1999;
FEATURES Location/Qualifiers
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
Db 18 TTGGGTTGGGTTGGG 1

RESULT 714
LOCUS AR075539 18 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 36 from patent US 5958680.
ACCESSION AR075539
VERSION AR075539.1 GI:10002285
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
```

```
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: US 5958680-A 36 28-SEP-1999;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1017 GGTGGGATGGGCTGG 1034
||||| ||||| |||||
Db 18 GGTGGGTTGGGTTGG 1

RESULT 715
LOCUS AR078882 18 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 26 from patent US 5965370.
ACCESSION AR078882
VERSION AR078882.1 GI:10005628
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowser,L.M.
TITLE Antisense modulation of RhoG expression
JOURNAL Patent: US 5965370-A 26 12-OCT-1999;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 CCGCTGGATGGGCACATC 1524
||||| ||||| |||||
Db 1 CAGCAGGATGGGCACATC 18

RESULT 716
LOCUS I20478 18 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 57 from patent US 5514577.
ACCESSION I20478
VERSION I20478.1 GI:1600833
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Draper,K.G., Crooke,S.T., Mirabelli,C.K., Ecker,D.J., Hanecak,R.C.,
        Anderson,K.P., Brown-Driver,V.L. and Wyatt,J.R.
TITLE Oligonucleotide therapies for modulating the effects of herpes
        viruses
JOURNAL Patent: US 5514577-A 57 07-MAY-1996;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGG 1036
||||| ||||| |||||
```

```
Db 1 TTGGGGTTGGGTTGGG 18

RESULT 717
LOCUS AR187555 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 3043 from patent US 6346398.
ACCESSION AR187555
VERSION AR187555.1 GI:20233520
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
        related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 3043 12-FEB-2002;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGGC 790
||||| ||||| |||||
Db 18 GAGTTGTAGTCTGGGGC 1

RESULT 718
LOCUS AR215621 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 169 from patent US 6410323.
ACCESSION AR215621
VERSION AR215621.1 GI:23313877
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Roberts,M.L. and Cowser,L.M.
TITLE Antisense modulation of human Rho family gene expression
JOURNAL Patent: US 6410323-A 169 25-JUN-2002;
FEATURES
    source
        1..18
            /organism="unknown"
            /mol_type="genomic DNA"
Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1507 CCGCTGGATGGGCACATC 1524
||||| ||||| |||||
Db 1 CAGCAGGATGGGCACATC 18

RESULT 719
LOCUS AR231295 18 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 32 from patent US 6451968.
ACCESSION AR231295
VERSION AR231295.1 GI:27272226
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
        Coull,J.M., Kiely,J. and Griffith,M.
```

```

TITLE      Peptide nucleic acids
JOURNAL    Patent: US 6451968-A 32 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAGAGAAAAAAAAACAAA 1

RESULT 720
LOCUS      AR231296          18 bp      DNA          linear          PAT 20-DEC-2002
DEFINITION Sequence 33 from patent US 6451968.
ACCESSION  AR231296
VERSION     AR231296.1 GI:27272227
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
            Coull,J.M., Kiely,J. and Griffith,M.
TITLE     Peptide nucleic acids
JOURNAL   Patent: US 6451968-A 33 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAGAGAAAAAAAAACAAA 1

RESULT 721
LOCUS      AR306483          18 bp      DNA          linear          PAT 12-JUN-2003
DEFINITION Sequence 35 from patent US 6548298.
ACCESSION  AR306483
VERSION     AR306483.1 GI:31696322
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE     Mammalian telomerase
JOURNAL   Patent: US 6548298-A 35 15-APR-2003;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGG 1036
Db 18 TTGGGGTTGGGTTGGG 1

TITLE      Peptide nucleic acids
JOURNAL    Patent: US 6451968-A 32 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAGAGAAAAAAAAACAAA 1

RESULT 721
LOCUS      AR306483          18 bp      DNA          linear          PAT 12-JUN-2003
DEFINITION Sequence 35 from patent US 6548298.
ACCESSION  AR306483
VERSION     AR306483.1 GI:31696322
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE     Mammalian telomerase
JOURNAL   Patent: US 6548298-A 35 15-APR-2003;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGG 1036
Db 18 TTGGGGTTGGGTTGGG 1

TITLE      Peptide nucleic acids
JOURNAL    Patent: US 6451968-A 32 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAGAGAAAAAAAAACAAA 1

RESULT 722
LOCUS      AR306484          18 bp      DNA          linear          PAT 12-JUN-2003
DEFINITION Sequence 36 from patent US 6548298.
ACCESSION  AR306484
VERSION     AR306484.1 GI:31696323
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE     Mammalian telomerase
JOURNAL   Patent: US 6548298-A 36 15-APR-2003;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1017 GGTGGGGATGGGCTGG 1034
Db 18 GGTGGGGTTGGGTTGG 1

TITLE      Peptide nucleic acids
JOURNAL    Patent: US 6451968-A 32 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAGAGAAAAAAAAACAAA 1

RESULT 723
LOCUS      AR324069          18 bp      RNA          linear          PAT 17-AUG-2003
DEFINITION Sequence 1471 from patent US 6566127.
ACCESSION  AR324069
VERSION     AR324069.1 GI:33709877
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 18)
AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
JOURNAL   Patent: US 6566127-A 1471 20-MAY-2003;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGGC 790
Db 18 GAGTTGTAGTCTGGGGC 1

TITLE      Peptide nucleic acids
JOURNAL    Patent: US 6451968-A 32 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGG 1036
Db 18 TTGGGGTTGGGTTGGG 1

TITLE      Peptide nucleic acids
JOURNAL    Patent: US 6451968-A 32 17-SEP-2002;
FEATURES   Location/Qualifiers
source     1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match      0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAGAGAAAAAAAAACAAA 1

RESULT 724
LOCUS      AX032592          18 bp      DNA          linear          PAT 20-SEP-2000
DEFINITION Sequence 38 from Patent EP1016715.
ACCESSION  AX032592
VERSION     AX032592.1 GI:10279530
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1
AUTHORS   Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
            Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
            Wyatt,J.R.
TITLE     Oligonucleotides having a conserved g4 core sequence
JOURNAL   Patent: EP 1016715-A 38 05-JUL-2000;
```

```
ISIS PHARMACEUTICALS INC (US)
  Location/Qualifiers
    1..18
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGG 1036
  ||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGG 18

RESULT 725
LOCUS AX032608 18 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 54 from Patent EP1016715.
ACCESSION AX032608
VERSION AX032608.1 GI:10279546
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
  1
  AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
  Wyatt,J.R.
  TITLE Oligonucleotides having a conserved g4 core sequence
  JOURNAL Patent: EP 1016715-A 54 05-JUL-2000;
  ISIS PHARMACEUTICALS INC (US)
FEATURES
  source
    1..18
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGG 1036
  ||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGG 18

RESULT 726
LOCUS AX032665 18 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 111 from Patent EP1016715.
ACCESSION AX032665
VERSION AX032665.1 GI:10279603
KEYWORDS
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
  1
  AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
  Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
  Wyatt,J.R.
  TITLE Oligonucleotides having a conserved g4 core sequence
  JOURNAL Patent: EP 1016715-A 111 05-JUL-2000;
  ISIS PHARMACEUTICALS INC (US)
FEATURES
  source
    1..18
    /organism="unidentified"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32644"

Query Match
  Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGGATGGGCTGGGG 1036
  ||||| ||||| |||||
Db 1 TTGGGGTTGGGGTTGGGG 18

RESULT 727
LOCUS AX082574 18 bp DNA linear PAT 28-FEB-2001
DEFINITION Sequence 25 from Patent WO0111047.
ACCESSION AX082574
VERSION AX082574.1 GI:13184684
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1
  AUTHORS Bowman,B.M. and Wang,K.
  TITLE Dna sequences isolated from human colonic epithelial cells
  JOURNAL Patent: WO 0111047-A 25 15-FEB-2001;
  Bayer Corporation (US)
FEATURES
  source
    1..18
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match
  Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
  Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1617 CTCAGTTCAGTTCATCCCAT 1634
  ||||| ||||| |||||
Db 18 CTCAGTTCATTCATCCCAT 1

RESULT 728
LOCUS BD088263 18 bp DNA linear PAT 27-AUG-2002
DEFINITION A method of arraying genome clone.
ACCESSION BD088263
VERSION BD088263.1 GI:22633873
KEYWORDS JP 2001321190-A/507.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
  1 (bases 1 to 18)
  AUTHORS Soeda,E.
  TITLE A method of arraying genome clone
  JOURNAL Patent: JP 2001321190-A 507 20-NOV-2001;
  THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
  GENOTECHS
COMMENT OS Artificial Sequence
  PN JP 2001321190-A/507
  PD 20-NOV-2001
  PF 12-MAR-2001 JP 2001068285
  PI EIICHI SOEDA
  PC C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
  C12N15/00
  CC Description of Artificial Sequence:Synthetic DNA FH Key
  LOCATION/Qualifiers
  FT source
    1..18
    /organism='Artificial Sequence'

FEATURES
  source
    1..18
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match
  Best Local Similarity 0.8%; Score 14.8; DB 1; Length 18;
```

```
Best Local Similarity 88.9%; Pred. No. 5.4e+02; Indels 0; Gaps 0;
Matches 16; Conservative 0; Mismatches 2;

Qy 683 CACAGCCAGTGAGGGGCT 700
||||| |||||||
Db 1 CACAGCTGTGAGGGGCT 18

RESULT 729
BD169501/c
LOCUS BD169501 18 bp DNA linear PAT 17-JAN-2003
DEFINITION A gene coding for aceto-lactate-synthetase.
ACCESSION BD169501
VERSION BD169501.1 GI:27875313
KEYWORDS WO 0244385-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Shimizu,T., Nakayama,I., Nagayama,K., Fukuda,A., Tanaka,Y. and Kaku,K.
TITLE A gene coding for aceto-lactate-synthetase
JOURNAL Patent: WO 0244385-A 2 06-JUN-2002;
KUMIAI CHEMICAL INDUSTRY CO LTD, NATIONAL INSTITUTE OF
AGROBIOLOGICAL SCIENCES,TSUTOMU SHIMIZU, ISHIZUE NAKAYAMA,KOZO
NAGAYAMA,ATSUNORI FUKUDA,YOSHIYUKI TANAKA,KOICHIRO KAKU
COMMENT OS Artificial Sequence
PN WO 0244385-A/2
PD 06-JUN-2002
PF 16-NOV-2001 WO 2001JP010014
PR 29-NOV-2000 JP 00P 362630
PI TSUTOMU SHIMIZU, ISHIZUE NAKAYAMA,KOZO NAGAYAMA,ATSUNORI
FUKUDA,
PI YOSHIYUKI TANAKA,KOICHIRO KAKU
PC C12N15/60,C12N9/88,C12N5/14,A01H5/00
CC Description of Artificial Sequence:primer
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Artificial Sequence'.
FEATURES
source
1..18
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1010 AAGATGTTGGTGGGATG 1027
||||| |||||||
Db 18 AAGAGGTGTTGGTGATG 1

RESULT 730
BD176184/c
LOCUS BD176184 18 bp DNA linear PAT 18-MAR-2003
DEFINITION Mammalian telomerase.
ACCESSION BD176184
VERSION BD176184.1 GI:29121890
KEYWORDS JP 2002272489-A/43.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau,S., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: JP 2002272489-A 43 24-SEP-2002;
GERON CORP
COMMENT OS Unidentified
PN JP 2002272489-A/43
PD 24-SEP-2002
PF 06-MAR-2002 JP 2002061125

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1010 AAGATGTTGGTGGGATG 1027
||||| |||||||
Db 18 AAGAGGTGTTGGTGATG 1

RESULT 730
BD176184/c
LOCUS BD176184 18 bp DNA linear PAT 18-MAR-2003
DEFINITION Mammalian telomerase.
ACCESSION BD176184
VERSION BD176184.1 GI:29121891
KEYWORDS JP 2002272489-A/44.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau,S., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: JP 2002272489-A 44 24-SEP-2002;
GERON CORP
COMMENT OS Unidentified
PN JP 2002272489-A/44
PD 24-SEP-2002
PF 06-MAR-2002 JP 2002061125
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/482115 PI BRYANT
VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Mammalian telomerase
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Unidentified'.
FEATURES
source
1..18
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGG 1036
||||| |||||||
Db 18 TTGGGGTTGGGTTGGG 1

RESULT 731
BD176185/c
LOCUS BD176185 18 bp DNA linear PAT 18-MAR-2003
DEFINITION Mammalian telomerase.
ACCESSION BD176185
VERSION BD176185.1 GI:29121891
KEYWORDS JP 2002272489-A/44.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Villeponteau,S., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: JP 2002272489-A 44 24-SEP-2002;
GERON CORP
COMMENT OS Unidentified
PN JP 2002272489-A/44
PD 24-SEP-2002
PF 06-MAR-2002 JP 2002061125
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/482115 PI BRYANT
VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Mammalian telomerase
FH Key Location/Qualifiers
FT source 1..18
FT /organism='Unidentified'.
FEATURES
source
1..18
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGG 1036
||||| |||||||
Db 18 TTGGGGTTGGGTTGGG 1

RESULT 732
AB069090
LOCUS AB069090 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-etsG4981
```

```

at lp36.
ACCESSION AB069090
VERSION AB069090.1 GI:15129894
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Mochishashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 7p35-p36
JOURNAL Chromosomes 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii, A.
JOURNAL Direct Submission
TITLE Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1..18
/note="forward primer for human STS sts-stSG4981 at lp36
sts-stSG4981 obtained from clones B277F18, B370B7, B133B1,
B137C2, B182L10, B123L12, B200L1, B200L2, B215B22, Human
BAC library RPCI-11"
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 683 CACAGCCTGTGAGGGGCT 700
|||||
Db 1 CACAGCCTGTGAGGGGCT 18

RESULT 733
AX129282
LOCUS AX129282
DEFINITION Sequence 500 from Patent WO0130362.
ACCESSION AX129282
VERSION AX129282.1 GI:14135587
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 500 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="cdk4 ribozyme binding site"
Query Match 0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 905 GCCAGCCTCCAGGATG 922

at lp36.
ACCESSION AB069090
VERSION AB069090.1 GI:15129894
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K.,
Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H.,
Mochishashi, A., Ohira, M., Nakagawara, A., Liu, S., Hoshi, M., Horii, A.,
and Soeda, E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 7p35-p36
JOURNAL Chromosomes 74 (1), 55-70 (2001)
MEDLINE 21269192
PUBMED 11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii, A.
JOURNAL Direct Submission
TITLE Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp,
Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature
1..18
/note="forward primer for human STS sts-stSG4981 at lp36
sts-stSG4981 obtained from clones B277F18, B370B7, B133B1,
B137C2, B182L10, B123L12, B200L1, B200L2, B215B22, Human
BAC library RPCI-11"
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 683 CACAGCCTGTGAGGGGCT 700
|||||
Db 1 CACAGCCTGTGAGGGGCT 18

RESULT 733
AX129282
LOCUS AX129282
DEFINITION Sequence 500 from Patent WO0130362.
ACCESSION AX129282
VERSION AX129282.1 GI:14135587
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Robbins, J.M. and Tritz, R.
TITLE Ribozyme therapy for the treatment of proliferative skin and eye
diseases
JOURNAL Patent: WO 0130362-A 500 03-MAY-2001;
IMMUSOL, INC. (US)
FEATURES
source
1..19
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="cdk4 ribozyme binding site"
Query Match 0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 905 GCCAGCCTCCAGGATG 922

RESULT 734
AX411902/c
LOCUS AX411902/c
DEFINITION Sequence 2 from Patent WO0226968.
ACCESSION AX411902
VERSION AX411902.1 GI:21444367
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 2 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
FEATURES
source
1..19
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="based on Homo sapiens"
Query Match 0.8%; Score 14.8; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 900 COTGAGCCAGCCTCCAGA 917
|||||
Db 18 COTGAGCCAGCCTCTAGA 1

RESULT 735
AR137265/c
LOCUS AR137265
DEFINITION Sequence 12 from patent US 6197505.
ACCESSION AR137265
VERSION AR137265.1 GI:14478774
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Norberg, L., Torbjorn, A., Andersson, M., Kristina, and
Lindstrom, P., Harry, Rutger.
TITLE Methods for assessing cardiovascular status and compositions for
use thereof
JOURNAL Patent: US 6197505-A 12 06-MAR-2001;
FEATURES
source
1..16
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1385 AGCCAGGTCAGGAGGA 1400
|||||
Db 16 AGCCAGGTCAGGGGGA 1

RESULT 736
BD231248/c
LOCUS BD231248
DEFINITION Genes for assessing cardiovascular status and compositions for use
thereof.
ACCESSION BD231248
VERSION BD231248.1 GI:33041018
KEYWORDS JP 2002527079-A/12.

```


SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 (bases 1 to 16)
Norberg,L.T., Andersson,M.K., Lindstrom,P.H.R. and Jonsson,L.
AUTHORS
Genes for assessing cardiovascular status and compositions for use
TITLE
thereof
JOURNAL
Patent: JP 2002527079-A 12 27-AUG-2002;
PAIRSEAKENSINGU AB
COMMENT
OS Artificial Sequence
PN JP 2002527079-A/12
PD 27-AUG-2002
PF 13-OCT-1999 JP 2000576056
PR 14-OCT-1998 US 60/104286,14-OCT-1998 US 60/104302 PI
LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM,
PI LENA JONSSON
PC C12Q1/68,C12N15/09//G01N33/53,G01N33/566,C12N15/00 CC Genes
for assessing cardiovascular status
and compositions for
CC use thereof
FH Key Location/Qualifiers
FT source 1..16
FT /organism='Artificial Sequence'.
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1385 AGCCAGGTCAGGAGGA 1400
|||||
Db 16 AGCCAGGTCAGGAGGA 1
RESULT 737
AX037387/c
LOCUS
AX037387 16 bp DNA linear PAT 16-NOV-2000
DEFINITION
Sequence 12 from Patent WO0056922.
ACCESSION
AX037387
VERSION
AX037387.1 GI:11226812
KEYWORDS
synthetic construct
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1
Norberg,L.T., Olaisson,E., Jonsson,L., Lindstrom,P.H. and
Sanders,R.
TITLE
Genetic polymorphism and polymorphic pattern for assessing disease
status, and compositions for use thereof
JOURNAL
Patent: WO 0056922-A 12 28-SEP-2000;
NORBERG LEIF TORBJORN (SE) ; OLAISSON ERIK (SE) ; JONSSON LENA (SE)
; GEMINI GENOMICS AB (SE) ; LINDSTROM PER HARRY RUTGER (SE) ;
SANDERS RHIANNON (SE)
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer"
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1385 AGCCAGGTCAGGAGGA 1400
|||||
Db 16 AGCCAGGTCAGGAGGA 1

RESULT 738
BD075139/c
LOCUS
BD075139 16 bp DNA linear PAT 27-AUG-2002
DEFINITION
Methods for assessing cardiovascular status and compositions for
use thereof.
ACCESSION
BD075139 GI:22620742
VERSION
BD075139.1
KEYWORDS
JP 2001519660-A/12.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 16)
Norberg,L.T., Andersson,M.K. and Lindstrom,P.H.R.
AUTHORS
Methods for assessing cardiovascular status and compositions for
use thereof
TITLE
Patent: JP 2001519660-A 12 23-OCT-2001;
JOURNAL
EURONA MEDICAL AB
COMMENT
OS Artificial Sequence
PN JP 2001519660-A/12
PD 23-OCT-2001
PF 01-APR-1998 JP 1998542530
PR 04-APR-1997 US 60/042930
PI LEIF TORBJORN NORBERG,MARIA KRISTINA ANDERSSON,PER HARRY PI
RUTGER LINDSTROM
PC C12Q1/68,C07K14/72,C07K14/575,C12N9/48
CC Description of Artificial Sequence: PCR PRIMER PH Key
Location/Qualifiers
FT source 1..16
FT /organism='Artificial Sequence'.
FEATURES
source
1..16
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1385 AGCCAGGTCAGGAGGA 1400
|||||
Db 16 AGCCAGGTCAGGAGGA 1
RESULT 739
AX216921
LOCUS
AX216921 17 bp RNA linear PAT 07-SEP-2001
DEFINITION
Sequence 2363 from Patent WO0159103.
ACCESSION
AX216921
VERSION
AX216921.1 GI:15526982
KEYWORDS
synthetic construct
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1
Blatt,L., McSwiggen,J. and Chowrira,B.M.
AUTHORS
Method and reagent for the modulation and diagnosis of cd20 and
TITLE
nogo gene expression
JOURNAL
Patent: WO 0159103-A 2363 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      861 AGGAAGAGGAAGAGGA 876
Db      2 AGGAGGAGGAAGAGGA 17

RESULT 740
LOCUS   AX218059
DEFINITION Sequence 3501 from Patent WO0159103.
ACCESSION AX218059
VERSION   AX218059.1 GI:15528120
KEYWORDS synthetic construct
SOURCE   synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS  Blatt, L., Mcswiggen, J. and Chowrira, B.M.
TITLE    Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL  nogo gene expression
PATENT:  WO 0159103-A 3501 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES Location/Qualifiers
source      1..17
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Nucleic Acid"

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1008 AGAAGATGGTGTGGG 1023
Db      2 AGAAGAAGTGGTGTGGG 17

RESULT 741
LOCUS   AX422499
DEFINITION Sequence 835 from Patent WO0188124.
ACCESSION AX422499
VERSION   AX422499.1 GI:21525881
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS  Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and
TITLE    Randi, A.M.
JOURNAL  Method and reagent for the inhibition of erg
PATENT:  WO 0188124-A 835 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES Location/Qualifiers
source      1..17
            /organism="Homo sapiens"
            /mol_type="unassigned RNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      268 GCACCTCCAGCCACC 283
Db      2 GCCCTCCAGCCACC 17

RESULT 742
LOCUS   AX692522/c
DEFINITION Sequence 5254 from Patent EP1281758.
ACCESSION AX692522
VERSION   AX692522.1 GI:29415480
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS  Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE    Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
JOURNAL  mdz12
PATENT:  EP 1281758-A 5254 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source      1..17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 5.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAA 1751
Db      17 AAAAAAAAAAAAAAGAA 2

RESULT 743
LOCUS   A63079
DEFINITION Sequence 6 from Patent WO9720197.
ACCESSION A63079
VERSION   A63079.1 GI:3716943
KEYWORDS unidentified
SOURCE   unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS  Arguello, R., Avakian, H. and Madrigal, A.
TITLE    METHOD FOR IDENTIFYING AN UNKNOWN ALLELE
JOURNAL  Patent: WO 9720197-A 6 05-JUN-1997;
ANTHONY NOLAN BONE MARROW TRUS (GB)
COMMENT   Other publication AU 7703796 19970619.
FEATURES Location/Qualifiers
source      1..18
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"

Query Match      0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      907 CAGCCTCCAGAGGATG 922
Db      2 CACCCTCCAGAGGATG 17

RESULT 744
LOCUS   AR095850
DEFINITION Sequence 71 from patent US 6004814.
ACCESSION AR095850
VERSION   AR095850.1 GI:10024110
KEYWORDS Unknown.
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Bennett, C.Frank. and Cowsert, L.M.
TITLE    Antisense modulation of CD71 expression

QY      907 CAGCCTCCAGAGGATG 922
Db      2 CACCCTCCAGAGGATG 17

RESULT 744
LOCUS   AR095850
DEFINITION Sequence 71 from patent US 6004814.
ACCESSION AR095850
VERSION   AR095850.1 GI:10024110
KEYWORDS Unknown.
SOURCE   Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS  Bennett, C.Frank. and Cowsert, L.M.
TITLE    Antisense modulation of CD71 expression

```

```

JOURNAL Patent: US 6004814-A 71 21-DEC-1999;
FEATURES Location/Qualifiers
    source
        1..18
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 729 GGCTTCTGGGCCCTC 744
Db 3 GGCTTCTGGGCCCTC 18

RESULT 745
AR266237/c
LOCUS AR266237 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 49 from patent US 6492173.
ACCESSION AR266237
VERSION AR266237.1 GI:29695083
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Cowsett,L.M.
TITLE Antisense inhibition of cyclin D2 expression
JOURNAL Patent: US 6492173-A 49 10-DEC-2002;
FEATURES Location/Qualifiers
    source
        1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1518 GCACATCTTGTGCAAG 1533
Db 17 GCACATCTTGTGCAAG 2

RESULT 746
AR268656
LOCUS AR268656 18 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 6 from patent US 6500614.
ACCESSION AR268656
VERSION AR268656.1 GI:29699271
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Arguello,R., Avakian,H. and Madrigal,A.
TITLE Method for identifying an unknown allele
JOURNAL Patent: US 6500614-A 6 31-DEC-2002;
FEATURES Location/Qualifiers
    source
        1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 907 CAGCCTCAGAGGATG 922
Db 2 CAGCCTCAGAGGATG 17

RESULT 747
AR392120/c
LOCUS AR392120 18 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 35 from patent US 6613567.
ACCESSION AR392120
VERSION AR392120.1 GI:40116010
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Bennett,C.F. and Cowsett,L.M.
TITLE Antisense inhibition of Her-2 expression
JOURNAL Patent: US 6613567-A 35 02-SEP-2003;
FEATURES Location/Qualifiers
    source
        1..18
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1650 TCTCCCTGACATCCAC 1665
Db 16 TCTCCCTGACATCCAC 1

RESULT 748
AX115223/c
LOCUS AX115223 18 bp DNA linear PAT 11-MAY-2001
DEFINITION Sequence 346 from Patent WO0129262.
ACCESSION AX115223
VERSION AX115223.1 GI:14032165
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 346 26-APR-2001;
FEATURES Location/Qualifiers
    source
        1..18
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Primer"

Query Match
Best Local Similarity 0.8%; Score 14.4; DB 1; Length 18;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 64 TTCTGGAGTCCCAAC 79
Db 18 TTCTGGAGTCCCAAC 3

RESULT 749
D00269S07
LOCUS D00269S07 18 bp DNA linear PRI 21-SEP-2002
DEFINITION Homo sapiens gene for tyrosine hydroxylase, exon 6, partial
sequence.
ACCESSION D00275
VERSION D00275.1 GI:220105
KEYWORDS
SEGMENT 7 of 24
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS O'Malley,K.L., Anhalt,M.J., Martin,B.M., Kelsoe,J.R., Winfield,S.L.
and Ginne,E.I.

```

TITLE Isolation and characterization of the human tyrosine hydroxylase gene: identification of 5' alternative splice sites responsible for multiple mRNAs

JOURNAL MEDLINE PUBMED Biochemistry 26 (22), 6910-6914 (1987)

REFERENCE 2892528

AUTHORS 2 (bases 1 to 18)

Kobayashi,K., Kaneda,N., Ichinose,H., Kishi,F., Nakazawa,A., Kurosawa,Y., Fujita,K. and Nagatsu,T.

TITLE Structure of the human tyrosine hydroxylase gene: alternative splicing from a single gene accounts for generation of four mRNA types

JOURNAL MEDLINE PUBMED J. Biochem. 103 (6), 907-912 (1988)

COMMENT 2902075

In [1], they determined the nucleotide sequences of all exons and their surrounding regions of human TH gene, and the exon/intron boundaries are shown. The boundaries were determined by comparing the genomic DNA sequence with the cDNA sequence. The human TH gene is split into 14 exons. In [1], they concluded that the four types of human TH mRNA are produced through alternative splicing from a single gene.

FEATURES Location/Qualifiers

source
1..18
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="GHTH-E20"
/tissue_type="placenta"
/note="54 bp after segment 6"
exon
1..8
/product="tyrosine hydroxylase"
/note="AA 244 at 1"
intron
9..>18
/number=6

Query Match 0.8%; Score 14.4; DB 1; Length 18;

Best Local Similarity 93.8%; Pred. No. 6e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 15; Conservative 0;

QY 684 ACAGGCAGTGAGGGGC 699

Db 2 ACAGGCAGTGAGGGGC 17

RESULT 750

LOCUS AR146849

DEFINITION Sequence 4 from patent US 6218597.

ACCESSION AR146849

VERSION AR146849.1 GI:15110038

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)

AUTHORS Port,J.David. and Bristow,M.R.

TITLE Transgenic model and treatment for heart disease

JOURNAL Patent: US 6218597-A 4 17-APR-2001;

FEATURES Location/Qualifiers

source
1..19
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 6.4e+02;

Matches 15; Conservative 1; Indels 0; Gaps 0;

QY 110 CAGCGCTCGGGGCTT 125

Db 2 CAGCGCTCGGGGCTT 17

RESULT 751

LOCUS AR393609

DEFINITION Sequence 148 from patent US 6617122.

ACCESSION AR393609

VERSION AR393609.1 GI:40120337

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 19)

AUTHORS Hayden,M.R., Brooks-Wilson,A.R. and Pimstone,S.N.

TITLE Process for identifying modulators of ABC1 activity

JOURNAL Patent: US 6617122-A 148 09-SEP-2003;

FEATURES Location/Qualifiers

source
1..19
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 6.4e+02; Mismatches 1; Indels 0; Gaps 0;

QY 1184 GCTCCAGCCCATCCT 1199

Db 4 GCTACAGCCCATCCT 19

RESULT 752

LOCUS AX130721

DEFINITION Sequence 1939 from Patent WO0130362.

ACCESSION AX130721

VERSION AX130721.1 GI:14137026

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Robbins,J.M. and Tritz,R.

TITLE Ribozyme therapy for the treatment of proliferative skin and eye diseases

JOURNAL Patent: WO 0130362-A 1939 03-MAY-2001;

FEATURES Location/Qualifiers

source
1..19
/organism="Homo sapiens"
/mol_type="unassigned DNA"

QY 1518 GCACATCTTGTGCAG 1533

Db 2 GCACATCTTGTGCAG 17

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 6.4e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 753

LOCUS AX659402

DEFINITION Sequence 4 from Patent WO02102824.

ACCESSION AX659402

VERSION AX659402.1 GI:29161632

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Beimfohr, C. and Snaidr, J.
TITLE Method for specific fast detection of relevant bacteria in drinking water
JOURNAL Patent: WO 02102824-A 4 27-DEC-2002;
Vermicon AG (DE)
FEATURES Location/Qualifiers
source 1..19
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="oligonucleotide"

Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.3%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 753 CCACCTTCCTCTCCCA 768
|||||
Db 1 CCACCTTCCTCTCCCA 16

RESULT 754
E52143/c
LOCUS E52143
DEFINITION TSA7005 gene.
ACCESSION E52143
VERSION E52143.1 GI:18629626
KEYWORDS JP 2001025389-A/3.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ogawara, T., Suzuki, M. and Ozaki, K.
TITLE TSA7005 gene
JOURNAL Patent: JP 2001025389-A 3 30-JAN-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unknown
PN JP 2001025389-A/3
PD 30-JAN-2001
PF 15-JUL-1999 JP 1999201279
PR
PI TSUYOSHI OGAWARA, MIKIO SUZUKI, KOICHI OZAKI
PC C12N15/09, C07K14/47, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10//A61K31/00,
PC A61K38/00, A61K48/00, C12P21/02, C12N15/00, C12N5/00, A61K37/02 CC

FT Key Location/Qualifiers
FT source 1..16
/organism='Unknown'.
FEATURES source Location/Qualifiers
source 1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.7e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
:|||||
Db 15 DAAAAAAAAAAAAA 1

RESULT 755
E53842/c
LOCUS E53842
DEFINITION LUNX gene and method for detecting micrometastasis of cancer.
ACCESSION E53842
VERSION E53842.1 GI:18633612
KEYWORDS JP 2001078772-A/3.
SOURCE unidentified
ORGANISM unidentified

unclassified.
1 (bases 1 to 16)
Kadota, M., Fujiwara, Y., Watanabe, R. and Ozaki, K.
TITLE LUNX gene and method for detecting micrometastasis of cancer
JOURNAL Patent: JP 2001078772-A 3 27-MAR-2001;
OTSUKA PHARMACEUT CO LTD
COMMENT OS Unidentified
PN JP 2001078772-A/3
PD 27-MAR-2001
PF 07-SEP-1999 JP 1999253186
PR
PI MORITO KADOTA, YOSHIYUKI FUJIWARA, RYUJI WATANABE, KOICHI OZAKI
PC C12N15/09, C07K14/82, C07K16/32, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10, C12Q1/68,
PC G01N33/15, G01N33/50, G01N33/566, G01N33/574//A61K31/713, PC
A61K35/12, A61K35/76,
PC A61K39/395, A61K39/395, A61K48/00, A61P35/00, A61P35/04, C12P21/08,
PC C12N15/00,
PC C12N5/00
CC
FT Key Location/Qualifiers
FT source 1..16
/organism='Unidentified'.
FEATURES source Location/Qualifiers
source 1..16
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14.2; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 5.7e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1749
:|||||
Db 15 BAAAAAAAAAAAAA 1

RESULT 756
AR029886
LOCUS AR029886
DEFINITION Sequence 75 from patent US 5861244.
ACCESSION AR029886
VERSION AR029886.1 GI:5943100
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Wang, C.-G. and Heppburn, A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 75 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..14
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
:|||||
Db 1 AAAAAAAAAAAAAA 14

RESULT 757
AR029887/c
LOCUS AR029887
DEFINITION Sequence 76 from patent US 5861244.
ACCESSION AR029887
VERSION AR029887.1 GI:5943101
KEYWORDS

```

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Wang, C.-G. and Heburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 76 19-JAN-1999;
FEATURES     Location/Qualifiers
              source
              1..14
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 758
AR168510/c AR168510 14 bp DNA linear PAT 17-DEC-2001
LOCUS      Sequence 26 from patent US 6287858.
ACCESSION  AR168510
VERSION     AR168510.1 GI:17904466
KEYWORDS    '
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      D'Andrea, A.D. and Zhu, Y.
TITLE        Deubiquitinating enzymes that regulate cell growth
JOURNAL      Patent: US 6287858-A 26 11-SEP-2001;
FEATURES     Location/Qualifiers
              source
              1..14
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1

RESULT 759
AR174024/c AR174024 14 bp DNA linear PAT 17-DEC-2001
LOCUS      Sequence 14 from patent US 6306624.
ACCESSION  AR174024
VERSION     AR174024.1 GI:17914344
KEYWORDS    '
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Petkovich, P. Martin., White, J.A., Beckett, B.R. and Jones, G.
TITLE        Retinoid metabolizing protein
JOURNAL      Patent: US 6306624-A 14 23-OCT-2001;
FEATURES     Location/Qualifiers
              source
              1..14
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1747

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Wang, C.-G. and Heburn, A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 76 19-JAN-1999;
FEATURES     Location/Qualifiers
              source
              1..14
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 760
BD237464 14 bp DNA linear PAT 17-JUL-2003
LOCUS      Nucleic acid having blocked terminals modified with an acid-stable
DEFINITION skeleton and therapeutic method thereof.
ACCESSION  BD237464
VERSION     BD237464.1 GI:33047234
KEYWORDS    '
SOURCE      synthetic construct
ORGANISM     synthetic construct
              artificial sequences.
              1 (bases 1 to 14)
REFERENCE    Dale, R.M.K., Gatton, S.L. and Arrow, A.
AUTHORS      Nucleic acid having blocked terminals modified with an acid-stable
TITLE        skeleton and therapeutic method thereof
JOURNAL      Patent: JP 2002534434-A 2 15-OCT-2002;
FEATURES     OLIGOS ETC INC
              OS Artificial Sequence
              PN JP 2002534434-A/2
              PD 15-OCT-2002
              PF 16-DEC-1999 JP 2000592300
              PR 30-DEC-1998 US 09/223498, 19-JUL-1999 US 09/356069 PI
              RODERIC M K DALE, STEVEN L GATTON, AMY ARROW
              PC C07H21/00, A61K9/127, A61K31/7088, A61K47/44, A61K48/00,
              A61P3/00,
              PC A61P17/02, A61P29/00, A61P31/04, A61P31/10, A61P31/12, A61P35/00,
              C12N5/10,
              PC C12N15/09, C12N15/00, C12N5/00
              CC Nucleic acid having blocked terminals modified with an acid-
              CC skeleton and therapeutic method thereof
              CC Key
              FH Location/Qualifiers
              FT source
              1..14
              /organism="Artificial Sequence".
              Location/Qualifiers
              1..14
              /organism="synthetic construct"
              /mol_type="genomic DNA"
              /db_xref="taxon:32630"

Query Match      0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 14

RESULT 761
AR222460 14 bp DNA linear PAT 26-SEP-2002
LOCUS      Sequence 20 from patent US 6429300.
DEFINITION AR222460
ACCESSION  AR222460
VERSION     AR222460.1 GI:23329991
KEYWORDS    '
SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS      Kurz, M., Lohse, P. and Wagner, R.
TITLE        Peptide acceptor ligation methods
JOURNAL      Patent: US 6429300-A 20 06-AUG-2002;
FEATURES     Location/Qualifiers
              source
              1..14
              /organism="unknown"
              /mol_type="genomic DNA"

Query Match      0.8%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 14;

```

```
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 762
AR364948/c
LOCUS AR364948 14 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 4 from patent US 5453496.
ACCESSION AR364948
VERSION AR364948.1 GI:34428168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE Polynucleotide phosphorodithioate
JOURNAL Patent: US 5453496-A 4 26-SEP-1995;
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 763
AR364949
LOCUS AR364949 14 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 5 from patent US 5453496.
ACCESSION AR364949
VERSION AR364949.1 GI:34428169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Caruthers,M.H., Marshall,W.S., Brill,W. and Nielsen,J.
TITLE Polynucleotide phosphorodithioate
JOURNAL Patent: US 5453496-A 5 26-SEP-1995;
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 764
AX048406/c
LOCUS AX048406 14 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071747.
ACCESSION AX048406
VERSION AX048406.1 GI:12225570
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct

artificial sequences.
1
REFERENCE
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
production and use of the same
JOURNAL Patent: WO 0071747-A 5 30-NOV-2000;
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Region A"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 765
AX827014
LOCUS AX827014 14 bp RNA linear PAT 12-DEC-2003
DEFINITION Sequence 11 from Patent EP1344835.
ACCESSION AX827014
VERSION AX827014.1 GI:39837221
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Rabbani,E., Stavrianopoulos,J.G., Donegan,J.J., Coleman,J. and
Liu,D.
TITLE Real-time nucleic acid detection processes and compositions
JOURNAL Patent: EP 1344835-A 11 17-SEP-2003;
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Primer"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 766
AX839906
LOCUS AX839906 14 bp RNA linear PAT 16-DEC-2003
DEFINITION Sequence 11 from Patent EP1348713.
ACCESSION AX839906
VERSION AX839906.1 GI:39978437
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
processes and other processes for using same in nucleic acid
determinations and analyses
JOURNAL Patent: EP 1348713-A 11 01-OCT-2003;
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Primer"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 767
AX839906
LOCUS AX839906 14 bp RNA linear PAT 16-DEC-2003
DEFINITION Sequence 11 from Patent EP1348713.
ACCESSION AX839906
VERSION AX839906.1 GI:39978437
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Stavrianopoulos,J.G. and Rabbani,E.
TITLE Labeling reagents and labeled targets, target labeling
processes and other processes for using same in nucleic acid
determinations and analyses
JOURNAL Patent: EP 1348713-A 11 01-OCT-2003;
FEATURES
    source
        Location/Qualifiers
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned RNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Primer"

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 768
AX048406/c
LOCUS AX048406 14 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 5 from Patent WO0071747.
ACCESSION AX048406
VERSION AX048406.1 GI:12225570
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
```

```
source
1..14
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Description of Artificial Sequence: Primer"

Query Match
Best Local Similarity 0.8%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
DB 1 AAAAAAAAAAAAAA 14

RESULT 767
BD073890/c
LOCUS BD073890 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073890
VERSION BD073890.1 GI:22619493
KEYWORDS JP 2001512698-A/15.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 15 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/15
PD 28-AUG-2001
PE 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM,SUZANNE HOSTER,MANFRED KUBBIES PC
C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N15/09, PC
C12P21/02,
PC C12P21/08,C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Isolation of novel aging factor gene P23
FH Key Location/Qualifiers
FT source 1..14
FEATURES
source
1..14
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.8%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1747
DB 14 ACAAAAAAAAAAAAAA 1

RESULT 768
BD084127
LOCUS BD084127 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084127
VERSION BD084127.1 GI:22629737
KEYWORDS JP 2001525663-A/15.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 14)

AUTHORS Feder,J.N., Krommal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tsuchihashi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 15 11-DEC-2001;
PROGENITOR INC
COMMENT OS Homo sapiens (human)
PN JP 2001525663-A/15
PD 11-DEC-2001
PE 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KROMMAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
and new genes in the region of the human CC hemochromatosis gene
FH key Location/Qualifiers
FT source 1..14
FEATURES
source
1..14
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.8%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
DB 1 AAAAAAAAAAAAAA 14

RESULT 769
BD096963/c
LOCUS BD096963 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Oligonucleotide for SNP detection.
ACCESSION BD096963
VERSION BD096963.1 GI:22642551
KEYWORDS JP 2001346579-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Komiyama,M. and Asanuma,H.
TITLE Oligonucleotide for SNP detection
JOURNAL Patent: JP 2001346579-A 2 18-DEC-2001;
MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT OS Artificial Sequence
PN JP 2001346579-A/2
PD 18-DEC-2001
PE 02-JUN-2000 JP 2000165441
PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
PC C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
PC C12N15/00,
PC C12N15/00,
CC Oligonucleotide for SNP detection
FH key Location/Qualifiers
FT modified base 1.
FEATURES
source
1..14
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.8%; Score 14; DB 1; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
DB 14 AAAAAAAAAAAAAA 1
```



```

RESULT 770
BD096965/c
LOCUS          BD096965          14 bp      DNA          linear          PAT 27-AUG-2002
DEFINITION     Oligonucleotide for SNP detection.
ACCESSION      BD096965
VERSION        BD096965.1  GI:22642553
KEYWORDS       JP 2001346579-A/4.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Komiya,M. and Asanuma,H.
TITLE          Oligonucleotide for SNP detection
JOURNAL        Patent: JP 2001346579-A 4 18-DEC-2001;
                MAKOTO KOMIYAMA,HIROYUKI ASANUMA
COMMENT        OS Artificial Sequence
                PN JP 2001346579-A/4
                PD 18-DEC-2001
                PF 02-JUN-2000  JP 2000165441
                PI MAKOTO KOMIYAMA,HIROYUKI ASANUMA
                PC C12N15/09,C12N15/09,C12Q1/68,G01N21/78,G01N33/53,G01N33/566,
                PC C12N15/00,
                CC Oligonucleotide for SNP detection
                FH Key
                FT modified base 1.
FEATURES       source
                1..14
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 771
BD132850/c
LOCUS          BD132850          14 bp      DNA          linear          PAT 18-SEP-2002
DEFINITION     Methods of nucleic acid detection.
ACCESSION      BD132850
VERSION        BD132850.1  GI:23227795
KEYWORDS       JP 2002509443-A/1.
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Weisburg,W.G., Stull,P.D. and Reshatoff,M.R.
TITLE          Methods of nucleic acid detection
JOURNAL        Patent: JP 2002509443-A 1 26-MAR-2002;
                GEN PROBE INC
COMMENT        OS Artificial Sequence
                PN JP 2002509443-A/1
                PD 26-MAR-2002
                PF 30-OCT-1998  JP 1999526687
                PR 31-OCT-1997  US 60/063969
                PI WILLIAM G WEISBURG,PAUL D STULL,MICHAEL R RESHATOFF PC
                CC Description of Artificial Sequence: synthetic oligonucleotide
                FH Key
                FT Location/Qualifiers
                1..14
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 1; Gaps 14;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 772
BD176795/c
LOCUS          BD176795          14 bp      DNA          linear          PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176795
VERSION        BD176795.1  GI:29122507
KEYWORDS       WO 02074951-A/42.
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 42 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/42
                PD 26-SEP-2002
                PF 13-MAR-2002  WO 2002JP002338
                PR 15-MAR-2001  JP 01P 073959
                PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
                CC Synthetic DNA
                FH Key
                FT Location/Qualifiers
                1..14
                /organism="Artificial Sequence".
                source
                1..14
                /organism="synthetic construct"
                /mol_type="genomic DNA"
                /db_xref="taxon:32630"

Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 773
BD176800/c
LOCUS          BD176800          14 bp      DNA          linear          PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176800
VERSION        BD176800.1  GI:29122512
KEYWORDS       WO 02074951-A/47.
SOURCE         synthetic construct
ORGANISM       synthetic construct
                artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 47 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/47.
                PD 26-SEP-2002

```

PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA HIROSE, JUN SAKAI PC
C12N15/09, C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
/organism="Artificial Sequence".
FEATURES
source
1..14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAA 1747
Db 14 ACAAAAAAAAAAAAA 1

RESULT 774
BD176803/c
LOCUS
DEFINITION
14 bp DNA linear PAT 18-MAR-2003
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION
BD176803
VERSION
BD176803.1 GI:29122515
KEYWORDS
WO 02074951-A/50.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
1 (bases 1 to 14)
Yamamoto, M., Yamamoto, N., Hirose, K. and Sakai, J.
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
Patent: WO 02074951-A 50 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD, MIKIO YAMAMOTO, NAOKI YAMAMOTO,
KUNITAKA HIROSE, JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/50
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA HIROSE, JUN SAKAI PC
C12N15/09, C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
/organism="Artificial Sequence".
FEATURES
source
1..14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAA 1748
Db 14 CAAAAAAAAAAAAAAAA 1

RESULT 775
BD176804/c
LOCUS
DEFINITION
14 bp DNA linear PAT 18-MAR-2003
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION
BD176804

BD176804.1 GI:29122516
WO 02074951-A/51.
synthetic construct
synthetic construct
artificial sequences.
1 (bases 1 to 14)
Yamamoto, M., Yamamoto, N., Hirose, K. and Sakai, J.
Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
Patent: WO 02074951-A 51 26-SEP-2002;
KOREHA CHEMICAL INDUSTRY CO LTD, MIKIO YAMAMOTO, NAOKI YAMAMOTO,
KUNITAKA HIROSE, JUN SAKAI
OS Artificial Sequence
PN WO 02074951-A/51
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO, NAOKI YAMAMOTO, KUNITAKA HIROSE, JUN SAKAI PC
C12N15/09, C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
/organism="Artificial Sequence".
FEATURES
source
1..14 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

RESULT 776
AR055852/c
LOCUS
DEFINITION
Sequence 56 from patent US 5837542.
ACCESSION
AR055852
VERSION
AR055852.1 GI:5981429
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Grimm, S., Stinchcomb, D.T., McSwiggan, J., Sullivan, S. and
Draper, K.G.
TITLE
Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL
Patent: US 5837542-A 56 17-NOV-1998;
FEATURES
Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 CCCACGAGCAGCA 270
Db 14 CCCACGAGCAGCA 1

RESULT 777
AR056156/c
LOCUS
DEFINITION
Sequence 360 from patent US 5837542.
ACCESSION
AR056156
VERSION
AR056156.1 GI:5981733

[illegible]

```
VERSION AR113917.1 GI:14094239
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 363 17-OCT-2000;
FEATURES
    source
        1..15
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1
RESULT 783
AR114151/c
LOCUS AR114151 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 597 from patent US 6132967.
ACCESSION AR114151
VERSION AR114151.1 GI:14094473
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of
intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 597 17-OCT-2000;
FEATURES
    source
        1..15
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1
RESULT 784
AR114151/c
LOCUS AR114151 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 3 from patent US 5576427.
ACCESSION AR114151
VERSION AR114151.1 GI:1819856
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook,P.D., Delecki,D.J. and Guinasso,C.
TITLE Acyclic nucleoside analogs and oligonucleotide sequences containing
them
JOURNAL Patent: US 5576427-A 3 19-NOV-1996;
FEATURES
    source
        1..15
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 CCCACGGAGCAGCA 270
Db 14 CCCACGGAGCAGCA 1
RESULT 785
AR114151/c
LOCUS AR114151 15 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 4 from patent US 5576427.
ACCESSION AR114151
VERSION AR114151.1 GI:1819857
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Cook,P.D., Delecki,D.J. and Guinasso,C.
TITLE Acyclic nucleoside analogs and oligonucleotide sequences containing
them
JOURNAL Patent: US 5576427-A 4 19-NOV-1996;
FEATURES
    source
        1..15
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 786
AR114151/c
LOCUS AR114151 15 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 16 from patent US 5658780.
ACCESSION AR114151
VERSION AR114151.1 GI:2479410
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE Rel a targeted ribozymes
JOURNAL Patent: US 5658780-A 16 19-AUG-1997;
FEATURES
    source
        1..15
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 727 CAGGCTTCGGGCC 740
Db 1 CAGGCTTCGGGCC 14
RESULT 787
AR241870/c
LOCUS AR241870 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 158 from patent US 6472154.
ACCESSION AR241870
```

```

VERSION AR241870.1 GI:27287682
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 158 29-OCT-2002;
FEATURES Location/Qualifiers
source
1..15
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db ||| ||||| |||||
15 AAAAAAAAAAAAAA 1

RESULT 788
AX632881/c
LOCUS AX632881 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 20 from Patent EP1260586.
ACCESSION AX632881
VERSION AX632881.1 GI:28468495
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 20 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 257 CCCACGGAGCAGCA 270
Db ||| ||||| |||||
14 CCCACGGAGCAGCA 1

RESULT 789
AX633195/c
LOCUS AX633195 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 334 from Patent EP1260586.
ACCESSION AX633195
VERSION AX633195.1 GI:28468809
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 20 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db ||| ||||| |||||
14 AAAAAAAAAAAAAA 1

RESULT 790
AX633201/c
LOCUS AX633201 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 340 from Patent EP1260586.
ACCESSION AX633201
VERSION AX633201.1 GI:28468815
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 340 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES Location/Qualifiers
source
1..15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db ||| ||||| |||||
14 AAAAAAAAAAAAAA 1

RESULT 791
AX633299/c
LOCUS AX633299 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 438 from Patent EP1260586.
ACCESSION AX633299
VERSION AX633299.1 GI:28468913
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes

```



```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mezes,P.S., Gourlie,B.B., Rixon,M.W., Schlom,J., Kaplan,D.A. and
Anderson,W.H.Kerr.
TITLE Family of high affinity, modified antibodies for cancer treatment
JOURNAL Patent: US 593813-A 23 30-NOV-1999;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 797
LOCUS ARI40675 16 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 23 from patent US 6207815.
ACCESSION ARI40675
VERSION ARI40675.1 GI:14483171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mezes,P.S., Gourlie,B.B., Rixon,M.W., Schlom,J., Kaplan,D.A. and
Anderson,W.H.Kerr.
TITLE Family of high affinity, modified antibodies for cancer treatment
JOURNAL Patent: US 593813-A 23 30-NOV-1999;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 798
LOCUS ARI40675 16 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 23 from patent US 6207815.
ACCESSION ARI40675
VERSION ARI40675.1 GI:14483171
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mezes,P.S., Gourlie,B.B., Rixon,M.W., Schlom,J., Kaplan,D.A. and
Anderson,W.H.Kerr.
TITLE Family of high affinity, modified antibodies for cancer treatment
JOURNAL Patent: US 593813-A 23 30-NOV-1999;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 799
LOCUS ARI40688 16 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 39 from patent US 6207815.
ACCESSION ARI40688
VERSION ARI40688.1 GI:14483184
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mezes,P.S., Gourlie,B.B., Rixon,M.W., Schlom,J., Kaplan,D.A. and
Anderson,W.H.Kerr.
TITLE Family of high affinity, modified antibodies for cancer treatment
JOURNAL Patent: US 6207815-A 39 27-MAR-2001;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16

RESULT 800
LOCUS I16032 16 bp DNA linear PAT 03-APR-1996
DEFINITION Sequence 6 from patent US 5473060.
ACCESSION I16032
VERSION I16032.1 GI:1250940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 801
LOCUS I28367/c 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION I28367
VERSION I28367.1 GI:1819143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3

RESULT 802
LOCUS I28367/c 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 6 from patent US 5571677.
ACCESSION I28367
VERSION I28367.1 GI:1819143
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M. and Lloyd,D.H.
TITLE Oligonucleotide clamps having diagnostic applications
JOURNAL Patent: US 5473060-A 6 05-DEC-1995;
FEATURES Location/Qualifiers
source
1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3
```

```
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
        macromolecular structures
JOURNAL Patent: US 5571677-A 6 05-NOV-1996;
FEATURES Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3
RESULT 802
LOCUS AR428275
DEFINITION Sequence 23 from patent US 6641999.
ACCESSION AR428275
VERSION AR428275.1 GI:40187730
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mezes,P.S., Gourlie,B., Rixon,M.W. and Anderson,W.H.K.
TITLE Probing method for identifying antibodies specific for selected
        antigens
JOURNAL Patent: US 6641999-A 23 04-NOV-2003;
FEATURES Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16
RESULT 803
LOCUS AR428288
DEFINITION Sequence 39 from patent US 6641999.
ACCESSION AR428288
VERSION AR428288.1 GI:40187743
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Mezes,P.S., Gourlie,B., Rixon,M.W. and Anderson,W.H.K.
TITLE Probing method for identifying antibodies specific for selected
        antigens
JOURNAL Patent: US 6641999-A 39 04-NOV-2003;
FEATURES Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1396 GAGGAGACTGTGAG 1409
Db 3 GAGGAGACTGTGAG 16
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
        macromolecular structures
JOURNAL Patent: US 5571677-A 6 05-NOV-1996;
FEATURES Location/Qualifiers
        source
            1..16
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 16 AAAAAAAAAAAAAA 3
RESULT 804
LOCUS AX359760
DEFINITION Sequence 64 from Patent WO0200691.
ACCESSION AX359760
VERSION AX359760.1 GI:18675467
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Vernet,C.A., Tchernev,V., Putturajan,M., Malyankar,U.M., Gusev,V.,
        Herrmann,J.L., Macdougall,J.R., Rastelli,L., Zhong,H., Spytek,K.A.,
        Shenoy,S., Gerlach,V.L., Gangolli,E.A., Stone,D.J. and
        Smithson,G.
TITLE Novel polynucleotides and polypeptides encoded thereby
        Patent: WO 0200691-A 64 03-JAN-2002;
JOURNAL Curagen Corporation (US)
FEATURES Location/Qualifiers
        source
            1..16
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match 0.8%; Score 14; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
RESULT 805
LOCUS AR187060/c
DEFINITION Sequence 2548 from patent US 6346398.
ACCESSION AR187060
VERSION AR187060.1 GI:20233025
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
        related to levels of vascular endothelial growth factor receptor
        Patent: US 6346398-A 2548 12-FEB-2002;
JOURNAL
FEATURES Location/Qualifiers
        source
            1..17
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749
Db 17 AAAAAAAAAAAAAA 4
RESULT 806
LOCUS AR187065/c
DEFINITION Sequence 2553 from patent US 6346398.
ACCESSION AR187065
VERSION AR187065.1 GI:20233030
KEYWORDS
```


[illegible]

```

DEFINITION Sequence 1506 from Patent EP1239051.
ACCESSION AX531997
VERSION AX531997.1 GI:25255760
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M.
TITLE Human poeh-like protein 1
JOURNAL Patent: EP 1239051-A 1506 11-SEP-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
source
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 897 GCCCTGAGCCAGC 910
Db 14 GCCCTGAGCCAGC 1

RESULT 812
AX724616/c
LOCUS AX692529 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 5261 from Patent EP1281758.
ACCESSION AX692529
VERSION AX692529.1 GI:29415487
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 5261 05-FEB-2003;
JOURNAL Aeomica, Inc. (US)
FEATURES
source
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAA 1748
Db 14 CAAAAAATAAAAAA 1

RESULT 813
AX724616/c
LOCUS AX724616 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2303 from Patent WO03025176.
ACCESSION AX724616
VERSION AX724616.1 GI:30503959
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2303 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
Patent: WO 03025176-A 2303 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

QY 336 GGGACCGGAGGATC 349
Db 14 GGGACCGGAGGATC 1

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 336 GGGACCGGAGGATC 349
Db 14 GGGACCGGAGGATC 1

RESULT 814
AX728102/c
LOCUS AX728102 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5789 from Patent WO03025176.
ACCESSION AX728102
VERSION AX728102.1 GI:30507445
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5789 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1286 CTTTCACAGTGGAT 1299
Db 15 CTTTCACAGTGGAT 2

RESULT 815
AX728167/c
LOCUS AX728167 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5854 from Patent WO03025176.
ACCESSION AX728167
VERSION AX728167.1 GI:30507510
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5854 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
Patent: WO 03025176-A 5854 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

QY 1286 CTTTCACAGTGGAT 1299
Db 15 CTTTCACAGTGGAT 2

RESULT 815
AX728167/c
LOCUS AX728167 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5854 from Patent WO03025176.
ACCESSION AX728167
VERSION AX728167.1 GI:30507510
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5854 27-MAR-2003;
JOURNAL Molecular Engines Laboratories (FR)
FEATURES
source
Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
Patent: WO 03025176-A 5854 27-MAR-2003;
Molecular Engines Laboratories (FR)
Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

QY 1286 CTTTCACAGTGGAT 1299
Db 15 CTTTCACAGTGGAT 2
```

[illegible]

```

FT source 1..17
FT /organism='Homo sapiens (human)'
FEATURES
  source
    1..17
    Location/Qualifiers
      /organism="Homo sapiens"
      /mol_type="genomic RNA"
      /db_xref="taxon:9606"

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.4e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 768 AGCCGAGGTGAAG 781
Db 14 AGCCGAGGTGAAG 1

RESULT 820
AX116603/c
LOCUS
DEFINITION
ACCESSION AX116603
VERSION AX116603.1 GI:14033545
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  Picoult-Newburg, L. and Pohl, M.
  Genotyping reagents, kits and methods of use thereof
  Patent: WO 0129262-A 1726 26-APR-2001;
  Orchid BioSciences, Inc. (US)
FEATURES
  source
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Primer"

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 278 CCCACCCAGGTC 291
Db 18 CCCACCCAGGTC 5

RESULT 821
AX661797/c
LOCUS
DEFINITION
ACCESSION AX661797
VERSION AX661797.1 GI:29162860
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  Hinkel, C.A., Kimmerly, W.J. and Yang, L.
  Methods of analysis of nucleic acids
  Patent: WO 02061121-A 11 08-AUG-2002;
  Syngenta Participations AG (CH)
FEATURES
  source
    1..18
    /organism="synthetic construct"
    /mol_type="unassigned DNA"
    /db_xref="taxon:32630"
    /note="Hybridization Tag"

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;

QY 1122 CQTGGAGGAGGG 1135
Db 15 CQTGGAGGAGGG 2

RESULT 822
AX685128/c
LOCUS
DEFINITION
ACCESSION AX685128
VERSION AX685128.1 GI:29371479
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  Lieber, C.M., Woolley, A.T., Hamm, J.I. and Housman, D.
  Direct haplotyping using carbon nanotube probes
  Patent: WO 0222889-A 5 21-MAR-2002;
  PRESIDENT AND FELLOWS OF HARVARD COLLEGE (US); Massachusetts
  Institute Of Technology (US)
FEATURES
  source
    1..18
    Location/Qualifiers
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic PNA label"

  misc_feature 7..8
    /note="Lys"

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 6.8e+02; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2;

QY 1734 ACAAANNAANNA 1749
Db 16 ACAAANNAANNA 1

RESULT 823
BD088131
LOCUS
DEFINITION
ACCESSION BD088131
VERSION BD088131.1 GI:22633741
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1
  Soeda, E.
  A method of arraying genome clone
  Patent: JP 2001321190-A 375 20-NOV-2001;
  THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
  GENOTECHS
COMMENT
  OS Artificial Sequence
  PN JP 2001321190-A/375
  PD 20-NOV-2001
  PF 12-MAR-2001 JP 2001069285
  PI EIICHI SOEDA
  PC C12N15/09, C12N15/09, C12M1/00, C12Q1/68, G01N33/53, G01N33/566, PC
  C12N15/00
  CC C12N15/00
  CC Description of Artificial Sequence: Synthetic DNA FH Key
  FT source
    1..18
    Location/Qualifiers
      /organism="Artificial Sequence"

FEATURES
  source
    1..18
    Location/Qualifiers
      /organism="synthetic construct"
      /mol_type="genomic DNA"
      /db_xref="taxon:32630"

```

```

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 TCCAGCACACGCAG 396
DB 1 TCCAGCACACGCAG 14

RESULT 824
AB068968
LOCUS AB068968 18 bp DNA linear SYN 21-MAY-2003
DEFINITION Synthetic construct DNA, forward primer for human STS sts-D29643 at
ACCESSION AB068968
VERSION AB068968.1 GI:15129772
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
Morohashi,A., Ohira,M., Nakagawara,A., Iibu,S., Hoshi,M., Horii,A.
and Soeda,E.
TITLE A BAC-based STS-content map spanning a 35-Mb region of human
chromosome 1p35-p36
JOURNAL Genomics 74 (1), 55-70 (2001)
MEDLINE 21269192
PubMed 11374902
REFERENCE 2 (bases 1 to 18)
AUTHORS Horii,A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
Miyagi 980-8575, Japan (E-mail:horie@mail.cc.tohoku.ac.jp,
Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES
source 1..18
/molecule="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
misc_feature 1..18
/note="forward primer for human STS sts-D29643 at 1p36
sts-D29643 obtained from clones B72P17, B200J11, B200J12,
B367G13, B73C17, Human BAC library RPCI-11"

Query Match      0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 383 TCCAGCACACGCAG 396
DB 1 TCCAGCACACGCAG 14

RESULT 825
AR045403/c
LOCUS AR045403 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 196 from patent US 5817796.
ACCESSION AR045403
VERSION AR045403.1 GI:5966868
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylylate residues
JOURNAL Patent: US 5817796-A 196 06-OCT-1998;
FEATURES
source 1..17

```

```

/organism="unknown"
/mol_type="unassigned DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 AGGAAGAGGAGGAGGAG 877
DB 17 AGAAGAGGAGGAGGAG 1

RESULT 826
BD241460
LOCUS BD241460 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241460
VERSION BD241460.1 GI:33051230
KEYWORDS JP 2002525127-A/407.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 407 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/407
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N33/58,G01N37/00, PC
G01N37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
Key Location/Qualifiers
FT source 1..17
/organism="Homo sapiens (human)".
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 720 AGCTCTTCAGGCTTCTG 736
DB 1 AGACTCTTAGGCTTCTG 17

RESULT 827
BD241462
LOCUS BD241462 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241462
VERSION BD241462.1 GI:33051232
KEYWORDS JP 2002525127-A/409.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Landers,J.E., Jordan,B., Housman,D.E. and Charest,A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 409 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)

```

PN JP 2002525127-A/409
 PD 13-AUG-2002
 PF 24-SEP-1999 JP 2000572407
 PR 25-SEP-1998 US 60/101757
 FI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
 C12N15/09, C12Q1/68, G01N33/53, G01N33/566, G01N33/58, G01N37/00, PC
 G01N37/00,
 PC C12N15/00
 CC Methods and products related to genotyping and DNA analysis FH
 Key source Location/Qualifiers
 FT source 1. .17
 FT Location/Qualifiers
 1. .17 /Organism='Homo sapiens (human)'.
 /Organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 720 AGCTCTCAGGCTTCTG 736
 || ||||| ||||| |||||
 DB 1 AGACTCTTAGGCTTCTG 17

RESULT 828
 BD254403
 LOCUS
 DEFINITION
 Regulation of repressor genes using nucleic acid molecules.
 ACCESSION
 BD254403
 VERSION
 BD254403.1 GI:33064173
 KEYWORDS
 JP 2002541795-A/2196.
 SOURCE
 unclassified
 ORGANISM
 unclassified
 REFERENCE
 1 (bases 1 to 17)
 AUTHORS
 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE
 Regulation of repressor genes using nucleic acid molecules
 JOURNAL
 Patent: JP 2002541795-A 2196 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 OS Eukaryote
 COMMENT
 PN JP 2002541795-A/2196
 PD 10-DEC-2002
 PR 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
 FI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
 C12P21/02,
 PC
 C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
 C12R1:91),
 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
 PC A61K37/02,
 PC (C12N5/00, C12R1:91)
 CC Regulation of repressor genes using nucleic acid molecules FH
 Key source Location/Qualifiers
 FT source 1. .17
 FT Location/Qualifiers
 1. .17 /Organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 231 CCGCGGACCCCGGGC 247
 || ||||| ||||| |||||
 DB 1 CCACGGCTCCCGGGC 17

RESULT 828
 BD254403
 LOCUS
 DEFINITION
 Regulation of repressor genes using nucleic acid molecules.
 ACCESSION
 BD254403
 VERSION
 BD254403.1 GI:33064173
 KEYWORDS
 JP 2002541795-A/2196.
 SOURCE
 unclassified
 ORGANISM
 unclassified
 REFERENCE
 1 (bases 1 to 17)
 AUTHORS
 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE
 Regulation of repressor genes using nucleic acid molecules
 JOURNAL
 Patent: JP 2002541795-A 2196 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 OS Eukaryote
 COMMENT
 PN JP 2002541795-A/2196
 PD 10-DEC-2002
 PR 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
 FI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
 C12P21/02,
 PC
 C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
 C12R1:91),
 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
 PC A61K37/02,
 PC (C12N5/00, C12R1:91)
 CC Regulation of repressor genes using nucleic acid molecules FH
 Key source Location/Qualifiers
 FT source 1. .17
 FT Location/Qualifiers
 1. .17 /Organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 231 CCGCGGACCCCGGGC 247
 || ||||| ||||| |||||
 DB 1 CCACGGCTCCCGGGC 17

RESULT 829
 BD254747
 LOCUS
 DEFINITION
 Regulation of repressor genes using nucleic acid molecules.
 ACCESSION
 BD254747
 VERSION
 BD254747.1 GI:33064517
 KEYWORDS
 JP 2002541795-A/2540.
 SOURCE
 unclassified
 ORGANISM
 unclassified
 REFERENCE
 1 (bases 1 to 17)
 AUTHORS
 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE
 Regulation of repressor genes using nucleic acid molecules
 JOURNAL
 Patent: JP 2002541795-A 2540 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 OS Eukaryote
 COMMENT
 PN JP 2002541795-A/2540
 PD 10-DEC-2002
 PF 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
 FI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
 C12P21/02,
 PC
 C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
 C12R1:91),
 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
 PC A61K37/02,
 PC (C12N5/00, C12R1:91)
 CC Regulation of repressor genes using nucleic acid molecules FH
 Key source Location/Qualifiers
 FT source 1. .17
 FT Location/Qualifiers
 1. .17 /Organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1239 TGGCTGCTTCACCTGGC 1255
 ||||| ||||| ||||| |||||
 DB 1 TGGCTCCTTGACCTGCG 17

RESULT 830
 BD255543
 LOCUS
 DEFINITION
 Regulation of repressor genes using nucleic acid molecules.
 ACCESSION
 BD255543
 VERSION
 BD255543.1 GI:33065313
 KEYWORDS
 JP 2002541795-A/3336.
 SOURCE
 unclassified
 ORGANISM
 unclassified
 REFERENCE
 1 (bases 1 to 17)
 AUTHORS
 Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
 TITLE
 Regulation of repressor genes using nucleic acid molecules
 JOURNAL
 Patent: JP 2002541795-A 3336 10-DEC-2002;
 RIBOZYME PHARMACEUTICALS INC
 OS Eukaryote
 COMMENT
 PN JP 2002541795-A/3336
 PD 10-DEC-2002
 PF 11-APR-2000 JP 2000611654
 PR 12-APR-1999 US 60/129390
 FI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
 C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
 C12P21/02,
 PC
 C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
 C12R1:91),
 PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
 PC A61K37/02,
 PC (C12N5/00, C12R1:91)
 CC Regulation of repressor genes using nucleic acid molecules FH
 Key source Location/Qualifiers
 FT source 1. .17
 FT Location/Qualifiers
 1. .17 /Organism="unidentified"
 /mol_type="genomic DNA"
 /db_xref="taxon:32644"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 6.8e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 231 CCGCGGACCCCGGGC 247
 || ||||| ||||| |||||
 DB 1 CCACGGCTCCCGGGC 17

PC	C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC C12R1:91),
PC	A61K37/02, (C12P21/02,C12R1:91), (C12P21/02,C12N5/00,C12N5/00, PC A61K37/02, (C12N5/00,C12R1:91)
CC	Regulation of repressor genes using nucleic acid molecules FH
Key	Location/Qualifiers
FT	1..17
FT	Location/Qualifiers
FEATURES	source
	1..17
	/organism="unidentified"
	/mol_type="genomic DNA"
	/db_xref="taxon:32644"
Query Match	0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 6.8e+02;
Matches 15;	Conservative 0; Mismatches 2; Indels 0; Gaps 0
Qy	1731 TTTACAAAAA 1747
Db	17 TTCACAAAGAAAAA 1
RESULT 831	
BD255580	17 bp DNA linear PAT 17-JUL-2003
LOCUS	BD255580
DEFINITION	Regulation of repressor genes using nucleic acid molecules.
ACCESSION	BD255580
VERSION	BD255580.1 GI:33065350
KEYWORDS	JP 2002541795-A/3373.
SOURCE	unidentified
ORGANISM	unclassified.
REFERENCE	1 (bases 1 to 17)
AUTHORS	Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE	Regulation of repressor genes using nucleic acid molecules
JOURNAL	Patent: JP 2002541795-A 3373 10-DEC-2002;
COMMENT	RIBOZYME PHARMACEUTICALS INC
OS	Eukaryote
PN	JP 2002541795-A/3373
PD	10-DEC-2002
PF	11-APR-2000 JP 2000611654
PR	12-APR-1999 US 60/129390
PI	LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC C12P21/02,
PC	C12P21/02,C12P21/02//A61K31/711, (C12N5/10,C12R1:91), (C12P21/02, PC C12R1:91),
PC	(C12P21/02,C12R1:91), (C12P21/02,C12N5/00,C12N5/00, PC A61K37/02,
PC	(C12N5/00,C12R1:91)
CC	Regulation of repressor genes using nucleic acid molecules FH
Key	Location/Qualifiers
FT	1..17
FT	Location/Qualifiers
FEATURES	source
	1..17
	/organism="unidentified"
	/mol_type="genomic DNA"
	/db_xref="taxon:32644"
Query Match	0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity	88.2%; Pred. No. 6.8e+02;
Matches 15;	Conservative 0; Mismatches 2; Indels 0; Gaps 0
Qy	1071 CTTTGTATGTTCTACAT 1087
Db	1 CTTTGTATTTCTTCAT 17

```
C12R1:91),
PC (C12P21/02,C12R1:91), (C12P21/02,C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
1..17
/organism="Eukaryote".
FEATURES
source
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACAAATAAATAAATAA 1750
||||| |||||||
Db 17 ACAAATAAATAAATAA 1
||||| |||||||
RESULT 834
BD258580/c
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258580
VERSION BD258580.1 GI:33068350
KEYWORDS unidentifed
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6373 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/6373
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
1..17
/organism="Eukaryote".
FEATURES
source
1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1733 TACAAAAATAAATAAATAA 1749
||||| |||||||
Db 17 TACAAAAATAAATAAATAA 1
||||| |||||||
RESULT 835
BD272764
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Tissue-specific and pathogen-specific toxic agents and ribozymes.
ACCESSION BD272764
VERSION BD272764.1 GI:33082532
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Norris, J., Clawson, G., Westwater, C., Schofield, D., Schmidt, M.,
Hoel, B., Dolan, J. and Pan, W.H.
TITLE Tissue-specific and pathogen-specific toxic agents and ribozymes
JOURNAL Patent: JP 2002541822-A 13 10-DEC-2002;
MUSC FOUNDATION FOR RESEARCH DEVELOPMENT, THE PENN STATE RESEARCH
FOUNDATION
COMMENT OS Artificial Sequence
PN JP 2002541822-A/13
PD 10-DEC-2002
PF 14-APR-2000 JP 2000611726
PR 14-APR-1999 US 09/291902.13-APR-2000 US 09/548449 PI
JAMES NORRIS, GARY CLAWSON, CAROLINE WESTWATER, DAVID SCHOFIELD, PI
MICHAEL SCHMIDT, BRIAN HOEL, JOSEPH DOLAN, WEI HUA PAN PC
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, A61P31/04, PC
C12N7/00,
PC C12N9/00, C12N15/00, A61K37/02
CC promoter
FH Key Location/Qualifiers
FT source 1..17
FT Location/Qualifiers
1..17
/organism="Artificial Sequence".
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1020 TGGGATGGGCTGGG 1036
||||| |||||||
Db 1 TGGGGTGGGGTGGG 17
||||| |||||||
RESULT 836
IS2455/c
LOCUS 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 196 from patent US 5646042.
ACCESSION IS2455
VERSION IS2455.1 GI:2473656
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.
TITLE C-myb targeted ribozymes
JOURNAL Patent: US 5646042-A 196 08-JUL-1997;
FEATURES
source
1..17
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 861 AGGAAGAGGAGGAG 877
||||| |||||||
Db 17 AGAAGAGGAGGAG 1
||||| |||||||
RESULT 837
```


LOCUS	AR186642	17 bp	DNA	linear	PAT 20-APR-2002
DEFINITION	Sequence 2130 from patent US 6346398.				
ACCESSION	AR186642				
VERSION	AR186642.1	GI:20232607			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6346398-A 2130 12-FEB-2002;				
FEATURES	Location/Qualifiers				
source	1..17				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.8%; Score 13.8; DB 1; Length 17;				
Best Local Similarity	88.2%; Pred. No. 6.8e+02;				
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	771 CCGAGGTGAAGTCTGGG 787				
Db					
	17 CCGAGTTGTAGTCTGGG 1				
RESULT 838					
AR187066/c		17 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR187066				
DEFINITION	Sequence 2554 from patent US 6346398.				
ACCESSION	AR187066				
VERSION	AR187066.1	GI:20233031			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6346398-A 2554 12-FEB-2002;				
FEATURES	Location/Qualifiers				
source	1..17				
	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	0.8%; Score 13.8; DB 1; Length 17;				
Best Local Similarity	88.2%; Pred. No. 6.8e+02;				
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1732 TTACAAAAAAAAAAAAA 1748				
Db					
	17 TTGGAAAAAAAAAAAAA 1				
RESULT 839					
AR187067/c		17 bp	DNA	linear	PAT 20-APR-2002
LOCUS	AR187067				
DEFINITION	Sequence 2555 from patent US 6346398.				
ACCESSION	AR187067				
VERSION	AR187067.1	GI:20233032			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 17)				
AUTHORS	Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6346398-A 2555 12-FEB-2002;				
FEATURES	Location/Qualifiers				

LOCUS AR192332 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7820 from patent US 6346398.
ACCESSION AR192332
VERSION AR192332.1 GI:20238297
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7820 12-FEB-2002;
FEATURES
Location/Qualifiers
source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1735 CAAAAAATACAAAAA 1751
||||| ||||| |||||
Db 17 CAAAAAATACAAAAA 1
RESULT 843
AR192333/c
LOCUS AR192333 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7821 from patent US 6346398.
ACCESSION AR192333
VERSION AR192333.1 GI:20238298
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7821 12-FEB-2002;
FEATURES
Location/Qualifiers
source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1735 CAAAAAATACAAAAA 1751
||||| ||||| |||||
Db 17 CAAAAAATACAAAAA 1
RESULT 844
AR192335/c
LOCUS AR192335 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 7823 from patent US 6346398.
ACCESSION AR192335
VERSION AR192335.1 GI:20238300
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J., Stinchcomb, D. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 7823 12-FEB-2002;
FEATURES
Location/Qualifiers
source
1. .17

/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACACAAAAAATACAAAAA 1750
||||| ||||| |||||
Db 17 ACACAAAAAATACAAAAA 1
RESULT 845
AR196416/c
LOCUS AR196416 17 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 881 from patent US 6350934.
ACCESSION AR196416
VERSION AR196416.1 GI:20245853
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Zwack, M.G., Edington, B.E., McSwiggen, J.A., Merlo, P., Ann.Owens., Guo, L., Skokut, T.A., Young, S.A., Folkerts, O. and Merlo, D.J.
TITLE Nucleic acid encoding delta-9 desaturase
JOURNAL Patent: US 6350934-A 881 26-FEB-2002;
FEATURES
Location/Qualifiers
source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1733 TACAAAAAATACAAAAA 1749
||||| ||||| |||||
Db 17 TACAAAAAATACAAAAA 1
RESULT 846
AR204408/c
LOCUS AR204408 17 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 3 from patent US 6365729.
ACCESSION AR204408
VERSION AR204408.1 GI:21501052
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Tyagi, S., Kramer, F.R. and Vartikian, R.
TITLE High specificity primers, amplification methods and kits
JOURNAL Patent: US 6365729-A 3 02-APR-2002;
FEATURES
Location/Qualifiers
source
1. .17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 242 CGGGGCCACACCGGCC 258
||||| ||||| |||||
Db 17 CGCGCGGACACCGGCC 1
RESULT 847
AR262702/c
LOCUS AR262702 17 bp DNA linear PAT 29-JAN-2003
DEFINITION Sequence 3 from patent US 631140.

```
ACCESSION AR262702
VERSION AR262702.1 GI:28074345
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Mollet,B., Germond,J.E. and Lapierre,L.
TITLE Mobile genetic elements as tools for genetic modification of L.
delbrueckii or L. helveticus
JOURNAL Patent: US 6331140-A 3 18-DEC-2001;
FEATURES
    source
        Location/Qualifiers
            /organism="unknown"
            /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1672 GACTTTGTGACCAAAATG 1688
Db 17 GACATTGTACCAAAAGG 1

RESULT 848
AR286095
LOCUS AR286095 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 467 from patent US 6528640.
ACCESSION AR286095
VERSION AR286095.1 GI:29723691
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpelsky,A.,
TITLE Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
JOURNAL Synthetic ribonucleic acids with RNase activity
FEATURES
    source
        Location/Qualifiers
            Patent: US 6528640-A 467 04-MAR-2003;

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1151 GCTACGTGGCCACCCTG 1167
Db 1 GCTACGTGGCCCCCTG 17

RESULT 849
AR286192/c
LOCUS AR286192 17 bp RNA linear PAT 10-APR-2003
DEFINITION Sequence 564 from patent US 6528640.
ACCESSION AR286192
VERSION AR286192.1 GI:29723788
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpelsky,A.,
TITLE Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
JOURNAL Synthetic ribonucleic acids with RNase activity
FEATURES
    source
        Location/Qualifiers
            Patent: US 6528640-A 564 04-MAR-2003;

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1748
Db 17 TTGAAAAA 1

RESULT 852
AR323677/c
LOCUS AR323677 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1079 from patent US 6566127.
ACCESSION AR323677
```

```
Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 232 CGCGGCACCGGGGCC 248
Db 17 CGCGGCTGCCCGGGGCC 1

RESULT 850
AR323273/c
LOCUS AR323273 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 675 from patent US 6566127.
ACCESSION AR323273
VERSION AR323273.1 GI:33709081
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 675 20-MAY-2003;
FEATURES
    source
        Location/Qualifiers
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 771 CCGAGGTGAAGTCTGGG 787
Db 17 CCGAGTTGTAGTCTGGG 1

RESULT 851
AR323676/c
LOCUS AR323676 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1078 from patent US 6566127.
ACCESSION AR323676
VERSION AR323676.1 GI:33709484
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1078 20-MAY-2003;
FEATURES
    source
        Location/Qualifiers
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1748
Db 17 TTGAAAAA 1

RESULT 852
AR323677/c
LOCUS AR323677 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 1079 from patent US 6566127.
ACCESSION AR323677
```

```
VERSION AR323677.1 GI:33709485
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1079 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1747
Db 17 TTTGGAAAAA 1

RESULT 853
AR326200/c
LOCUS AR326200 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3602 from patent US 6566127.
ACCESSION AR326200
VERSION AR326200.1 GI:33712008
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3602 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1747
Db 17 TTTGGAAAAA 1

RESULT 854
AR326201/c
LOCUS AR326201 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3603 from patent US 6566127.
ACCESSION AR326201
VERSION AR326201.1 GI:33712009
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3603 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAA 1752
Db 17 AAACAAAAA 1

RESULT 855
AR326202/c
LOCUS AR326202 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3604 from patent US 6566127.
ACCESSION AR326202
VERSION AR326202.1 GI:33712010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3604 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 CAAAAA 1751
Db 17 CAAAAA 1

RESULT 856
AR326203/c
LOCUS AR326203 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3605 from patent US 6566127.
ACCESSION AR326203
VERSION AR326203.1 GI:33712011
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3605 20-MAY-2003;
FEATURES Location/Qualifiers
source
1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAA 1750
Db 17 AAAAAA 1

RESULT 857
AR326205/c
LOCUS AR326205 17 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 3607 from patent US 6566127.
ACCESSION AR326205
VERSION AR326205.1 GI:33712013
```



```
ORGANISM      synthetic construct
              artificial sequences.
REFERENCE     1
AUTHORS      Herrnstadt,C. and Davis,R.E.
TITLE        Single nucleotide polymorphisms in mitochondrial genes that segreg
              ate with alzheimer's disease
JOURNAL      Patent: WO 0063441-A 68 26-OCT-2000;
              MITOKOR (US)
FEATURES     source
              Location/Qualifiers
              1..17
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="PCR primer"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1450 AAGTGGGAGGAGTGTTGG 1466
          ||| ||||| ||||| |||||
Db      17 AAGGGGATGAGTGTTGG 1

RESULT 863
AX215933/c
LOCUS      AX215933
DEFINITION Sequence 1375 from Patent WO0159103.
ACCESSION AX215933
VERSION    AX215933.1 GI:15525976
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
           nogo gene expression
JOURNAL    Patent: WO 0159103-A 1375 16-AUG-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ;
           McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   source
           Location/Qualifiers
           1..17
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Nucleic Acid"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1329 CTTTCACAGAGTTTG 1345
          ||||| ||||| |||||
Db      17 CTTTCACAGAACTTTG 1

RESULT 864
AX216915
LOCUS      AX216915
DEFINITION Sequence 2357 from Patent WO0159103.
ACCESSION AX216915
VERSION    AX216915.1 GI:15526976
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
           nogo gene expression
JOURNAL    Patent: WO 0159103-A 2357 16-AUG-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ;
           McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   source
           Location/Qualifiers
           1..17
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Nucleic Acid"

ORGANISM      synthetic construct
              artificial sequences.
REFERENCE     1
AUTHORS      Herrnstadt,C. and Davis,R.E.
TITLE        Single nucleotide polymorphisms in mitochondrial genes that segreg
              ate with alzheimer's disease
JOURNAL      Patent: WO 0063441-A 68 26-OCT-2000;
              MITOKOR (US)
FEATURES     source
              Location/Qualifiers
              1..17
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="PCR primer"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      861 AGGAGAGGAGGAGGAG 877
          ||||| ||||| ||||| |||||
Db      1 AGGAGGAGAGGAGGAG 17

RESULT 865
AX216916
LOCUS      AX216916
DEFINITION Sequence 2358 from Patent WO0159103.
ACCESSION AX216916
VERSION    AX216916.1 GI:15526977
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
           nogo gene expression
JOURNAL    Patent: WO 0159103-A 2358 16-AUG-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ;
           McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   source
           Location/Qualifiers
           1..17
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Nucleic Acid"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      861 AGGAGAGGAGGAGGAG 877
          ||||| ||||| ||||| |||||
Db      1 AGGAGAGGAGGAGGAG 17

RESULT 866
AX216925
LOCUS      AX216925
DEFINITION Sequence 2367 from Patent WO0159103.
ACCESSION AX216925
VERSION    AX216925.1 GI:15526986
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
           nogo gene expression
JOURNAL    Patent: WO 0159103-A 2367 16-AUG-2001;
           RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ;
           McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   source
           Location/Qualifiers
           1..17
           /organism="synthetic construct"
           /mol_type="unassigned RNA"
           /db_xref="taxon:32630"
           /note="Nucleic Acid"
```

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 861 AGGAAGAGGAGGAG 877
Db 1 AGGAAGAGGAGGAG 17

RESULT 867
AX218302
LOCUS AX218302 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3744 from Patent WO0159103.
ACCESSION AX218302
VERSION AX218302.1 GI:15528363
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
JOURNAL nogo gene expression
Patent: WO 0159103-A 3744 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1. 17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 860 CAGGAAGAGGAGGAGGA 876
Db 1 CAAGAAGAGGAAGA 17

RESULT 868
AX272523
LOCUS AX272523 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 92 from Patent WO0162911.
ACCESSION AX272523
VERSION AX272523.1 GI:16545260
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 92 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)

FEATURES
source 1. 17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 203 CCAGAGCCCTCAGGGG 219
Db 1 CCAGAGCTCCCGAGGGG 17

RESULT 869
AX272706
LOCUS AX272706 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 275 from Patent WO0162911.
ACCESSION AX272706
VERSION AX272706.1 GI:16545443
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 275 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)

FEATURES
source 1. 17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 202 GCCAGAGCCCTCAGGG 218
Db 1 GCCAGAGCTCCCGAGGG 17

RESULT 870
AX272707
LOCUS AX272707 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 276 from Patent WO0162911.
ACCESSION AX272707
VERSION AX272707.1 GI:16545444
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., Hamblin, P.A. and
Ellis, J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 276 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)

FEATURES
source 1. 17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 204 CAGAGCCCTCAGGGGA 220
Db 1 CAGAGCTCCCGAGGGGA 17

RESULT 871
AX272804/c
LOCUS AX272804 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 373 from Patent WO0162911.
ACCESSION AX272804
VERSION AX272804.1 GI:16545541
KEYWORDS

```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
TITLE       Method and reagent for the inhibition of grid
JOURNAL     Patent: WO 0162911-A 373 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES    Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned RNA"
                /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 GGCATATTGCGGAGGC 1149.
Db 17 GGCATATTGCGGAGGC 1

RESULT 872
AX272952/c
LOCUS       AX272952          17 bp    RNA        linear    PAT 29-OCT-2001
DEFINITION Sequence 521 from Patent WO0162911.
ACCESSION  AX272952
VERSION     AX272952.1 GI:16545689
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
            Ellis,J.H.
TITLE       Method and reagent for the inhibition of grid
JOURNAL     Patent: WO 0162911-A 521 30-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES    Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned RNA"
                /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1135 GCATATTGCGGAGGCTG 1151
Db 17 GCATATTGCGGAGGCTG 1

RESULT 873
AX361147/c
LOCUS       AX361147          17 bp    DNA        linear    PAT 15-FEB-2002
DEFINITION Sequence 31 from Patent EP1177789.
ACCESSION  AX361147
VERSION     AX361147.1 GI:18693793
KEYWORDS
SOURCE      Rattus sp.
            Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
AUTHORS     Fluhmann,B., Heim,M., Hunziker,W. and Weber,P.
TITLE       Use of phycanic acid for the treatment of diabetes
JOURNAL     Patent: EP 117789-A 31 06-FEB-2002;

SOURCE      Roche Vitamins AG (CH)
            Location/Qualifiers
            source
              1..17
                /organism="Rattus sp."
                /mol_type="unassigned DNA"
                /db_xref="taxon:10118"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 694 AGGGGCTGCGGCCACC 710
Db 17 AGGGGCTGCTGACCACC 1

RESULT 874
AX422503
LOCUS       AX422503          17 bp    RNA        linear    PAT 18-JUN-2002
DEFINITION Sequence 839 from Patent WO0188124.
ACCESSION  AX422503
VERSION     AX422503.1 GI:21525885
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
            Randi,A.M.
TITLE       Method and reagent for the inhibition of erg
JOURNAL     Patent: WO 0188124-A 839 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES    Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned RNA"
                /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 273 CCAGCCCCCAGGGG 289
Db 1 CCAGCCCCCAGGGG 17

RESULT 875
AX422924
LOCUS       AX422924          17 bp    RNA        linear    PAT 18-JUN-2002
DEFINITION Sequence 1260 from Patent WO0188124.
ACCESSION  AX422924
VERSION     AX422924.1 GI:21526306
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
            Randi,A.M.
TITLE       Method and reagent for the inhibition of erg
JOURNAL     Patent: WO 0188124-A 1260 22-NOV-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES    Location/Qualifiers
            source
              1..17
                /organism="Homo sapiens"
                /mol_type="unassigned RNA"
                /db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 273 CCAGCCCCCAGGGG 289
Db 1 CCAGCCCCCAGGGG 17
```


Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 31 AGAGGAAAAAAGC 47
|||||
Db 1 AGAGGAATGMAAAGC 17

RESULT 876
AX423181
LOCUS AX423181 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1517 from Patent WO0188124.
ACCESSION AX423181
VERSION AX423181.1 GI:21526563
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, P.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1517 22-NOV-2001;
FEATURES RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 AGGAGAGGAGGAGG 877
|||||
Db 1 AGGAAGGCGAGAG 17

RESULT 877
AX499077
LOCUS AX499077 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 384 from Patent EP1229046.
ACCESSION AX499077
VERSION AX499077.1 GI:23381370
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 384 07-AUG-2002;
FEATURES Aeonica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 855 CCTCGAGGAGGAA 871
|||||
Db 1 CCTGCGGAGGAGAA 17

RESULT 878
AX499340/c
LOCUS AX499340 17 bp DNA linear PAT 27-SEP-2002

DEFINITION Sequence 647 from Patent EP1229046.
ACCESSION AX499340
VERSION AX499340.1 GI:23381633
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 647 07-AUG-2002;
FEATURES Aeonica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAG 868
|||||
Db 17 TGGCCCTGCAGGAGCG 1

RESULT 879
AX531998/c
LOCUS AX531998 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1507 from Patent EP1239051.
ACCESSION AX531998
VERSION AX531998.1 GI:25255762
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1507 11-SEP-2002;
FEATURES Aeonica, Inc. (US)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 893 AGTGCCCTGAGCCAG 909
|||||
Db 17 AGAGCCCTGAGCCAG 1

RESULT 880
AX544715/c
LOCUS AX544715 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 228 from Patent EP1243660.
ACCESSION AX544715
VERSION AX544715.1 GI:25809926
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polyptide n-acetylglucosaminyltransferase 10

```
JOURNAL Patent: EP 1243660-A 228 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

  Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1025 ATGGGGCTGGGGTTGTG 1041
Db 17 ATGGGGCTGGGGCTGTG 1

RESULT 881
AX544716/c
LOCUS
DEFINITION Sequence 229 from Patent EPI243660.
ACCESSION AX544716
VERSION AX544716.1 GI:25809927
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Zhang, J., Gu, Y. and Nguyen, C.T.
  Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  Patent: EP 1243660-A 229 25-SEP-2002;
  Aeomica, Inc. (US)
FEATURES
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

  Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1024 GATGGGGCTGGGGTTGT 1040
Db 17 GATGGGGCTGGGGCTGT 1

RESULT 882
AX544717/c
LOCUS
DEFINITION Sequence 230 from Patent EPI243660.
ACCESSION AX544717
VERSION AX544717.1 GI:25809928
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Zhang, J., Gu, Y. and Nguyen, C.T.
  Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  Patent: EP 1243660-A 230 25-SEP-2002;
  Aeomica, Inc. (US)
FEATURES
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

  Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 GGATGGGGCTGGGGTTG 1039
Db 17 GGATGGGGCTGGGGCTG 1

RESULT 883
AX544744
LOCUS
DEFINITION Sequence 257 from Patent EPI243660.
ACCESSION AX544744
VERSION AX544744.1 GI:25809955
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Zhang, J., Gu, Y. and Nguyen, C.T.
  Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
  Patent: EP 1243660-A 257 25-SEP-2002;
  Aeomica, Inc. (US)
FEATURES
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

  Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 CCTGCAGCGCCCTGGCGC 1551
Db 1 CCTGAAGCCCTGTCTGC 17

RESULT 884
AX688347
LOCUS
DEFINITION Sequence 1079 from Patent EPI281758.
ACCESSION AX688347
VERSION AX688347.1 GI:29411047
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 Shannon, M., Gu, Y. and Nguyen, C.T.
  Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
  mdz12
  Patent: EP 1281758-A 1079 05-FEB-2003;
  Aeomica, Inc. (US)
FEATURES
  source
    1..17
      /organism="Homo sapiens"
      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

  Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 17;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAGAG 868
Db 1 TGGCCCTGCAGGAGTG 17

RESULT 885
AX698573/c
LOCUS
DEFINITION Sequence 62 from Patent WO03010335.
```

ACCESSION AX698573
VERSION AX698573.1 GI:29499401
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mirel,D.B., Erlich,H.A., Bugawan,T.L., Noble,J.A. and Valdez,A.M.
TITLE I1-4 receptor sequence variation associated with type 1 diabetes
JOURNAL Patent: WO 03010335-A 62 06-FEB-2003;
Roche Diagnostics GmbH (DE); F. HOFFMANN-LA ROCHE AG (CH)
FEATURES
source 1..17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="allele specific PCR primer"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 898 CCCTGAGCCAGCCTCC 914
Db 17 CCCTGAGCCAGTCACC 1
RESULT 886
AX727700
LOCUS AX727700 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5387 from Patent WO03025176.
ACCESSION AX727700
VERSION AX727700.1 GI:30507043
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 5387 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1..17
Location/Qualifiers
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 801 GAGCCAGAGAGAGCCAG 817
Db 1 GATCCAGTGAGAGCCAG 17
RESULT 887
AX730844
LOCUS AX730844 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2478 from Patent WO03025175.
ACCESSION AX730844
VERSION AX730844.1 GI:30510187
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025175-A 2478 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1730 GTTTACAAAAA 1746
Db 1 GATCACAAAAA 17
RESULT 889
AX784081
LOCUS AX784081 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2412 from Patent WO03050284.
ACCESSION AX784081
VERSION AX784081.1 GI:32951930
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Guo,J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2412 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"

```
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1185 CTCCTGCGCCATCTCTGG 1201
||||| ||||| |||||
Db 1 CTCCTGCGCCATCTCTGG 17

RESULT 890
AX787049/c
LOCUS AX787049 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2 from Patent WO03040024.
ACCESSION AX787049
VERSION AX787049.1 GI:32954271
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Bohmann,K., Hohelsel,W., Koehler,B. and Dorn,I.
TITLE Assay based on doped nanoparticles
JOURNAL Patent: WO 03040024-A 2 15-MAY-2003;
Bayer Aktiengesellschaft (BE)
FEATURES
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 242 CGGGGCCACCCGCC 258
||||| ||||| |||||
Db 17 CGGGGCCACCCGCC 1

RESULT 891
BD144764/c
LOCUS BD144764 17 bp DNA linear PAT 17-JAN-2003
DEFINITION Use of phytanic acid for the treatment of diabetes.
ACCESSION BD144764
VERSION BD144764.1 GI:27850522
KEYWORDS JP 2002104964-A/31.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 17)
AUTHORS Fluehmann,B., Helm,M., Hunziker,W. and Weber,P.
TITLE Use of phytanic acid for the treatment of diabetes
JOURNAL Patent: JP 2002104964-A 31 10-APR-2002;
ROCHE VITAMINS AG
COMMENT
OS Rattus sp. (rat)
PN JP 2002104964-A/31
PD 10-APR-2002
PF 01-AUG-2001 JP 2001233070
PR 04-AUG-2000 EP 00116848.3
PI BEAT FLUEHMANN, MANUEL HELM, WILLI HUNZIKER, PETER WEBER PC
A61K31/20, A23L1/30, A61K31/16, A61K31/201, A61K31/215, A61P3/00, PC
A61P3/04,
PC A61P3/06, A61P3/10
CC Rat primary hepatocytes
FH Key Location/Qualifiers
FT source
1..17
/organism="Rattus sp. (rat)".
Location/Qualifiers

source
1..17
/organism="Rattus sp."
/mol_type="genomic DNA"
/db_xref="taxon:10118"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 694 AGGGGCTGGGCCACC 710
||||| ||||| |||||
Db 17 AGGGGCTGGGCCACC 1

RESULT 892
BD199007
LOCUS BD199007 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD199007
VERSION BD199007.1 GI:33008777
KEYWORDS JP 2002509721-A/2033.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Meswigen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 2033 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002509721-A/2033
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source
1..17
/organism="Homo sapiens (human)".
Location/Qualifiers

source
1..17
/organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1012 CATGTGGTTGGGATGG 1028
||||| ||||| |||||
Db 1 CATGTGGTTGGGAGGG 17

RESULT 893
BD200582
LOCUS BD200582 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD200582
VERSION BD200582.1 GI:33010352
KEYWORDS JP 2002509721-A/3608.
```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1. (bases 1 to 17)
TITLE Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and McSwiggen, J.A.
JOURNAL Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
COMMENT RIBOZYME PHARMACEUTICALS INC
PATENT: JP 2002509721-A 3608 02-APR-2002;
OS Homo sapiens (human)
PN JP 2002509721-A/3608
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..17
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 717 GGGAGCCTCTCAGGCTT 733
Db 1 GGGAGCCTCTCAGGCTT 17
RESULT 894
BD200583 17 bp RNA linear PAT 17-JUL-2003
LOCUS Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
DEFINITION BD200583.1 GI:33010353
VERSION JP 2002509721-A/3609.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1. (bases 1 to 17)
TITLE Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and McSwiggen, J.A.
JOURNAL Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
COMMENT RIBOZYME PHARMACEUTICALS INC
PATENT: JP 2002509721-A 3609 02-APR-2002;
OS Homo sapiens (human)
PN JP 2002509721-A/3609
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K31/7125, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00

CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..17
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 6.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 719 GAGCCTCTCAGGCTTCT 735
Db 1 GAGCCTCTCTCGGCTTCT 17
RESULT 895
A14818/c 18 bp DNA linear PAT 16-MAY-1994
LOCUS Nucleotide sequence 12 from patent number EP0298807.
DEFINITION A14818
ACCESSION A14818
VERSION A14818.1 GI:513808
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1. (bases 1 to 18)
AUTHORS Stern, T., Courtney, M. and Lecocq, J.P.
TITLE Method for the production of stable cell lines from transgenic animals for the production of specific proteins; tumour cell lines and proteins obtained
JOURNAL Patent: EP 0298807-A 12 11-JAN-1989;
MORETTIN, Enrico
FEATURES
source
1..18
/organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 740 CCTCCCGGGCGCCCTC 756
Db 17 CCATCCCGGGCGCCCTC 1
RESULT 896
A64610 18 bp DNA linear PAT 29-MAR-1999
LOCUS Sequence 29 from Patent WO9728186.
DEFINITION A64610
ACCESSION A64610
VERSION A64610.1 GI:4530708
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Caput, D., Ferrara, P. and Kaghad, A.M.
TITLE PURIFIED SR-p70 PROTEIN
JOURNAL Patent: WO 9728186-A 29 07-AUG-1997;
COMMENT SANOFI SA (FR)
Other publication AU 1727597 19970822
Other publication FR 2744455 19970808.
FEATURES
source
1..18
/organism='unidentified'

```
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
  0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 GCTGCTGGGTCTCTGG 854
  ||| ||| ||| ||| |||
Db 2 GCAGCTTGGGTCTCTGG 18

RESULT 897
AR083836/c
LOCUS
DEFINITION Sequence 52 from patent US 5977316.
ACCESSION AR083836
VERSION AR083836.1 GI:10010607
SOURCE
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 18)
  Chatterjee,M., Foon,K.A. and Chatterjee,S.K.
  TITLE Monoclonal antibody 1A7 and related polypeptides
  JOURNAL Patent: US 5977316-A 52 02-NOV-1999;
  FEATURES
    source
      1..18
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 TTGGCCCTTCATCTG 313
  ||| ||| ||| ||| |||
Db 17 TTGGCCCTTCATCTG 1

RESULT 898
AR106852
LOCUS
DEFINITION Sequence 13 from patent US 6107092.
ACCESSION AR106852
VERSION AR106852.1 GI:12821382
KEYWORDS
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 18)
  Cowser,L.M., Bennett,C.Frank, and O'Malley,B.W.
  TITLE Antisense modulation of SRA expression
  JOURNAL Patent: US 6107092-A 13 22-AUG-2000;
  FEATURES
    source
      1..18
      /organism="unknown"
      /mol_type="unassigned DNA"

Query Match
  0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 768 AGGCCGAGTGAAGTCT 784
  ||| ||| ||| ||| |||
Db 2 AGGCCGAGTGAAGTCT 18

RESULT 899
AR106931
LOCUS
DEFINITION Sequence 92 from patent US 6107092.
ACCESSION AR106931
```

```
VERSION AR106931.1 GI:12821461
KEYWORDS
SOURCE
  Unknown.
  Unclassified.
REFERENCE 1 (bases 1 to 18)
  Cowser,L.M., Bennett,C.Frank, and O'Malley,B.W.
  TITLE Antisense modulation of SRA expression
  JOURNAL Patent: US 6107092-A 92 22-AUG-2000;
  FEATURES
    Location/Qualifiers
      source
        1..18
        /organism="unknown"
        /mol_type="unassigned DNA"

Query Match
  0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 768 AGGCCGAGTGAAGTCT 784
  ||| ||| ||| ||| |||
Db 1 AGGCCGAGTGAAGTCT 17

RESULT 900
E40556/c
LOCUS
DEFINITION Novel serine protease.
ACCESSION E40556
VERSION E40556.1 GI:18628999
KEYWORDS
  JP 2001046065-A/21.
  synthetic construct
  SOURCE
    ORGANISM
      artificial sequences.
REFERENCE 1 (bases 1 to 18)
  Tsuruoka,N., Yamashiro,K., Mitsui,S. and Yamaguchi,N.
  AUTHORS
  TITLE Novel serine protease
  JOURNAL Patent: JP 2001046065-A 21 20-FEB-2001;
  COMMENT
    SUNTORY LTD
    OS Artificial Sequence
    PN JP 2001046065-A/21
    PD 20-FEB-2001
    PF 03-AUG-1999 JP 1999220522
    PR
    PI NOBUO TSURUOKA,KYOKO YAMASHIRO,SHINICHI MITSUI, PI NOZOMI
    YAMAGUCHI
    PC C12N15/09,C07K14/435,C07K16/40,C12N1/15,C12N1/19,C12N1/21, PC
    C12N5/10,
    PC C12N9/50,C12P21/02,C12Q1/68,G01N33/15,G01N33/50//A61K31/00, PC
    A61K38/48,
    PC A61K38/55,A61K45/00,A61K48/00,C12N15/00,C12N5/00,A61K37/547,
    CC A61K37/64
    FH Key
    FT Location/Qualifiers
    FT
      Location/Qualifiers
        1..18
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"

Query Match
  0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 360 GTGGGTGGGTCCCATG 376
  ||| ||| ||| ||| |||
Db 17 GTGGGTGGGTCCCATG 1

RESULT 901
E51022
LOCUS
```

DEFINITION	Improved production of isoprenoid.									
ACCESSION	E51022									
VERSION	E51022.1 GI:13023244									
KEYWORDS	JP 200050884-A/25.									
SOURCE	synthetic construct									
ORGANISM	synthetic construct									
REFERENCE	1 (bases 1 to 18)									
AUTHORS	Tatsuo,H., Kazuyuki,O. and Yutaka,S.									
TITLE	Improved production of isoprenoid									
JOURNAL	Patent: JP 200050884-A 25 22-FEB-2000;									
COMMENT	F. HOFFMANN LA ROCHE AG									
	OS Artificial Sequence									
	PN JP 2000050884-A/25									
	PD 22-FEB-2000									
	PR 06-MAY-1999 JP 1999126015									
	PF 06-MAY-1998 EP 98108210.0									
	PI TATSUO HOSHINO, KAZUYUKI OJIMA, YUTAKA SETOYUCHI PC									
	C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P7/04, PC									
	C12P23/00, C12N15/00,									
	PC C12N5/00									
	CC									
	FH Key									
	FT source									
	Location/Qualifiers									
	1. .18									
	/organism="Artificial Sequence".									
FEATURES	source									
	Location/Qualifiers									
	1. .18									
	/organism="synthetic construct"									
	/mol_type="genomic DNA"									
	/db_xref="taxon:32630"									
Query Match	0.8%; Score 13.8; DB 1; Length 18;									
Best Local Similarity	88.2%; Pred. No. 7.2e+02;									
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	28 GGAAGAGGAAAAAAAA 44									
Db	1 GGAAGAGGAGAGAGAAA 17									
RESULT 902										
I82163/c	I82163 18 bp DNA linear PAT 10-JUN-1998									
LOCUS	Sequence 9 from patent US 5712098.									
DEFINITION	I82163									
ACCESSION	I82163									
VERSION	I82163.1 GI:3210460									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 18)									
AUTHORS	Tsuchihashi Z., Gnirke A., Thomas, W.J., Drayna, D.T., Ruddy, D.,									
TITLE	Wolff, R.K. and Feder, J.N.									
	Hereditary hemochromatosis diagnostic markers and diagnostic									
	methods									
JOURNAL	Patent: US 5712098-A 9 27-JAN-1998;									
FEATURES	Location/Qualifiers									
	source									
	1. .18									
	/organism="unknown"									
	/mol_type="unassigned DNA"									
Query Match	0.8%; Score 13.8; DB 1; Length 18;									
Best Local Similarity	88.2%; Pred. No. 7.2e+02;									
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	1237 CCTGGCTGCTTCACCTG 1253									
Db	18 CCTGGTGTCTCCACCTG 2									
RESULT 903										
AR132884/c	AR132884 18 bp DNA linear PAT 20-APR-2002									
LOCUS	Sequence 9 from patent US 5712098.									
DEFINITION	I82163									
ACCESSION	I82163									
VERSION	I82163.1 GI:3210460									
KEYWORDS	Unknown.									
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 18)									
AUTHORS	Tsuchihashi Z., Gnirke A., Thomas, W.J., Drayna, D.T., Ruddy, D.,									
TITLE	Wolff, R.K. and Feder, J.N.									
	Hereditary hemochromatosis diagnostic markers and diagnostic									
	methods									
JOURNAL	Patent: US 5712098-A 9 27-JAN-1998;									
FEATURES	Location/Qualifiers									
	source									
	1. .18									
	/organism="unknown"									
	/mol_type="unassigned DNA"									
Query Match	0.8%; Score 13.8; DB 1; Length 18;									
Best Local Similarity	88.2%; Pred. No. 7.2e+02;									
Matches	15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	1237 CCTGGCTGCTTCACCTG 1253									
Db	18 CCTGGTGTCTCCACCTG 2									

```

DEFINITION Sequence 8372 from patent US 6346398.
ACCESSION AR192884
VERSION AR192884.1 GI:20238849
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 8372 12-FEB-2002;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGG 789
||||| |||||||
DB 18 GAGTTGTAGTCTGGGG 2

RESULT 904
AR195017
LOCUS AR195017 18 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 2 from patent US 6350580.
ACCESSION AR195017
VERSION AR195017.1 GI:20244454
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sorge,J.A.
TITLE Methods for detection of a target nucleic acid using a probe comprising secondary structure
JOURNAL Patent: US 6350580-A 2 26-FEB-2002;
FEATURES
source
1..18
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
||||| |||||||
DB 1 AAAAAATAATAAAAAAAAA 17

RESULT 905
AR217329
LOCUS AR217329 18 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 48 from patent US 6416948.
ACCESSION AR217329
VERSION AR217329.1 GI:23317010
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
REFERENCE 1 (bases 1 to 18)
AUTHORS Pilarowski,L.M., Beich,A.R. and Szczeppek,A.J.
TITLE Methods for detection of rearranged DNA
JOURNAL Patent: US 6416948-A 48 09-JUL-2002;
FEATURES
source
1..18
/organism="unknown"
/mol_type="genomic DNA"

```

```
Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 982 TACTTTGGCCAGTGTGG 998
Db 1 TACTTTGACCAGTGGGG 17

RESULT 906
AR222132 18 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION Sequence 60 from patent US 6429014.
ACCESSION AR222132
VERSION AR222132.1 GI:23329506
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Steele C.L., Bohlmann, J. and Croteau R.B.
TITLE Monoterpene synthases from grand fir (Abies grandis)
JOURNAL Patent: US 6429014-A 60 06-AUG-2002;
FEATURES
source
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 749 GCCCCACCTTCTCTC 765
Db 1 GCCACCACCTTCTCTC 17

RESULT 907
AR275355/c 18 bp DNA linear PAT 10-APR-2003
LOCUS
DEFINITION Sequence 52 from patent US 6509016.
ACCESSION AR275355
VERSION AR275355.1 GI:29708446
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Chatterjee, M., Foon, K.A. and Chatterjee, S.K.
TITLE Monoclonal antibody 1A7 and use for the treatment of melanoma and
JOURNAL Patent: US 6509016-A 52 21-JAN-2003;
FEATURES
source
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 TTGGCCCTTCCATCTG 313
Db 17 TTGGGCCCTTCCATCTG 1

RESULT 908
AR326626/c 18 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 4028 from patent US 6566127.
ACCESSION AR326626
VERSION AR326626.1 GI:33712434

KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions
JOURNAL Patent: US 6566127-A 4028 20-MAY-2003;
FEATURES
source
    /organism="unknown"
    /mol_type="unassigned RNA"

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGG 789
Db 18 GAGTTGTAGTCTGGGG 2

RESULT 909
AR349888 18 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 30 from patent US 6586202.
ACCESSION AR349888
VERSION AR349888.1 GI:33750789
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Hoshino, T., Ojima, K. and Setoguchi, Y.
TITLE Isoprenoid production
JOURNAL Patent: US 6586202-A 30 01-JUL-2003;
FEATURES
source
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 28 GGAAGAGGAGAGAGAGAA 44
Db 1 GGAAGAGGAGAGAGAGAA 17

RESULT 910
AR352433 18 bp DNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 2 from patent US 6589743.
ACCESSION AR352433
VERSION AR352433.1 GI:33757570
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 18)
AUTHORS Sorge, J.A.
TITLE Methods for detection of a target nucleic acid using a probe
JOURNAL Patent: US 6589743-A 2 08-JUL-2003;
FEATURES
source
    /organism="unknown"
    /mol_type="genomic DNA"

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```


Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 911
AR362789
LOCUS AR362789 18 bp DNA linear PAT 03-SEP-2003
DEFINITION Sequence 6 from patent US 5182262.
ACCESSION AR362789
VERSION AR362789.1 GI:34423191
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 18)
AUTHORS Leto, I.
TITLE Calmodulin binding peptide derivatives of non-erythroid alpha spectrin
JOURNAL Patent: US 5182262-A 6 26-JAN-1993;
FEATURES Location/Qualifiers
source 1..18
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1156 GTGGCCACCTGGAGAA 1172
Db 1 GTGGCCACCTGGCCAA 17

RESULT 912
AX012429
LOCUS AX012429 18 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 30 from Patent EP0955363.
ACCESSION AX012429
VERSION AX012429.1 GI:9998468
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Hoshino, T., Ojima, K. and Setoguchi, Y.
TITLE Dna sequences encoding enzymes involved in production of isoprenoids
JOURNAL Patent: EP 0955363-A 30 10-NOV-1999;
HOFMANN LA ROCHE (CH)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 28 GGAAGAGGAGGAGGAGAA 44
Db 1 GGAAGAGGAGGAGGAGAA 17

RESULT 913
AX135661
LOCUS AX135661 18 bp DNA linear PAT 29-MAY-2001
DEFINITION Sequence 2 from Patent WO0132922.
ACCESSION AX135661

VERSION AX135661.1 GI:14271931
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Sorge, J.A.
TITLE Methods for detection of a target nucleic acid sequence
JOURNAL Patent: WO 0132922-A 2 10-MAY-2001;
STRATAGENE (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="FEN nuclease cleavage product"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 914
AX172296/c
LOCUS AX172296 18 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0141815.
ACCESSION AX172296
VERSION AX172296.1 GI:14597478
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Clark, E.A., Golub, T.R., Hynes, R.O. and Lander, E.S.
TITLE Metastasis genes and uses thereof
JOURNAL Patent: WO 0141815-A 2 14-JUN-2001;
WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH (US); MASSACHUSETTS INSTITUTE OF TECHNOLOGY (US); Dana-Farber Cancer Institute Inc. (US)
FEATURES Location/Qualifiers
source 1..18
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1010 AAGATGTGTTGGGAT 1026
Db 17 AAGATTTGGTTGGGAT 1

RESULT 915
AX391641
LOCUS AX391641 18 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 22 from Patent EP1184468.
ACCESSION AX391641
VERSION AX391641.1 GI:19700247
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Yamamoto, N.C., Okamoto, T.C. and Suzuki, T.C.
TITLE Method for sequencing using probe arrays
JOURNAL Patent: EP 1184468-A 22 06-MAR-2002;

```

FEATURES
    source
        1. .18
            /location/Qualifiers
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Sample oligonucleotide"

Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 18;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGCTCGGGTTCAT 498
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 916
AX718767/c
LOCUS AX718767 18 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 331 from Patent WO20103043.
ACCESSION AX718767
VERSION AX718767.1 GI:29891334
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
    1
    AUTHORS Beinrohr,C. and Snaidr,J.
    TITLE Method for the specific fast detection of bacteria which is harmful
    JOURNAL Patent: WO 02103043-A 331 27-DEC-2002;
    FEATURES
        source
            1. .18
                /location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonukleotid"

Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 18;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1357 TCAGTGTGGGTGGGC 1373
Db 18 TCAGTGTGGGTGGGC 2

RESULT 919
AX785415/c
LOCUS AX785415 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 26 from Patent WO03050301.
ACCESSION AX785415
VERSION AX785415.1 GI:32953035
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
    1
    AUTHORS Gurling,H.M.
    TITLE Susceptibility locus for schizophrenia
    JOURNAL Patent: WO 03050301-A 26 19-JUN-2003;
    FEATURES
        source
            1. .18
                /location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 18;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 926 TGGATAGGCTGACGAAG 942
Db 17 TGGATAGGCTGACGAAG 1

RESULT 920
AX839747
LOCUS AX839747 18 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 15 from Patent EP1323823.

```

```

FEATURES
    source
        1. .18
            /location/Qualifiers
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Sample oligonucleotide"

Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 18;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGCTCGGGTTCAT 498
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 916
AX391790
LOCUS AX391790 18 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 22 from Patent EP1184467.
ACCESSION AX391790
VERSION AX391790.1 GI:19700374
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
    1
    AUTHORS Yamamoto,N., Okamoto,T., Tanaka,S. and Suzuki,T.
    TITLE Screening method for gene variation
    JOURNAL Patent: EP 1184467-A 22 06-MAR-2002;
    FEATURES
        source
            1. .18
                /location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Sample oligonucleotide"

Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 18;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGCTCGGGTTCAT 498
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 917
AX453798
LOCUS AX453798 18 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 22 from Patent EP1213361.
ACCESSION AX453798
VERSION AX453798.1 GI:21713467
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
    1
    AUTHORS Okamoto,T., Yamamoto,N. and Suzuki,T.
    TITLE Terminal labeled probe array and method of making it
    JOURNAL Patent: EP 1213361-A 22 12-JUN-2002;
    FEATURES
        source
            1. .18
                /location/Qualifiers
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthesized"

Query Match
    Best Local Similarity 0.8%; Score 13.8; DB 1; Length 18;
    Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```
ACCESSION AX839747
VERSION AX839747.1 GI:39922912
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Sheppard,P.O., Jaspers,S.R., Jelinek,L.J. and Whitmore,T.E.
TITLE Mammalian secretory peptide 9, antibodies against it and their use
JOURNAL Patent: EP 1323823-A 15 02-JUL-2003;
Zymogenetics Inc (US)
FEATURES
    source
    1..18
        Location/Qualifiers
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1570 ACCGTCACCACTGACTG 1586
    ||| ||||| |||||
Db 2 ACCTCCACCACTGACTG 18

RESULT 921
BD000033
LOCUS BD000033 18 bp DNA linear PAT 31-JAN-2002
DEFINITION Probe-coupling substrate, process for producing the same,
probe-array, method for detecting target substance, method for
specifying base sequence of single-stranded nucleic acid in
sample, and method for quantitating the target substance in the
sample.
ACCESSION BD000033
VERSION BD000033.1 GI:18623112
KEYWORDS JP 200270896-A/23.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Okamoto,H., Yamamoto,N. and Suzuki,T.
TITLE Probe-coupling substrate, process for producing the same,
probe-array, method for detecting target substance, method for
specifying base sequence of single-stranded nucleic acid in
sample, and method for quantitating the target substance in the
sample.
JOURNAL Patent: JP 200270896-A 23 03-OCT-2000;
CANON INC ANTEN PHARMACEUT CO LTD
COMMENT OS Artificial Sequence
PN JP 200270896-A/23
PD 03-OCT-2000
PF 28-JAN-1999 JP 1999019915
PR
PI HISASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC
C12Q1/68,C12M1/00,C12N15/09,G01N33/566,C12N15/00 CC
FH Key Location/Qualifiers
FT source 1..18
    /organism="Artificial Sequence".
FEATURES
    source
    1..18
        Location/Qualifiers
        /organism="synthetic construct"
        /mol_type="genomic DNA"
        /db_xref="taxon:32630"
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 482 ATGGGGGTCGGGGTCAT 498
    ||||| ||||| |||||
Db 2 ATGGGGCTCGGGTCAT 18

RESULT 922
BD106774
LOCUS BD106774 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Mammalian secretory peptide-9.
ACCESSION BD106774
VERSION BD106774.1 GI:23201592
KEYWORDS JP 2002503112-A/9.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 18)
AUTHORS Sheppard,P.O., Jelinek,L.J., Jaspers,S.R. and Whitmore,T.E.
TITLE Mammalian secretory peptide-9
JOURNAL Patent: JP 2002503112-A 9 29-JAN-2002;
ZyMOGENETICS INC
COMMENT OS Artificial Sequence
PN JP 2002503112-A/9
PD 29-JAN-2002
PF 02-JUL-1998 JP 1999507420
PR 03-JUL-1997 US 60/051704,03-JUL-1997 US 08/888088 PR
17-MAY-1998 US 60/085983,19-MAY-1998 US 09/081338 PR
17-JUN-1998 US 60/089899,17-JUN-1998 US 09/099005 PI PAUL O
SHEPPARD,LAURA J JELINEK,STEPHEN R JASPERS,THEODORE E PI
WHITMORE
PC C12N15/12,C12N15/62,C07K14/47,C07K16/18,C07K16/142,A61K38/17
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
    source
    1..18
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1570 ACCGTCACCACTGACTG 1586
    ||| ||||| |||||
Db 2 ACCTCCACCACTGACTG 18

RESULT 923
BD133644
LOCUS BD133644 18 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for screening mutated gene.
ACCESSION BD133644
VERSION BD133644.1 GI:23228589
KEYWORDS JP 2002071687-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 18)
AUTHORS Yamamoto,N., Okamoto,T., Suzuki,T. and Tanaka,S.
TITLE Method for screening mutated gene
JOURNAL Patent: JP 2002071687-A 22 12-MAR-2002;
CANON INC
COMMENT OS Artificial Sequence
PN JP 2002071687-A/22
PD 12-MAR-2002
PF 31-AUG-2000 JP 2000263396
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,SHINYA TANAKA
PC G01N33/53,C12M1/00,C12N15/09,C12Q1/68,G01N31/22,G01N33/566, PC
G01N37/00.
PC C12N15/00
CC Sample origonucleotide
FH Key Location/Qualifiers
FT source 1..18
    /organism="Artificial Sequence".
FEATURES
    source
    1..18
        Location/Qualifiers
        /organism="synthetic construct"
```

/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498
||||| ||||| |||||
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 924

BD135722 18 bp DNA linear PAT 18-SEP-2002
LOCUS
DEFINITION Method for detecting subjective component in specimen sample, and
substrate for detection used therefor.

ACCESSION BD135722
VERSION BD135722.1 GI:23230667
KEYWORDS JP 2002065274-A/26.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

1 (bases 1 to 18)

REFERENCE Yamamoto,N., Okamoto,T., Suzuki,T. and Shimizu,A.

AUTHORS Method for detecting subjective component in specimen sample, and
TITLE substrate for detection used therefor

JOURNAL Patent: JP 2002065274-A 26 05-MAR-2002;

CANON INC

COMMENT

OS Artificial Sequence
PN JP 2002065274-A/26
PD 05-MAR-2002
PF 31-AUG-2000 JP 2002063395
PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI,AKIRA SHIMIZU
PC C12N15/09,C12MI/00,C12MI/40,C12Q1/68,G01N31/22,G01N33/53, PC
G01N33/566,
PC G01N35/02,G01N37/10,G01N37/00,C12N15/00,G01N35/06 CC DNA
probe for hybridizing with gene encoding
mutated p53;named
CC in Table 1
FH Key Location/Qualifiers
FT source 1..18
FT /organism="synthetic construct"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32630"

FEATURES
source

Location/Qualifiers

1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498
||||| ||||| |||||
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 925

BD160988 18 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION Terminal-labeled probe-array and method for preparing it, and
method for evaluating target mass using the same.

ACCESSION BD160988
VERSION BD160988.1 GI:27866746
KEYWORDS JP 2002153284-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

1 (bases 1 to 18)

REFERENCE Okamoto,T., Yamamoto,N. and Suzuki,T.

AUTHORS Terminal-labeled probe-array and method for preparing it, and
TITLE

method for evaluating target mass using the same
Patent: JP 2002153284-A 22 28-MAY-2002;

CANON INC

OS Artificial Sequence

PN JP 2002153284-A/22

PD 28-MAY-2002

PF 24-NOV-2000 JP 2000357446

PI TADASHI OKAMOTO,NOBUKO YAMAMOTO,TOMOHIRO SUZUKI PC

C12N15/09,C12Q1/68,G01N31/22,G01N33/53,G01N33/566,G01N37/00, PC

C12N15/00

CC Description of Artificial Sequence:Synthesized FH Key

Location/Qualifiers

FT source 1..18

FT Location/Qualifiers

1..18 /organism="Artificial Sequence".

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498
||||| ||||| |||||
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 926

BD167483 18 bp DNA linear PAT 17-JAN-2003
LOCUS
DEFINITION A method of analyzing a base sequence of a nucleic acid.

ACCESSION BD167483

VERSION BD167483.1 GI:27873295

KEYWORDS WO 0233068-A/22.

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1 (bases 1 to 18)

AUTHORS Yamamoto,N., Okamoto,T. and Suzuki,T.

TITLE A method of analyzing a base sequence of a nucleic acid

JOURNAL Patent: WO 0233068-A 22 25-APR-2002;

CANON KK,NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI

OS Artificial Sequence

PN WO 0233068-A/22

PD 23-APR-2002

PF 18-OCT-2000 WO 2000JP007244

PI NOBUKO YAMAMOTO,TADASHI OKAMOTO,TOMOHIRO SUZUKI PC

C12N15/09,C12Q1/68,G01N33/566,G01N33/53

CC Sample orionucleotide

FH Key Location/Qualifiers

FT source 1..18

FT Location/Qualifiers

1..18 /organism="Artificial Sequence".

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498
||||| ||||| |||||
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 927

BD176966 18 bp DNA linear PAT 16-APR-2003
LOCUS
DEFINITION Method of analyzing nucleic acid base sequence.

```

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0
QY 1121 CCCTGAGAGAGGGGCA 1137
      ||||| ||||| |||||
Db 2 CCCTGAAGAGCGGGCA 18

RESULT 929
AX377095 15 bp DNA linear PAT 18-MAR-2002
LOCUS
DEFINITION Sequence 16 from Patent WO0212561.
ACCESSION AX377095
VERSION AX377095.1 GI:19573386
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Kazemi,A., Messer,C. and Tanguay,D.A.
TITLE Haplotypes of the orig1 gene
JOURNAL Patent: WO 0212561-A 16 14-FEB-2002;
Genaisance Pharmaceuticals, Inc. (US)
FEATURES
source 1..15
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 6.3e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1149 CTGCTACGTGGCCA 1162
      |||||:|||||
Db 2 CTCTAYGIGGGCA 15

RESULT 930
BD096968/c
LOCUS BD096968 18 bp DNA linear PAT 27-AUG-2002
DEFINITION SAG:apoptosis sensitivity gene.
ACCESSION BD096968
VERSION BD096968.1 GI:22642556
KEYWORDS JP 2001526063-A/3.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Sun,Y.
TITLE SAG:apoptosis sensitivity gene
JOURNAL Patent: JP 2001526063-A 3 18-DEC-2001;
WARNER LAMBERT CO
COMMENT OS Unidentified
PN JP 2001526063-A/3
PD 18-DEC-2001
PR 15-DEC-1998 JP 2000525451
PF 19-DEC-1997 US 60/068179,11-SEP-1998 US 60/099840 PI
YI SUN
PC C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P17/02,A61P35/00,
PC A61P39/06,
PC A61P43/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21 PC
,C12N5/10,C1201/68,
PC G01N33/50,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC
Strandedness: Single;
CC Topology: Linear;
CC /desc = 'oligonucleotide P1 downstream primer' FH Key
CC Location/Qualifiers
FT source 1..18
FT /organism='Unidentified'.
Location/Qualifiers
1..18
/organism="unidentified"
FEATURES
source

```

```
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.8%; Score 13.6; DB 1; Length 18;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1748
Db 18 YAAAAA15

RESULT 931
LOCUS AR084519
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION AR084519
VERSION AR084519.1 GI:10011290
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 8 09-NOV-1999;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTACAAAA1745
Db 1 TTTAAAAA15

RESULT 932
LOCUS BD244856
DEFINITION Oligonucleotide primer capable of making the non-specific double
strand formation unstable.
ACCESSION BD244856
VERSION BD244856.1 GI:33054626
KEYWORDS synthetic construct
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double
strand formation unstable
JOURNAL Patent: JP 2002532063-A 1 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
PN JP 2002532063-A/1
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
1..15
FT source
/organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.8%; Score 13.6; DB 1; Length 18;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1748
Db 18 YAAAAA15

RESULT 931
LOCUS AR084519
DEFINITION Sequence 8 from patent US 5981185.
ACCESSION AR084519
VERSION AR084519.1 GI:10011290
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Matson,R.S., Coassin,P.J., Rampal,J.B. and Caskey,C.Thomas.
TITLE Oligonucleotide repeat arrays
JOURNAL Patent: US 5981185-A 8 09-NOV-1999;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTACAAAA1745
Db 1 TTTAAAAA15

RESULT 932
LOCUS BD244856
DEFINITION Oligonucleotide primer capable of making the non-specific double
strand formation unstable.
ACCESSION BD244856
VERSION BD244856.1 GI:33054626
KEYWORDS synthetic construct
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Pelletier,J. and Das,M.
TITLE Oligonucleotide primer capable of making the non-specific double
strand formation unstable
JOURNAL Patent: JP 2002532063-A 1 02-OCT-2002;
COMMENT MCGILL UNIVERSITY
PN JP 2002532063-A/1
PD 02-OCT-2002
PF 06-OCT-1999 JP 2000574722
PR 07-OCT-1998 CA 2246623
PI JERRY PELLETIER,MANJULA DAS
PC C12N15/09,C12Q1/68,C12N15/00
CC Description of Artificial Sequence: synthetic oligonucleotide
FH Key Location/Qualifiers
1..15
FT source
/organism="Artificial Sequence".
FEATURES
source
Location/Qualifiers
1..15
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAA1750
Db 1 AAAAAA15

RESULT 933
LOCUS I28566
DEFINITION Sequence 19 from patent US 5571937.
ACCESSION I28566
VERSION I28566.1 GI:1819342
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5571937-A 19 05-NOV-1996;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGG 878
Db 1 AAGAGGAGGAGG 15

RESULT 934
LOCUS I58728
DEFINITION Sequence 19 from patent US 5652350.
ACCESSION I58728
VERSION I58728.1 GI:2477966
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 15)
AUTHORS Watanabe,K.A., Ren,W.-Y. and Weil,R.
TITLE Complementary DNA and toxins
JOURNAL Patent: US 5652350-A 19 29-JUL-1997;
FEATURES
source
Location/Qualifiers
1..15
/organism="unknown"
/mol_type="unassigned DNA"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 15;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGG 878
Db 1 AAGAGGAGGAGG 15

RESULT 935
LOCUS AR241876
DEFINITION Sequence 164 from patent US 6472154.
ACCESSION AR241876
VERSION AR241876.1 GI:27287688
KEYWORDS
```

```

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
TITLE        Polymorphic repeats in human genes
JOURNAL      Patent: US 6472154-A 164 29-OCT-2002;
FEATURES     Location/Qualifiers
             source
             1..15
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 936
LOCUS      AX147741 15 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 43 from Patent WO0136673.
ACCESSION  AX147741
VERSION     AX147741.1 GI:14346786
KEYWORDS   Pseudomonas sp.
SOURCE     Pseudomonas sp.
ORGANISM   Bacteria; Proteobacteria.

REFERENCE   1
AUTHORS     Apfel, H., Heesemann, J., Trebesius, K. and Autenrieth, I.
TITLE       Test for micro-organisms
JOURNAL     Patent: WO 0136673-A 43 25-MAY-2001;
            Creatogen Aktiengesellschaft (DE)
FEATURES    Location/Qualifiers
             source
             1..15
             /organism="Pseudomonas sp."
             /mol_type="unassigned DNA"
             /db_xref="taxon:306"

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 649 GCTGCCCGCCTTC 663
Db 1 GCTGCCCGCCTTC 15

RESULT 937
LOCUS      AR141562/2 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6146855.
ACCESSION  AR141562
VERSION     AR141562.1 GI:15101078
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE   1 (bases 1 to 16)
AUTHORS     Williams, K.Leslie., Vesey, G., Veal, D., Ashbolt, N.John. and
            Dorsch, M.
TITLE       Method for the detection of viable Cryptosporidium parvum oocysts
JOURNAL     Patent: US 6146855-A 2 14-NOV-2000;
FEATURES    Location/Qualifiers
             source
             1..16
             /organism="unknown"
             /mol_type="unassigned DNA"

Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.1e+02;

SOURCE      Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Garner, H.R., Wren, J.D., Minna, J.D. and Fondon, J.W. III.
TITLE        Polymorphic repeats in human genes
JOURNAL      Patent: US 6472154-A 164 29-OCT-2002;
FEATURES     Location/Qualifiers
             source
             1..15
             /organism="unknown"
             /mol_type="genomic DNA"

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 6.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAA 1747
Db 15 TACTAAAAAAAAAAAAA 1

RESULT 938
LOCUS      BD266224/2 16 bp DNA linear PAT 17-JUL-2003
DEFINITION Universal arrays.
ACCESSION  BD266224
VERSION     BD266224.1 GI:33075992
KEYWORDS   JP 2002539849-A/224.
SOURCE     synthetic construct
            synthetic construct
            artificial sequences.
            1 (bases 1 to 16)
REFERENCE   1
AUTHORS     Fan, J.B., Hirschhorn, J.N., Huang, X., Kaplan, P., Lander, E.S.,
            Lockhart, D.J., Ryder, T. and Sklar, P.
TITLE       Universal arrays
JOURNAL     Patent: JP 2002539849-A 224 26-NOV-2002;
            WHITEHEAD INSTITUTE FOR BIOMEDICAL RESEARCH, AFFYMETRIX INC
COMMENT     OS Artificial Sequence
            PN JP 2002539849-A/224
            PD 26-NOV-2002
            PF 27-MAR-2000 JP 2000608794
            PR 26-MAR-1999 US 60/126473, 23-JUN-1999 US 60/140359 PI
            JTIAN BING FAN, JOEL N HIRSCHORN, XIAOHUA
            HUANG, PAUL KAPLAN, ERIC
            PI S LANDER,
            PI DAVID J LOCKHART, THOMAS RYDER, PAMELA SKLAR
            PC C12Q1/68, C12M1/00, C12N15/09, C12N15/09, C12N15/09, G01N33/53, PC
            G01N33/566,
            PC G01N37/00, C12N15/00, C12N15/00, C12N15/00
            CC Primer
            FH Key
            FT source
            1..16
            Location/Qualifiers
            /organism="Artificial Sequence".

Query Match      0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 984 CTTTGGCCAGTGTGG 998
Db 15 CTTTGGCCAGTGTGG 1

RESULT 939
LOCUS      AX598384 16 bp DNA linear PAT 14-FEB-2003
DEFINITION Sequence 658 from Patent WO0244994.
ACCESSION  AX598384
VERSION     AX598384.1 GI:28398560
KEYWORDS   synthetic construct
            synthetic construct
            artificial sequences.
            1
REFERENCE   1
AUTHORS     Brower, A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
            Indig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichiev, V.,
            Neri, B.P., Reimer, N.D., Roeven, R.T., Skrzypczynski, Z., Ziarno, W.A.,
            Comerford, J., Stump, S. and Viegut, D.D.
TITLE       Systems and method for detection assay production and sale
JOURNAL     Patent: WO 0244994-A 658 06-JUN-2002;
            THIRD WAVE TECHNOLOGIES, INC. (US)
FEATURES    Location/Qualifiers

```

source 1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1533 GGCCTGCAGGCGCTG 1547
Db 1 GGCCTGCAGGCGCAG 15

RESULT 940
AR009007/c

LOCUS AR009007 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 16 from patent US 5756101.
ACCESSION AR009007
VERSION AR009007.1 GI:3967812
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Paolletti,E., de Taisne,C., Chang,S., Hui,G. and Siddiqui,W.
TITLE Malaria recombinant poxvirus
JOURNAL Patent: US 5756101-A 16 26-MAY-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1096 CAGCTTCGCGGCCAG 1110
Db 17 CAGCTTCGAGGCCAG 3

RESULT 941
AR010206/c

LOCUS AR010206 17 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5756702.
ACCESSION AR010206
VERSION AR010206.1 GI:3969011
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Lohman,K.L., Ostreerova,N.V., Van Cleve,M. and Reid,R.Alan.
TITLE Detection of nucleic acids in cells by thermophilic strand displacement amplification
JOURNAL Patent: US 5756702-A 4 26-MAY-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 CAAAGAGGAGTGC 842
Db 15 CAATGAGGAGTGC 1

RESULT 942
AR043128/c

LOCUS AR043128 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 12 from patent US 5814453.
ACCESSION AR043128
VERSION AR043128.1 GI:5964136
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beck,J.Joseph.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5814453-A 12 29-SEP-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 CCCCACTCCAGCCTC 626
Db 16 CACCACTCCAGCCTC 2

RESULT 943
AR045401/c

LOCUS AR045401 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 194 from patent US 5817796.
ACCESSION AR045401
VERSION AR045401.1 GI:5966866
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Stinchcomb,D.T., Draper,K., McSwiggen,J. and Jarvis,T.
TITLE C-myb ribozymes having 2'-5'-linked adenylyate residues
JOURNAL Patent: US 5817796-A 194 06-OCT-1998;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGGAGG 878
Db 17 AAGAGGAGGAGGAGG 3

RESULT 944
AR074628/c

LOCUS AR074628 17 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 12 from patent US 5955274.
ACCESSION AR074628
VERSION AR074628.1 GI:10001381
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Ligon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5955274-A 12 21-SEP-1999;
FEATURES Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"


```

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 612 CCCACTCCAGCCTC 626
   |||||
Db 16 CACCACTCCAGCCTC 2

RESULT 945
LOCUS AR098727/c 17 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 2 from patent US 6077669.
ACCESSION AR098727
VERSION AR098727.1 GI:12808493
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1. (bases 1 to 17)
AUTHORS Little,M.C. and Vonk,G.P.
TITLE Kit and method for fluorescence based detection assay
JOURNAL Patent: US 6077669-A 2 20-JUN-2000;
FEATURES
    source
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 828 CAATGAGGAAGCTGC 842
   |||||
Db 15 CAATGAGGAAGCTGC 1

RESULT 946
LOCUS BD238354 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for identifying nucleic acid.
ACCESSION BD238354
VERSION BD238354.1 GI:33048124
KEYWORDS JP 2002534099-A/8.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1. (bases 1 to 17)
AUTHORS Rothberg,J.M., Mckenna,M., Predki,P., Windemuth,A. and Shimkets,R.A.
TITLE Method for identifying nucleic acid
JOURNAL Patent: JP 2002534099-A 8 15-OCT-2002;
COMMENT CUPAGEN CORP
OS Artificial Sequence
PN JP 2002534099-A/8
PD 15-OCT-2002
PF 07-JAN-1999 US 60/115109,13-OCT-1999 US 09/417386 PI
JONATHAN M ROTHBERG,MICHAEL MCKENNA,PAUL PREDKI,ANDREAS PI
WINDMUTH,
PI RICHARD A SHIMKETS
CC C12N15/09,C12Q1/68//G01N33/50,G01N33/566,C12N15/00
PC Description of Artificial Sequence: PCR primer FH Key
FEATURES
    Location/Qualifiers
    FT source
    1..17
    /organism="Artificial Sequence".

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 828 CAAAGAGGAAGCTGC 842
   |||||
Db 15 CAATGAGGAAGCTGC 1

RESULT 947
LOCUS E35686/c 17 bp DNA linear PAT 18-JUN-2001
DEFINITION Detection assay with the use of fluorescence and kit therefor.
ACCESSION E35686
VERSION E35686.1 GI:13019158
KEYWORDS JP 1999225799-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1. (bases 1 to 17)
AUTHORS Michael,C.L. and Gren,P.V.
TITLE Detection assay with the use of fluorescence and kit therefor
JOURNAL Patent: JP 1999225799-A 2 24-AUG-1999;
COMMENT BECTON DICKINSON & CO
OS Artificial Sequence
PN JP 1999225799-A/2
PD 24-AUG-1999
PF 04-NOV-1998 JP 1998312790
PR 04-NOV-1997 US 08/964020
PI MICHAEL C LITTLE GREN P VONG
PC C12Q1/68,G01N11/78,G01N33/50//C12N15/09,C12N15/00 CC
FH Key
FT source
1..17
/organism="Artificial Sequence".

FEATURES
    source
    Location/Qualifiers
    1..17
    /organism="synthetic construct"
    /mol_type="genomic DNA"
    /db_xref="taxon:32630"

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 828 CAAAGAGGAAGCTGC 842
   |||||
Db 15 CAATGAGGAAGCTGC 1

RESULT 948
LOCUS I32068 17 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 12 from patent US 5585238.
ACCESSION I32068
VERSION I32068.1 GI:1822859
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1. (bases 1 to 17)
AUTHORS Ligon,J.M. and Beck,J.J.
TITLE Detection of fungal pathogens using the polymerase chain reaction
JOURNAL Patent: US 5585238-A 12 17-DEC-1996;
FEATURES
    Location/Qualifiers
    FT source
    1..17
    /organism="unknown"
    /mol_type="unassigned DNA"

Query Match          0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 612 CCCACTCCAGCCTC 626
   |||||

```

```
Db      16 CACCACTCCAGCTC 2
RESULT 949
I43322/c
LOCUS      17 bp      DNA      linear      PAT 07-OCT-1997
DEFINITION Sequence 4 from patent US 5631147.
ACCESSION I43322
VERSION I43322.1 GI:2468566
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Lohman,K.L., Ostreva,N.V., Cleve,M.V. and Reid,R.A.
TITLE Detection of nucleic acids in cells by thermophilic strand
displacement amplification
JOURNAL Patent: US 5631147-A 4 20-MAY-1997;
FEATURES
source
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 CAAAGAGGAGCTGC 842
Db 15 CAATGAGGAGCTGC 1

RESULT 952
AR187288/c
LOCUS      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 2776 from patent US 6346398.
ACCESSION AR187288
VERSION AR187288.1 GI:20233253
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2776 12-FEB-2002;
FEATURES
source
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAAGC 47
Db 17 AGGAAAAAAAAAGC 3

RESULT 953
AR187289/c
LOCUS      17 bp      DNA      linear      PAT 20-APR-2002
DEFINITION Sequence 2777 from patent US 6346398.
ACCESSION AR187289
VERSION AR187289.1 GI:20233254
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions
related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6346398-A 2777 12-FEB-2002;
FEATURES
source
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAAGC 47
Db 16 AGGAAAAAAAAAGC 2

RESULT 951
I95825/c
LOCUS      17 bp      DNA      linear      PAT 01-DEC-1998
DEFINITION Sequence 4 from patent US 5733752.
ACCESSION I95825
VERSION I95825.1 GI:3940295
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 17)
AUTHORS Lohman,K.L., Ostreva,N.V., Cleve,M.Van. and Reid,R.Alan.
TITLE Detection of nucleic acids in cells by thermophilic strand
```

```
RESULT 954
ARI87290/c
LOCUS       ARI87290               17 bp    DNA             linear    PAT 20-APR-2002
DEFINITION   Sequence 2778 from patent US 6346398.
ACCESSION   ARI87290
VERSION     ARI87290.1  GI:20233255
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6346398-A 2778 12-FEB-2002;
FEATURES
source      Location/Qualifiers
             1..17
             /organism="unknown"
             /mol_type="unassigned DNA"
Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAAAGC 47
Db 15 AGGAAAAAAAAGC 1

RESULT 955
ARI87290/c
LOCUS       ARI87290               17 bp    RNA             linear    PAT 17-AUG-2003
DEFINITION   Sequence 1300 from patent US 6566127.
ACCESSION   ARI87290
VERSION     ARI87290.1  GI:33709706
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1300 20-MAY-2003;
FEATURES
source      Location/Qualifiers
             1..17
             /organism="unknown"
             /mol_type="unassigned RNA"
Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAAAGC 47
Db 15 AGGAAAAAAAAGC 1

RESULT 956
ARI87290/c
LOCUS       ARI87290               17 bp    RNA             linear    PAT 17-AUG-2003
DEFINITION   Sequence 1301 from patent US 6566127.
ACCESSION   ARI87290
VERSION     ARI87290.1  GI:33709707
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1301 20-MAY-2003;
FEATURES
source      Location/Qualifiers
             1..17
             /organism="unknown"
             /mol_type="unassigned RNA"
Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAAAGC 47
Db 17 AGGAAAAAAAAGC 3

RESULT 957
ARI87290/c
LOCUS       ARI87290               17 bp    RNA             linear    PAT 17-AUG-2003
DEFINITION   Sequence 1302 from patent US 6566127.
ACCESSION   ARI87290
VERSION     ARI87290.1  GI:33709708
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 1302 20-MAY-2003;
FEATURES
source      Location/Qualifiers
             1..17
             /organism="unknown"
             /mol_type="unassigned RNA"
Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAAAGC 47
Db 16 AGGAAAAAAAAGC 2

RESULT 958
ARI87290/c
LOCUS       ARI87290               17 bp    RNA             linear    PAT 17-AUG-2003
DEFINITION   Sequence 5090 from patent US 6566127.
ACCESSION   ARI87290
VERSION     ARI87290.1  GI:33713496
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE       Method and reagent for the treatment of diseases or conditions
           related to levels of vascular endothelial growth factor receptor
JOURNAL     Patent: US 6566127-A 5090 20-MAY-2003;
FEATURES
source      Location/Qualifiers
             1..17
             /organism="unknown"
             /mol_type="unassigned RNA"
Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 530 AGCCCCCGCCACCTC 544
Db 3 AACCCCCGCCACCTC 17
```

```
RESULT 959
LOCUS AX146685/c 17 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 27 from Patent WO0134834.
ACCESSION AX146685
VERSION AX146685.1 GI:14285078
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Leffers, H., Jorgensen, M. and skakkeb K, N.E.
TITLE Endogenous gene expression assay
JOURNAL Patent: WO 0134834-A 27 17-MAY-2001;
Rigshospitalet (DK)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Primer sequence"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 33 AGGAAAAAAGGC 47
Db 17 AGAAAAAAGGC 3
RESULT 960
LOCUS AX216923 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2365 from Patent WO0159103.
ACCESSION AX216923
VERSION AX216923.1 GI:15526984
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2365 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 864 AAGAGAGAGAGG 878
Db 1 AGGAGAGAGAGG 15
RESULT 961
LOCUS AX218294 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3736 from Patent WO0159103.
ACCESSION AX218294
VERSION AX218294.1 GI:15528355
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3736 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1619 CAGTCCAGTTCCCA 1633
Db 16 CAGTCCAGTTCCCA 2
RESULT 963
LOCUS AX266016 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3407 from Patent WO0173002.
ACCESSION AX266016
VERSION AX266016.1 GI:16514815
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Kniec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3406 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1619 CAGTCCAGTTCCCA 1633
Db 16 CAGTCCAGTTCCCA 2
RESULT 963
LOCUS AX266016 17 bp DNA linear PAT 26-OCT-2001
DEFINITION Sequence 3407 from Patent WO0173002.
ACCESSION AX266016
VERSION AX266016.1 GI:16514815
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Kniec, E.B., Gamper, H.B. and Rice, M.C.
TITLE Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
JOURNAL Patent: WO 0173002-A 3407 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
```

FEATURES
source
Location/Qualifiers

1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1619 CAGTTCACGATCCCA 1633
Db 2 CAGTGCCAGTCCCA 16

RESULT 964
AX421847
LOCUS AX421847 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 183 from Patent WO0188124.
ACCESSION AX421847
VERSION AX421847.1 GI:21525229
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 183 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 655 CCAGCCTCCCCGTG 669
Db 1 CCAGCCTCCCCGTG 15

RESULT 965
AX422310/c
LOCUS AX422310 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 646 from Patent WO0188124.
ACCESSION AX422310
VERSION AX422310.1 GI:21525692
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 646 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 613 CCCACTCCAGCCTCT 627
Db 17 CCCACTCCAGCCTCT 3

RESULT 966
AX422498
LOCUS AX422498 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 834 from Patent WO0188124.
ACCESSION AX422498
VERSION AX422498.1 GI:21525880
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 834 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 268 GCATTCCAGCCCAC 282
Db 3 GCCCTCCAGCCCAC 17

RESULT 967
AX422545
LOCUS AX422545 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 881 from Patent WO0188124.
ACCESSION AX422545
VERSION AX422545.1 GI:21525927
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 881 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 655 CCAGCCTTTCCCGTG 669
Db 3 CCAGCCTTTCCCGTG 17

RESULT 968
AX422546
LOCUS AX422546 17 bp RNA linear PAT 18-JUN-2002

[illegible]

```

FEATURES             Location/Qualifiers
     source
       1..17
         /organism="Homo sapiens"
         /mol_type="unassigned DNA"
         /db_xref="taxon:9606"

Query Match
Best Local Similarity    0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1619 CAGTTCAGTTCCCA 1633
Db              |||||
               2 CAGTGCCAGTTCCCA 16

RESULT 964
AX421847          17 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION        Sequence 183 from Patent WO0188124.
ACCESSION         AX421847
VERSION           AX421847.1 GI:21525229
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
                  Randi,A.M.
TITLE             Method and reagent for the inhibition of erg
JOURNAL           Patent: WO 0188124-A 183 22-NOV-2001;
                  RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
       1..17
         /organism="Homo sapiens"
         /mol_type="unassigned RNA"
         /db_xref="taxon:9606"

Query Match
Best Local Similarity    0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      655 CCAGCCTTCCCCGTG 669
Db              |||||
               1 CCAGCCTTCCCCGTG 15

RESULT 965
AX422310/c        17 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION        Sequence 646 from Patent WO0188124.
ACCESSION         AX422310
VERSION           AX422310.1 GI:21525692
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
                  Randi,A.M.
TITLE             Method and reagent for the inhibition of erg
JOURNAL           Patent: WO 0188124-A 646 22-NOV-2001;
                  RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
       1..17
         /organism="Homo sapiens"
         /mol_type="unassigned RNA"
         /db_xref="taxon:9606"

Query Match
Best Local Similarity    0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      968
Db              |||||
               3 CCAGCCTTCCCCGTG 17

RESULT 968
AX422546          17 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION        Sequence 881 from Patent WO0188124.
ACCESSION         AX422545
VERSION           AX422545.1 GI:21525927
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
                  Randi,A.M.
TITLE             Method and reagent for the inhibition of erg
JOURNAL           Patent: WO 0188124-A 881 22-NOV-2001;
                  RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
       1..17
         /organism="Homo sapiens"
         /mol_type="unassigned RNA"
         /db_xref="taxon:9606"

Query Match
Best Local Similarity    0.8%; Score 13.4; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      655 CCAGCCTTCCCCGTG 669
Db              |||||
               3 CCAGCCTTCCCCGTG 17

RESULT 968
AX422546          17 bp RNA linear PAT 18-JUN-2002
LOCUS
DEFINITION        Sequence 881 from Patent WO0188124.
ACCESSION         AX422545
VERSION           AX422545.1 GI:21525927
KEYWORDS          Homo sapiens (human)
SOURCE            Homo sapiens
ORGANISM           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS           Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
                  Randi,A.M.
TITLE             Method and reagent for the inhibition of erg
JOURNAL           Patent: WO 0188124-A 881 22-NOV-2001;
                  RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
       1..17
         /organism="Homo sapiens"
         /mol_type="unassigned RNA"
         /db_xref="taxon:9606"

```

<p>DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 882 from Patent WO0188124. AX422546 AX422546.1 GI:21525928</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 882 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 655 CCAGCCTTCCCGTG 669 Db 2 CCAGCCTTCCCGTG 16</p>	<p>RESULT 969 AX423515/c LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 1851 from Patent WO0188124. AX423515 AX423515.1 GI:21526897</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 1851 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 655 CCAGCCTTCCCGTG 669 Db 2 CCAGCCTTCCCGTG 16</p>	<p>RESULT 970 AX423516/c LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 1852 from Patent WO0188124. AX423516 AX423516.1 GI:21526898</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 882 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 613 CCCACTCCAGCCTCT 627 Db 16 CCCACTCCAGCCTCT 2</p>	<p>RESULT 971 AX423699 LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 2035 from Patent WO0188124. AX423699 AX423699.1 GI:21527081</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 2035 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 861 AGGAAGCGAAGAGG 875 Db 2 AGGAAGCGAAGAGG 16</p>	<p>RESULT 972 AX423700 LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 2036 from Patent WO0188124. AX423700 AX423700.1 GI:21527082</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 2036 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 861 AGGAAGCGAAGAGG 875 Db 2 AGGAAGCGAAGAGG 16</p>	<p>RESULT 973 AX423700 LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 2036 from Patent WO0188124. AX423700 AX423700.1 GI:21527082</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 2036 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 861 AGGAAGCGAAGAGG 875 Db 2 AGGAAGCGAAGAGG 16</p>	<p>RESULT 974 AX423700 LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 2036 from Patent WO0188124. AX423700 AX423700.1 GI:21527082</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 2036 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 861 AGGAAGCGAAGAGG 875 Db 2 AGGAAGCGAAGAGG 16</p>	<p>RESULT 975 AX423700 LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE AUTHORS</p> <p>TITLE JOURNAL</p> <p>FEATURES source</p>	<p>Sequence 2036 from Patent WO0188124. AX423700 AX423700.1 GI:21527082</p> <p>Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</p> <p>1 Jarvis, T., von Carlowitz, I., Mcswiggen, J.A., McLaughlin, F.G. and Randi, A.M. Method and reagent for the inhibition of erg</p> <p>PATENT: WO 0188124-A 2036 22-NOV-2001; RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)</p> <p>Location/Qualifiers 1. .17 /organism="Homo sapiens" /mol_type="unassigned RNA" /db_xref="taxon:9606"</p>	<p>Query Match Best Local Similarity 0.8%; Score 13.4; DB 1; Length 17; Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>	<p>QY 861 AGGAAGCGAAGAGG 875 Db 2 AGGAAGCGAAGAGG 16</p>	<p>RESULT 976 AX423700 LOCUS DEFINITION Accession Version Keywords Source Organism</p> <p>REFERENCE </p>
---	--	---	---	---	--	---	---	---	---	---	---	---	--	---	---	---	--	---	---	---	--	---	---	---	--	---	---	---	--	---	---	--

```

/db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 861 AGGAAGAGGAGGAGG 875
Db 1 AGGAGGAGGAGGAGG 15

RESULT 973
AX499341/c
LOCUS AX499341 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 648 from Patent EP1229046.
ACCESSION AX499341
VERSION AX499341.1 GI:23381634
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 648 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
    1..17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAG 866
Db 16 TGGCCCTGCAGGAG 2

RESULT 974
AX499342/c
LOCUS AX499342 17 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 649 from Patent EP1229046.
ACCESSION AX499342
VERSION AX499342.1 GI:23381635
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Zhan, J.
TITLE Human testis expressed patched like protein
JOURNAL Patent: EP 1229046-A 649 07-AUG-2002;
Aeomica, Inc. (US)
FEATURES
source
    Location/Qualifiers
    1..17
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAG 866
Db 15 TGGCCCTGCAGGAG 1

RESULT 975
AX578565/c
LOCUS AX578565 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 403 from Patent WO0211674.
ACCESSION AX578565
VERSION AX578565.1 GI:27647767
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 403 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source
    Location/Qualifiers
    1..17
    /organism="Homo sapiens"
    /mol_type="unassigned RNA"
    /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 AGCCTCCAGGAGTG 922
Db 17 AGCCTCCGAGGAGTG 3

RESULT 976
AX580298/c
LOCUS AX580298 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 2136 from Patent WO0211674.
ACCESSION AX580298
VERSION AX580298.1 GI:27649500
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 2136 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES
source
    Location/Qualifiers
    1..17
    /organism="Homo sapiens"
    /mol_type="unassigned RNA"
    /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 AGCCTCCAGGAGTG 922
Db 16 AGCCTCCGAGGAGTG 2

RESULT 977
AX580299/c
LOCUS AX580299 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 2137 from Patent WO0211674.
ACCESSION AX580299

```

VERSION AX580299.1 GI:27649501
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (Clca-1)
JOURNAL Patent: WO 0211674-A 2137 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US); Syntex (U.S.A.) LLC (US);
Thompson, James (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 908 AGCTCCAGGATG 922
Db 15 AGCTCCGAGGATG 1
RESULT 978
AX672633/c
LOCUS AX672633 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1078 from Patent WO03004526.
ACCESSION AX672633
VERSION AX672633.1 GI:29330981
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1078 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1386 GCCAGTCAGGAGGA 1400
Db 17 GCCAGTCAGGTGGA 3
RESULT 979
AX673370/c
LOCUS AX673370 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1815 from Patent WO03004526.
ACCESSION AX673370
VERSION AX673370.1 GI:29331718
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1815 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 907 CAGCTCCAGGATG 921
Db 16 CAGCTCCAGGATG 2
RESULT 980
AX688345
LOCUS AX688345 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1077 from Patent EP1281758.
ACCESSION AX688345
VERSION AX688345.1 GI:29411045
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 1077 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 852 TGGCCCTGCAGGAAG 866
Db 3 TGGCCCTGCAGGCAG 17
RESULT 981
AX688346
LOCUS AX688346 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1078 from Patent EP1281758.
ACCESSION AX688346
VERSION AX688346.1 GI:29411046
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 1078 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

[illegible]

```
VERSION      AX722330.1  GI:30422831
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE       1
JOURNAL     Telerman,A., Anson,R. and Tuijnder,M.
            Sequences involved in phenomena of tumour suppression, tumour
FEATURES    reversion, apoptosis and/or virus resistance and their use as
            medicines.
            Patent: WO 03025176-A 17 27-MAR-2003;
            Molecular Engines Laboratories (FR)
            Location/Qualifiers
            1. .17
            /organism="Mus musculus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10090"
            source
            Query Match      0.8%; Score 13.4; DB 1; Length 17;
            Best Local Similarity 93.3%; Pred. No. 7.6e+02;
            Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTACAAAAA 1745
Db 3 TCTACAAAAA 17

RESULT 987
AX724812/C
LOCUS      AX724812      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 2499 from Patent WO03025176.
ACCESSION  AX724812
VERSION    AX724812.1  GI:30504155
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE     1
JOURNAL   Telerman,A., Anson,R. and Tuijnder,M.
            Sequences involved in phenomena of tumour suppression, tumour
FEATURES  reversion, apoptosis and/or virus resistance and their use as
            medicines.
            Patent: WO 03025176-A 2499 27-MAR-2003;
            Molecular Engines Laboratories (FR)
            Location/Qualifiers
            1. .17
            /organism="Mus musculus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:10090"
            source
            Query Match      0.8%; Score 13.4; DB 1; Length 17;
            Best Local Similarity 93.3%; Pred. No. 7.6e+02;
            Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 38 AAAAAAAGCCAGAA 52
Db 17 AAAAAAAGCCAGGA 3

RESULT 988
AX735928/C
LOCUS      AX735928      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 1518 from Patent WO03025177.
ACCESSION  AX735928
VERSION    AX735928.1  GI:30515205
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1
JOURNAL   Telerman,A., Anson,R. and Tuijnder,M.
            Sequences involved in phenomena of tumour suppression, tumour
FEATURES  reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 3635 27-MAR-2003;
            Molecular Engines Laboratories (FR)
            Location/Qualifiers
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            source
            Query Match      0.8%; Score 13.4; DB 1; Length 17;
            Best Local Similarity 93.3%; Pred. No. 7.6e+02;
            Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 862 GGAAGAGGAAGAGGA 876
Db 17 GGAAGAGGAGAGGA 3

RESULT 990
AX738045/C
LOCUS      AX738045      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3635 from Patent WO03025177.
ACCESSION  AX738045
VERSION    AX738045.1  GI:30517333
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1
JOURNAL   Telerman,A., Anson,R. and Tuijnder,M.
            Sequences involved in phenomena of tumour suppression, tumour
FEATURES  reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 3635 27-MAR-2003;
            Molecular Engines Laboratories (FR)
            Location/Qualifiers
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            source
            Query Match      0.8%; Score 13.4; DB 1; Length 17;
            Best Local Similarity 93.3%; Pred. No. 7.6e+02;
            Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 862 GGAAGAGGAAGAGGA 876
Db 17 GGAAGAGGAGAGGA 3

RESULT 990
AX738045/C
LOCUS      AX738045      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 3635 from Patent WO03025177.
ACCESSION  AX738045
VERSION    AX738045.1  GI:30517333
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE     1
JOURNAL   Telerman,A., Anson,R. and Tuijnder,M.
            Sequences involved in phenomena of tumour suppression, tumour
FEATURES  reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
            Patent: WO 03025177-A 3635 27-MAR-2003;
            Molecular Engines Laboratories (FR)
            Location/Qualifiers
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            source
            Query Match      0.8%; Score 13.4; DB 1; Length 17;
            Best Local Similarity 93.3%; Pred. No. 7.6e+02;
            Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 862 GGAAGAGGAAGAGGA 876
Db 17 GGAAGAGGAGAGGA 3
```

```

source      1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1311 GATCCACTGTATTGA 1325
Db 1 GATCCTCTGTATTGA 15

RESULT 991
AX738493/c
LOCUS      AX738493      17 bp      DNA      linear      PAT 08-MAY-2003
DEFINITION Sequence 4083 from Patent WO03025177.
ACCESSION  AX738493
VERSION     AX738493.1 GI:30517781
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
JOURNAL     Patent: WO 03025177-A 4083 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAAGA 3

RESULT 992
AX757892/c
LOCUS      AX757892      17 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION Sequence 1213 from Patent WO03040369.
ACCESSION  AX757892
VERSION     AX757892.1 GI:32252508
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 1213 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAAGA 3

RESULT 992
AX757892/c
LOCUS      AX757892      17 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION Sequence 1213 from Patent WO03040369.
ACCESSION  AX757892
VERSION     AX757892.1 GI:32252508
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 1213 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAAGA 3

RESULT 993
AX759206/c
LOCUS      AX759206      17 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION Sequence 2527 from Patent WO03040369.
ACCESSION  AX759206
VERSION     AX759206.1 GI:32253822
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 2527 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 862 GGAGAGGAGAGAGGA 876
Db 17 GGAGGAGGAGAGAGGA 3

RESULT 994
AX804339/c
LOCUS      AX804339      17 bp      DNA      linear      PAT 25-NOV-2003
DEFINITION Sequence 507 from Patent WO03060160.
ACCESSION  AX804339
VERSION     AX804339.1 GI:38521480
KEYWORDS    Oreochromis niloticus (Nile tilapia)
SOURCE      Oreochromis niloticus
ORGANISM    Oreochromis niloticus
REFERENCE   1
AUTHORS     Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE       Verification of food origin based on nucleic acid pattern
            recognition
JOURNAL     Patent: WO 03060160-A 507 24-JUL-2003;
            Genomar ASA (NO)
FEATURES    source
            1. .17
            /organism="Oreochromis niloticus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:8128"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1024 GATGGGCTGGGGTT 1038
Db 1 GATCGGGCTGGGGTT 15

```

```

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAAGA 3

RESULT 993
AX759206/c
LOCUS      AX759206      17 bp      DNA      linear      PAT 25-JUN-2003
DEFINITION Sequence 2527 from Patent WO03040369.
ACCESSION  AX759206
VERSION     AX759206.1 GI:32253822
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Telerman,A., Amson,R. and Tuijnder,M.
TITLE       Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
JOURNAL     Patent: WO 03040369-A 2527 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES    source
            1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 862 GGAGAGGAGAGAGGA 876
Db 17 GGAGGAGGAGAGAGGA 3

RESULT 994
AX804339/c
LOCUS      AX804339      17 bp      DNA      linear      PAT 25-NOV-2003
DEFINITION Sequence 507 from Patent WO03060160.
ACCESSION  AX804339
VERSION     AX804339.1 GI:38521480
KEYWORDS    Oreochromis niloticus (Nile tilapia)
SOURCE      Oreochromis niloticus
ORGANISM    Oreochromis niloticus
REFERENCE   1
AUTHORS     Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
TITLE       Verification of food origin based on nucleic acid pattern
            recognition
JOURNAL     Patent: WO 03060160-A 507 24-JUL-2003;
            Genomar ASA (NO)
FEATURES    source
            1. .17
            /organism="Oreochromis niloticus"
            /mol_type="unassigned DNA"
            /db_xref="taxon:8128"

Query Match      0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1024 GATGGGCTGGGGTT 1038
Db 1 GATCGGGCTGGGGTT 15

```

```

RESULT 995
BD000130/c
LOCUS      BD000130      17 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION Detection of nucleic acid in cell by thermophilic strand
substitutive amplification.
ACCESSION  BD000130
VERSION     BD000130.1  GI:18623209
KEYWORDS    JP 2000300281-A/4.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Romain, K.L., Osutero, N.V., Clive, M.V. and Lead, R.A.
TITLE       Detection of nucleic acid in cell by thermophilic strand
            substitutive amplification
JOURNAL     Patent: JP 2000300281-A 4 31-OCT-2000;
            BECTON DICKINSON & CO
COMMENT     OS Artificial Sequence
            PN JP 2000300281-A/4
            PD 31-OCT-2000
            PF 03-APR-2000 JP 2000101133
            PR 21-SEP-1995 US 08/531747,21-SEP-1995 US 08/531749 PI
            KENTON L ROMAINS,NATARI V OSUTERO,ROBA,MARK VAN CLIVE, PI ROBERT
            ALAN LEAD
            PC C12N15/09,C12Q1/68,C12N15/00
            CC
            FH Key Location/Qualifiers
            FT source 1..17 /organism='Artificial Sequence'.
FEATURES   source
            Location/Qualifiers
            1..17 /organism='synthetic construct'
            /mol_type='genomic DNA'
            /db_xref='taxon:32630'
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. NO. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 828 CAAGAGGAGCTGC 842
DB 15 CAATGAGGAGCTGC 1
RESULT 996
BD017427
LOCUS      BD017427      17 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Nucleic acid for assaying genus Shigella or genus Salmonella and
            detection method.
ACCESSION  BD017427
VERSION     BD017427.1  GI:22558603
KEYWORDS    JP 2001245677-A/38.
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Fukushima M., Kakinuma, K. and Kawaguchi, R.
TITLE       Nucleic acid for assaying genus Shigella or genus Salmonella and
            detection method
JOURNAL     Patent: JP 2001245677-A 38 11-SEP-2001;
            SRL INC,MARINE BIOTECHNOLOGY INSTITUTE CO LTD,NIPPON GENE CO LTD
COMMENT     OS Artificial Sequence
            PN JP 2001245677-A/38
            PD 11-SEP-2001
            PF 27-DEC-2000 JP 2000398087
            PI MASAO FUKUSHIMA,KENICHI KAKINUMA,RYUJI KAWAGUCHI PC
            C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
            G01N33/569//
            PC (C12Q1/68,C12R1:42),(C12Q1/68,C12R1:01),C12N15/00,C12N15/00 CC
            DNA probe for detecting Salmonella typhi, Salmonella CC
            typhimurium and
            CC Salmonella aerogenes
            CC
            FH Key Location/Qualifiers
            FT source 1..17 /organism='Artificial Sequence'.
FEATURES   source
            Location/Qualifiers
            1..17 /organism='synthetic construct'
            /mol_type='genomic DNA'
            /db_xref='taxon:32630'
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. NO. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 828 CAAGAGGAGCTGC 842
DB 15 CAATGAGGAGCTGC 1
RESULT 997
BD203288
LOCUS      BD203288      17 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION  BD203288
VERSION     BD203288.1  GI:33013058
KEYWORDS    JP 2002509721-A/6314.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE       Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
JOURNAL     Patent: JP 2002509721-A 6314 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS Homo sapiens (human)
            PN JP 2002509721-A/6314
            PD 02-APR-2002
            PF 24-MAR-1999 JP 2000541291
            PR 27-MAR-1998 US 60/079678
            PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
            A61P29/00,
            PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
            C12N5/00
            CC Method and reagent for treating diseases or conditions CC
            concerning molecule
            CC participating in vasculogenic response
            FH Key Location/Qualifiers
            FT source 1..17 /organism='Homo sapiens (human)'.
FEATURES   source
            Location/Qualifiers
            1..17 /organism='Homo sapiens'
            /mol_type='genomic RNA'
            /db_xref='taxon:9606'
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. NO. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 58 TTCTCTTCTCGAGT 72
DB 2 TTCTCTTCTCGAGT 16
RESULT 998
BD203289
LOCUS      BD203289      17 bp      RNA      linear      PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response.
ACCESSION  BD203289
VERSION     BD203289.1  GI:33013058
KEYWORDS    JP 2002509721-A/6314.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 17)
AUTHORS     Pavco, P.A., Roberts, E., Jarvis, T., Coeshott, C. and Mcswiggen, J.A.
TITLE       Method and reagent for treating diseases or conditions concerning
            molecule participating in vasculogenic response
JOURNAL     Patent: JP 2002509721-A 6314 02-APR-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS Homo sapiens (human)
            PN JP 2002509721-A/6314
            PD 02-APR-2002
            PF 24-MAR-1999 JP 2000541291
            PR 27-MAR-1998 US 60/079678
            PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
            PI JAMES A MCSWIGGEN
            PC
            C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
            A61P29/00,
            PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
            C12N5/00
            CC Method and reagent for treating diseases or conditions CC
            concerning molecule
            CC participating in vasculogenic response
            FH Key Location/Qualifiers
            FT source 1..17 /organism='Homo sapiens (human)'.
FEATURES   source
            Location/Qualifiers
            1..17 /organism='Homo sapiens'
            /mol_type='genomic RNA'
            /db_xref='taxon:9606'
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. NO. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 58 TTCTCTTCTCGAGT 72
DB 2 TTCTCTTCTCGAGT 16

```

```

molecule participating in vasculogenic response.
BD203289
VERSION BD203289.1 GI:33013059
KEYWORDS JP 2002509721-A/6315.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
REFERENCE
AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswiggen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 6315 02-APR-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002509721-A/6315
PD 02-APR-2002
PR 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..17
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 7.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 58 TTTCTTTCTGGAGT 72
Db 1 TTTCTTTCTGGAGT 15
RESULT 999
A52266/c
LOCUS A52266 Sequence 56 from Patent EP0705842. 14 bp DNA linear PAT 12-DEC-1997
DEFINITION
ACCESSION A52266
VERSION A52266.1 GI:2852046
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1
AUTHORS Bartnik,E.D. and Margerie,D.D.
TITLE Regulated genes by stimulation of chondrocytes with IL-1beta
JOURNAL Patent: EP 0705842-A 56 10-APR-1996;
COMMENT HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES
source
1..14
Location/Qualifiers
/organism='unidentified'
/mol_type='unassigned DNA'
/db_xref='taxon:32644'
Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1
RESULT 1001
E13671/c
LOCUS E13671
DEFINITION Primer.
ACCESSION E13671
VERSION E13671.1 GI:3252448
KEYWORDS JP 1997224672-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS Shibata,D., Kato,T. and Ota,H.
TITLE DNA CODING NEW DNA-CONNECTED PROTEIN
JOURNAL Patent: JP 1997224672-A 4 02-SEP-1997;
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224671-A/4
PD 02-SEP-1997
PF 19-FEB-1996 JP 1996031075
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
PC C12N15/09,C12N9/02,(C12N9/02,C12R1:91);
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial sequences'.
FEATURES
source
1..14
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1
RESULT 1001
E13671/c
LOCUS E13671
DEFINITION Primer.
ACCESSION E13671
VERSION E13671.1 GI:3252448
KEYWORDS JP 1997224672-A/4.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE
1 (bases 1 to 14)
AUTHORS Shibata,D., Kato,T. and Ota,H.
TITLE DNA CODING NEW DNA-CONNECTED PROTEIN
JOURNAL Patent: JP 1997224672-A 4 02-SEP-1997;
COMMENT MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO:KK
OS None
OC Artificial sequences.
PN JP 1997224672-A/4
PD 02-SEP-1997
PF 21-FEB-1996 JP 1996033973
PI SHIBATA DAISUKE, KATO TOMOHIKO, OTA HIROYUKI
```

PC C12N15/09,A01H5/00,C07H21/04,C07K14/415//C12N5/10,C12Q1/68; CC
strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
FH Key Location/Qualifiers
FT source 1..14
FT Location/Qualifiers
FEATURES
source
1..14
/organism="Artificial sequences".
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1
RESULT 1002
AR266627/c
LOCUS AR266627 14 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 65 from patent US 6495319.
ACCESSION AR266627
VERSION AR266627.1 GI:29695691
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS McClelland,M., Welsh,J. and Trenkle,T.
TITLE Reduced complexity nucleic acid targets and methods of using same
JOURNAL Patent: US 6495319-A 65 17-DEC-2002;
FEATURES
source
1..14
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 6.6e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAA 1748
Db 14 AAAAAAAAAAAAAA 1
RESULT 1003
AR012009/c
LOCUS AR012009 13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5763183.
ACCESSION AR012009
VERSION AR012009.1 GI:39699999
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Pesonen,U., Koulu,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE Allelic variation of the serotonin 5HT7 receptor
JOURNAL Patent: US 5763183-A 3 09-JUN-1998;
FEATURES
source
1..13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1004
AR012010/c
LOCUS AR012010 13 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 4 from patent US 5763183.
ACCESSION AR012010
VERSION AR012010.1 GI:3970000
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Pesonen,U., Koulu,M., Linnoila,M., Goldman,D. and Virkkunen,M.
TITLE Allelic variation of the serotonin 5HT7 receptor
JOURNAL Patent: US 5763183-A 4 09-JUN-1998;
FEATURES
source
1..13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1005
AR145368
LOCUS AR145368 13 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6211354.
ACCESSION AR145368
VERSION AR145368.1 GI:15107235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Horie,R. and Ishiguro,T.
TITLE Optically active DNA probe having phosphonic diester linkage
JOURNAL Patent: US 6211354-A 1 03-APR-2001;
FEATURES
source
1..13
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13
RESULT 1006
AR179431/c
LOCUS AR179431 13 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6326175.
ACCESSION AR179431
VERSION AR179431.1 GI:20220986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)

AUTHORS Guegler, K., Tan, R. and Rose, M.J.
 TITLE Methods and compositions for producing full length cDNA libraries
 JOURNAL Patent: US 6326175-A 6 04-DEC-2001;
 FEATURES Location/Qualifiers
 source 1..13
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1007
 E66853
 LOCUS 13 bp DNA linear PAT 18-JUN-2001
 DEFINITION DNA probe having optically active diphosphonate bond.
 ACCESSION E66853
 VERSION E66853.1 GI:13018113
 KEYWORDS JP 1999322783-A/1.
 SOURCE synthetic construct
 ORGANISM artificial construct
 REFERENCE 1 (bases 1 to 13)
 AUTHORS Ryuichi, H. and Takahiko, I.
 TITLE DNA probe having optically active diphosphonate bond
 JOURNAL Patent: JP 1999322783-A 1 24-NOV-1999;
 TOSOH CORP

OS Artificial Sequence
 PN JP 1999322783-A/1
 PD 24-NOV-1999
 PF 06-MAY-1998 JP 1998123298
 PR RYUICHI HORIE, TAKAHIKO ISHIGURO
 PI C07H21/04, C12N15/09, C12Q1/68, C12Q1/78, G01N33/50, PC
 G01N33/533,
 CC G01N33/566, G01N33/58
 FH Key Location/Qualifiers
 FT source 1..13
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1008
 E66854
 LOCUS 13 bp DNA linear PAT 18-JUN-2001
 DEFINITION DNA probe having optically active diphosphonate bond.
 ACCESSION E66854
 VERSION E66854.1 GI:13018114
 KEYWORDS JP 1999322783-A/2.
 SOURCE synthetic construct
 ORGANISM artificial construct
 REFERENCE 1 (bases 1 to 13)
 AUTHORS Ryuichi, H. and Takahiko, I.
 TITLE DNA probe having optically active diphosphonate bond

JOURNAL Patent: JP 1999322783-A 2 24-NOV-1999;
 TOSOH CORP
 COMMENT OS Artificial Sequence
 PN JP 1999322783-A/2
 PD 24-NOV-1999
 PF 06-MAY-1998 JP 1998123298
 PR RYUICHI HORIE, TAKAHIKO ISHIGURO
 PI C07H21/04, C12N15/09, C12Q1/68, C12Q1/78, G01N33/50, PC
 G01N33/533,
 CC G01N33/566, G01N33/58
 FH Key Location/Qualifiers
 FT source 1..13
 /organism="Artificial Sequence".

FEATURES
 source 1..13
 Location/Qualifiers
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1009
 AR205695/c
 LOCUS 13 bp DNA linear PAT 20-JUN-2002
 DEFINITION Sequence 6 from patent US 6369199.
 ACCESSION AR205695
 VERSION AR205695.1 GI:21503343
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 13)
 AUTHORS Guegler, K., Tan, R. and Rose, M.J.
 TITLE Fusion protein comprising an eIF-4E domain and an eIF-4G domain
 joined by a linker domain
 JOURNAL Patent: US 6369199-A 6 09-APR-2002;
 FEATURES Location/Qualifiers
 source 1..13
 /organism="unknown"
 /mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1010
 AR222459
 LOCUS 13 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 19 from patent US 6429300.
 ACCESSION AR222459
 VERSION AR222459.1 GI:23329990
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 13)
 AUTHORS Kurz, M., Lohse, P. and Wagner, R.
 TITLE Peptide acceptor ligation methods
 JOURNAL Patent: US 6429300-A 19 06-AUG-2002;

```

FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAA 13

RESULT 1011
LOCUS AR241741
DEFINITION Sequence 29 from patent US 6472154.
ACCESSION AR241741
VERSION AR241741.1 GI:27287553
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
    1 (bases 1 to 13)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 29 29-OCT-2002;
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="unknown"
                /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAA 13

RESULT 1012
LOCUS AX021144/c
DEFINITION Sequence 12 from Patent WO929898.
ACCESSION AX021144
VERSION AX021144.1 GI:10044796
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
    1
AUTHORS Berlin,K., Gut,I.G. and Lehrach,H.
TITLE Method for identifying nucleic acids by means of matrix-assisted
JOURNAL laser desorption/ionisation mass spectrometry
    Patent: WO 929898-A 12 17-JUN-1999;
    MAX PLANCK GESELLSCHAFT (DE); BERLIN KURT (DE); GUT IVO GLYNNE
    (DE); LEHRACH HANS (DE)
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="artificial sequence"

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAA 1

RESULT 1013
LOCUS AX048405/c
DEFINITION Sequence 4 from Patent WO0071747.
ACCESSION AX048405
VERSION AX048405.1 GI:12225569
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
    1
AUTHORS Boekenkamp,D., Hoppe,H.U. and Burgstaller,P.
TITLE Detection system for separating constituents of a sample and
JOURNAL production and use of the same
    Patent: WO 0071747-A 4 30-NOV-2000;
    Aventis Research & Technologies GmbH & Co. KG (DE)
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Region A"

Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 13;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAA 1

RESULT 1014
LOCUS AX104675/c
DEFINITION Sequence 867 from Patent WO0122972.
ACCESSION AX104675
VERSION AX104675.1 GI:13920872
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE
    1
AUTHORS Krieg,A.M., Schetter,C. and Vollmer,J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 867 05-APR-2001;
    UNIVERSITY OF IOWA RESEARCH FOUNDATION (US); Coley Pharmaceutical
    GmbH (DE)
FEATURES
    source
        Location/Qualifiers
            1..13
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
            misc_feature
                11..13
                    /note="PITC moiety attached at 3' end of sequence.
                    Has phosphodiester backbone."

Query Match
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAA 1

RESULT 1015
LOCUS AX104676/c
DEFINITION Sequence 868 from Patent WO0122972.
ACCESSION AX104676

```



```
VERSION AX104676.1 GI:13920873
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieger, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 868 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
misc_feature 11..13
/notes="Biotin moiety attached at 3' end of sequence.
Has phosphorothioate and phosphodiester chimeric backbone
with phosphodiester on 3' end."
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1016
AX235509/c
LOCUS AX235509 13 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 25 from Patent WO0149687.
ACCESSION AX235509
VERSION AX235509.1 GI:15593971
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wang, J. and Herdewijn, P.
TITLE Cyclohexene nucleic acids
JOURNAL Patent: WO 0149687-A 25 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES
source Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="DNA complement"
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1017
AX235510/c
LOCUS AX235510 13 bp RNA linear PAT 11-SEP-2001
DEFINITION Sequence 26 from Patent WO0149687.
ACCESSION AX235510
VERSION AX235510.1 GI:15593972
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Wang, J. and Herdewijn, P.
TITLE Cyclohexene nucleic acids
JOURNAL Patent: WO 0149687-A 25 12-JUL-2001;
K.U. LEUVEN RESEARCH & DEVELOPMENT (BE)
FEATURES
source Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/notes="oligomer used in this study"
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1018
AX355807/c
LOCUS AX355807 13 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 835 from Patent WO0197843.
ACCESSION AX355807
VERSION AX355807.1 GI:18620475
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 835 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic oligonucleotide-phosphodiester backbone"
misc_feature 13
/notes="FITC labeled"
Query Match 0.7%; Score 13; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1019
AX355808/c
LOCUS AX355808 13 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 836 from Patent WO0197843.
ACCESSION AX355808
VERSION AX355808.1 GI:18620476
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Weiner, G. and Hartmann, G.
TITLE Methods for enhancing antibody-induced cell lysis and treating
cancer
JOURNAL Patent: WO 0197843-A 836 27-DEC-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
source Location/Qualifiers
1..13
/organism="synthetic construct"
/mol_type="unassigned DNA"
```

/db_xref="taxon:32630"
 /note="Synthetic oligonucleotide-chimeric
 phosphorothioate/phosphodiester backbone with
 phosphodiester on 3' end"
 misc_difference 13
 /note="FITC labeled"

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1020
 AX547728/c
 LOCUS AX547728 13 bp DNA linear PAT 15-JAN-2003
 DEFINITION Sequence 867 from Patent WO02053141.
 ACCESSION AX547728
 VERSION AX547728.1 GI:25812872
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Bratzler, R.L.
 TITLE Inhibition of angiogenesis by nucleic acids
 JOURNAL Patent: WO 02053141-A 867 11-JUL-2002;
 Coley Pharmaceutical Group, Inc. (US)
 FEATURES
 source
 1. .13
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Has phosphodiester backbone."
 11. .13
 /note="Conjugated to FITC moiety."

misc_feature 11. .13

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1021
 AX547729/c
 LOCUS AX547729 13 bp DNA linear PAT 15-JAN-2003
 DEFINITION Sequence 868 from Patent WO02053141.
 ACCESSION AX547729
 VERSION AX547729.1 GI:25812873
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1
 AUTHORS Bratzler, R.L.
 TITLE Inhibition of angiogenesis by nucleic acids
 JOURNAL Patent: WO 02053141-A 868 11-JUL-2002;
 Coley Pharmaceutical Group, Inc. (US)
 FEATURES
 source
 1. .13
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Has phosphorothioate and phosphodiester chimeric
 backbone with phosphodiester on 3' end."
 11. .13
 /note="Conjugated to biotin moiety."

misc_feature 11. .13

Query Match 0.7%; Score 13; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
 Db 13 AAAAAAAAAAAAAA 1

RESULT 1022
 A88150/c
 LOCUS A88150 14 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 298 from Patent WO9833904.
 ACCESSION A88150
 VERSION A88150.1 GI:6736720
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Brysch, W. and Schlingensiefen, K.
 TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
 JOURNAL Patent: WO 9833904-A 298 06-AUG-1998;
 BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
 FEATURES
 source
 1. .14
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 0.7%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1577 CCACCTGACTGCTG 1589
 Db 14 CCACCTGACTGCTG 2

RESULT 1023
 A90117/c
 LOCUS A90117 14 bp DNA linear PAT 22-JAN-2000
 DEFINITION Sequence 298 from Patent EP0856579.
 ACCESSION A90117
 VERSION A90117.1 GI:6738631
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 14)
 AUTHORS Brysch, W.D. and Schlingensiefen, K.D.
 TITLE An antisense oligonucleotide preparation method
 JOURNAL Patent: EP 0856579-A 298 05-AUG-1998;
 BIOGNOSTIK GES (DE)
 FEATURES
 source
 1. .14
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 0.7%; Score 13; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1577 CCACCTGACTGCTG 1589
 Db 14 CCACCTGACTGCTG 2

RESULT 1024
 A97593/c
 LOCUS A97593 14 bp DNA linear PAT 26-JAN-2000

```
DEFINITION Sequence 3 from Patent WO9915681.
ACCESSION A97593
VERSION A97593.1 GI:6780897
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Roberts,J.A. and Paul,W.
TITLE CONTROL POP DEHISCENCE OR SHATTER
JOURNAL Patent: WO 9915681-A 3 01-APR-1999;
BIOGENMA UK LIMITED (GB); ROBERTS JEREMY ALAN (GB)
FEATURES
    source
        1..14
            /organism="unidentified"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32644"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1
RESULT 1025
AR004935/c AR004935 14 bp DNA linear PAT 04-DEC-1998
LOCUS
DEFINITION Sequence 2 from patent US 5747299.
ACCESSION AR004935
VERSION AR004935.1 GI:3965814
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Bloom,D., Fathman,C.Garrison. and Slaymaker,S.
TITLE Anergy genes
JOURNAL Patent: US 5747299-A 2 05-MAY-1998;
FEATURES
    source
        1..14
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1
RESULT 1026
AR036791 AR036791 14 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 33 from patent US 5800984.
ACCESSION AR036791
VERSION AR036791.1 GI:5954647
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Vary,C.P.H.
TITLE Nucleic acid sequence detection by triple helix formation at primer
site in amplification reactions
JOURNAL Patent: US 5800984-A 33 01-SEP-1998;
FEATURES
    source
        1..14
            /organism="unknown"
Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1
RESULT 1027
AR051240 AR051240 14 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 8 from patent US 5830658.
ACCESSION AR051240
VERSION AR051240.1 GI:5974604
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Grvaznov,S.M.
TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 8 03-NOV-1998;
FEATURES
    source
        1..14
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 13
RESULT 1028
AR067459/c AR067459 14 bp DNA linear PAT 29-SEP-1999
LOCUS
DEFINITION Sequence 8 from patent US 5851764.
ACCESSION AR067459
VERSION AR067459.1 GI:5998681
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Fisher,P.B. and Shen,R.
TITLE Human prostate tumor inducing gene-1 and uses thereof
JOURNAL Patent: US 5851764-A 8 22-DEC-1998;
FEATURES
    source
        1..14
            /organism="unknown"
            /mol_type="unassigned DNA"
Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1
RESULT 1029
AR127787 AR127787 14 bp DNA linear PAT 16-MAY-2001
LOCUS
DEFINITION Sequence 8 from patent US 6180777.
ACCESSION AR127787
```

```
VERSION      AR127787.1  GI:14114382
KEYWORDS     Unknown.
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 14)
AUTHORS     Horn,T.
TITLE       Synthesis of branched nucleic acids
JOURNAL     Patent: US 6180777-A 8 30-JAN-2001;
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1030
AR174022/c
LOCUS      AR174022      14 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 15 from patent US 6306624.
ACCESSION  AR174022
VERSION     AR174025.1  GI:17914345
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   1 (bases 1 to 14)
REFERENCE  Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE      Retinoid metabolizing protein
JOURNAL    Patent: US 6306624-A 15 23-OCT-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1033
AR174022/c
LOCUS      AR174022      14 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 12 from patent US 6306624.
ACCESSION  AR174022
VERSION     AR174022.1  GI:17914342
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   1 (bases 1 to 14)
REFERENCE  Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE      Retinoid metabolizing protein
JOURNAL    Patent: US 6306624-A 12 23-OCT-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1031
AR174023/c
LOCUS      AR174023      14 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION Sequence 13 from patent US 6306624.
ACCESSION  AR174023
VERSION     AR174023.1  GI:17914343
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   1 (bases 1 to 14)
REFERENCE  Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE      Retinoid metabolizing protein
JOURNAL    Patent: US 6306624-A 13 23-OCT-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1034
AR241806/c
LOCUS      AR241806      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 94 from patent US 6472154.
ACCESSION  AR241806
VERSION     AR241806.1  GI:27287618
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   1 (bases 1 to 14)
REFERENCE  Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE      Retinoid metabolizing protein
JOURNAL    Patent: US 6306624-A 15 23-OCT-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1033
AR174023/c
LOCUS      AR174023      14 bp      DNA      linear      PAT 06-FEB-1997
DEFINITION Sequence 8 from patent US 5571677.
ACCESSION  I28369
VERSION     I28369.1    GI:1819145
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   1 (bases 1 to 14)
REFERENCE  Gryaznov,S.M.
TITLE      Convergent synthesis of branched and multiply connected
            macromolecular structures
JOURNAL    Patent: US 5571677-A 8 05-NOV-1996;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13

RESULT 1034
AR241806/c
LOCUS      AR241806      14 bp      DNA      linear      PAT 20-DEC-2002
DEFINITION Sequence 94 from patent US 6472154.
ACCESSION  AR241806
VERSION     AR241806.1  GI:27287618
KEYWORDS   Unknown.
SOURCE     Unclassified.
ORGANISM   1 (bases 1 to 14)
REFERENCE  Petkovich,P.Martin., White,J.A., Beckett,B.R. and Jones,G.
TITLE      Retinoid metabolizing protein
JOURNAL    Patent: US 6306624-A 15 23-OCT-2001;
FEATURES   Location/Qualifiers
            source
            1..14
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1747
Db 1 CAAAAAAAAAAAAA 13
```

```
REFERENCE 1 (bases 1 to 14)
AUTHORS Garner,H.R., Wren,J.D., Minna,J.D. and Fondon,J.W. III.
TITLE Polymorphic repeats in human genes
JOURNAL Patent: US 6472154-A 94 29-OCT-2002;
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1035
AR349924/c
LOCUS AR349924 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 18 from patent US 6586204.
ACCESSION AR349924
VERSION AR349924.1 GI:33750834
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene E124, compositions, and methods of use
JOURNAL Patent: US 6586204-A 18 01-JUL-2003;
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1748
Db 14 CAAAAAAAAAAAAA 1
RESULT 1036
AR349926/c
LOCUS AR349926 14 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 20 from patent US 6586204.
ACCESSION AR349926
VERSION AR349926.1 GI:33750836
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 14)
AUTHORS Lehar,S.M. and Guild,B.C.
TITLE Apoptosis gene E124, compositions, and methods of use
JOURNAL Patent: US 6586204-A 20 01-JUL-2003;
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1
```

```
RESULT 1037
AX016298/c
LOCUS AX016298 14 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO9949046.
ACCESSION AX016298
VERSION AX016298.1 GI:10041861
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Roberts,J.A., Wyatt,P. and Whitelaw,C.
TITLE Signal transduction protein involved in plant dehiscence
JOURNAL Patent: WO 9949046-A 1 30-SEP-1999;
        ROBERTS JEREMY ALAN (GB); BIOGENMA UK LTD (GB); WYATT PAUL (GB);
        WHITELAW CATHERINE (GB)
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="oligo dT anchor primer 7"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1
RESULT 1038
AX642208/c
LOCUS AX642208 14 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 26 from Patent WO02061082.
ACCESSION AX642208
VERSION AX642208.1 GI:28474656
KEYWORDS
SOURCE
    ORGANISM
        synthetic construct
        artificial sequences.
REFERENCE 1
AUTHORS Day,R.
TITLE Zis-sr nucleic acid and amino acid sequences involved in the
        regulated secretory pathway and/or the regulation of the
        neuroendocrine phenotype (nep)
JOURNAL Patent: WO 02061082-A 26 08-AUG-2002;
        Universite de Sherbrooke (CA)
FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Oligonucleotide"
Query Match
Best Local Similarity 0.7%; Score 13; DB 1; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1747
Db 13 CAAAAAAAAAAAAA 1
RESULT 1039
AX659630/c
LOCUS AX659630 14 bp DNA linear PAT 03-APR-2003
DEFINITION Sequence 24 from Patent WO02103014.
ACCESSION AX659630
VERSION AX659630.1 GI:29161812
KEYWORDS
```

```

SOURCE      synthetic construct
ORGANISM    synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Al-Mahmood,S.
TITLE       Antisense oligonucleotides which can inhibit the formation of
            capillary tubes by endothelial cells
JOURNAL     Patent: WO 02103014-A 24 27-DEC-2002;
            Al-Mahmood, Salman (FR)
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Oligonucleotide anti-sens"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1747
Db 13 CAAAAA1

RESULT 1040
BD065663/c
LOCUS      14 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD065663
VERSION     BD065663.1 GI:22611266
KEYWORDS   JP 2001511000-A/298.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS    Schlingensiefen,K.H. and Brysch,W.
TITLE      An antisense oligonucleotide preparation method
JOURNAL    Patent: JP 2001511000-A 298 07-AUG-2001;
            BIOLOGISCHES INSTITUT FÜR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT    OS Unknown
            PN JP 2001511000-A/298
            PD 07-AUG-2001
            PF 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEFEN,WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source
            1..14
            /organism='Unknown'.
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1577 CCACTGACTGCTG 1589
Db 14 CCACTGACTGCTG 2

RESULT 1041
BD073881/c
LOCUS      14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION  BD073881
VERSION     BD073881.1 GI:22619484
KEYWORDS   JP 2001512698-A/6.

```

```

SOURCE      unidentified
ORGANISM    unidentified
            unclassified.
REFERENCE   1 (bases 1 to 14)
AUTHORS     Suishelm,K., Hosier,S. and Kubbies,M.
TITLE       Isolation of novel aging factor gene P23
JOURNAL     Patent: JP 2001512698-A 6 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS Unidentified
            PN JP 2001512698-A/6
            PD 28-AUG-2001
            PF 05-AUG-1998 JP 2000506375
            PR 08-AUG-1997 US 08/908873
            PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02.
            PC C12P21/08,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Isolation of novel aging factor gene P23
            FH Key
            Location/Qualifiers
            FT source
            1..14
            /organism='Unidentified'.
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1747
Db 13 CAAAAA1

RESULT 1042
BD073884/c
LOCUS      14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION  BD073884
VERSION     BD073884.1 GI:22619487
KEYWORDS   JP 2001512698-A/9.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 14)
AUTHORS     Suishelm,K., Hosier,S. and Kubbies,M.
TITLE       Isolation of novel aging factor gene P23
JOURNAL     Patent: JP 2001512698-A 9 28-AUG-2001;
            UNIVERSITY OF WASHINGTON
COMMENT     OS Unidentified
            PN JP 2001512698-A/9
            PD 28-AUG-2001
            PF 05-AUG-1998 JP 2000506375
            PR 08-AUG-1997 US 08/908873
            PI KAREN SUISHELM,SUZANNE HOSIER,MANFRED KUBBIES PC
            C12Q1/68,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N15/09, PC
            C12P21/02.
            PC C12P21/08,C12N15/00
            CC Strandedness: Single;
            CC Topology: Linear;
            CC Isolation of novel aging factor gene P23
            FH Key
            Location/Qualifiers
            FT source
            1..14
            /organism='Unidentified'.
FEATURES    Location/Qualifiers
            source
            1..14
            /organism="unidentified"
            /mol_type="genomic DNA"
            /db_xref="taxon:32644"

```

```

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1747
Db 13 CAAAAA1

RESULT 1043
BD073887/c
LOCUS BD073887 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Isolation of novel aging factor gene P23.
ACCESSION BD073887
VERSION BD073887.1 GI:22619490
KEYWORDS JP 2001512698-A/12.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 14)
AUTHORS Suishelm,K., Hosier,S. and Kubbies,M.
TITLE Isolation of novel aging factor gene P23
JOURNAL Patent: JP 2001512698-A 12 28-AUG-2001;
UNIVERSITY OF WASHINGTON
COMMENT OS Unidentified
PN JP 2001512698-A/12
PD 28-AUG-2001
PF 05-AUG-1998 JP 2000506375
PR 08-AUG-1997 US 08/908873
PI KAREN SUISHELM, SUZANNE HOSIER, MANFRED KUBBIES PC
C12P21/02, C12P21/08, C12N15/00
PC C12P21/08, C12N15/00
CC Strandedness: Single;
CC Topology: linear;
CC Isolation of novel aging factor gene P23
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Unidentified'.
FEATURES
source
1..14
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA1747
Db 13 CAAAAA1

RESULT 1044
BD084126/c
LOCUS BD084126 14 bp DNA linear PAT 27-AUG-2002
DEFINITION Polymorphisms and new genes in the region of the human
hemochromatosis gene.
ACCESSION BD084126
VERSION BD084126.1 GI:22629736
KEYWORDS JP 2001525663-A/14.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 14)
AUTHORS Feder,J.N., Kronmal,G.S., Lauer,P.M., Ruddy,D.A., Thomas,W.J.,
Tauchihaehi,Z. and Wolff,R.K.
TITLE Polymorphisms and new genes in the region of the human
hemochromatosis gene
JOURNAL Patent: JP 2001525663-A 14 11-DEC-2001;

```

```

PROGENTIOR INC
OS Homo sapiens (human)
PN JP 2001525663-A/14
PD 11-DEC-2001
PF 30-SEP-1997 JP 1998516815
PR 01-OCT-1996 US 08/724394, 07-MAY-1997 US 08/852495 PI
JOHN N FEDER,GREGORY S KRONMAL,PETER M LAUER,DAVID A RUDDY, PI
WINSTON J THOMAS,ZENTA TSUCHIHASHI,ROGER K WOLFF PC
C07H21/04,C12Q1/68,C12N15/63,C12N15/85,C12P21/02 CC Polymorphisms
and new genes in the region of the human CC hemochromatosis gene
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..14
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA1748
Db 14 AAAAAA2

RESULT 1045
BD176796
LOCUS BD176796 14 bp DNA linear PAT 18-MAR-2003
DEFINITION Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression.
ACCESSION BD176796
VERSION BD176796.1 GI:29122508
KEYWORDS WO 02074951-A/43.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 14)
AUTHORS Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE Method of constructing cDNA tag for identifying expressed gene and
method of analyzing gene expression
JOURNAL Patent: WO 02074951-A 43 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/43
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial Sequence'.
FEATURES
source
1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match      0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA1748
Db 1 AAAAAA13

RESULT 1046

```

```
BD176797
LOCUS          BD176797          14 bp      DNA          linear      PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176797.1 GI:29122509
VERSION        WO 02074951-A/44.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 44 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/44
                PD 26-SEP-2002
                PR 13-MAR-2002 WO 2002JP002338
                PI 15-MAR-2001 JP 01P 073959
                PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
                C12N15/09,C12Q1/68
                CC Synthetic DNA
                FH Key Location/Qualifiers
                FT source 1..14 /organism='Artificial Sequence'.

FEATURES
  source
  1..14
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1047
BD176798
LOCUS          BD176798          14 bp      DNA          linear      PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176798.1 GI:29122510
VERSION        WO 02074951-A/45.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 45 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/45
                PD 26-SEP-2002
                PR 13-MAR-2002 WO 2002JP002338
                PI 15-MAR-2001 JP 01P 073959
                PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
                C12N15/09,C12Q1/68
                CC Synthetic DNA
                FH Key Location/Qualifiers
                FT source 1..14 /organism='Artificial Sequence'.

FEATURES
  source
  1..14
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1047
BD176798
LOCUS          BD176798          14 bp      DNA          linear      PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176798.1 GI:29122510
VERSION        WO 02074951-A/45.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 45 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/45
                PD 26-SEP-2002
                PR 13-MAR-2002 WO 2002JP002338
                PI 15-MAR-2001 JP 01P 073959
                PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
                C12N15/09,C12Q1/68
                CC Synthetic DNA
                FH Key Location/Qualifiers
                FT source 1..14 /organism='Artificial Sequence'.

FEATURES
  source
  1..14
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1047
BD176798
LOCUS          BD176798          14 bp      DNA          linear      PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176798.1 GI:29122510
VERSION        WO 02074951-A/45.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 45 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/45
                PD 26-SEP-2002
                PR 13-MAR-2002 WO 2002JP002338
                PI 15-MAR-2001 JP 01P 073959
                PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
                C12N15/09,C12Q1/68
                CC Synthetic DNA
                FH Key Location/Qualifiers
                FT source 1..14 /organism='Artificial Sequence'.

FEATURES
  source
  1..14
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 1 AAAAAAAAAAAAAA 13

RESULT 1047
BD176801
LOCUS          BD176801          14 bp      DNA          linear      PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176801.1 GI:29122513
VERSION        WO 02074951-A/48.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
JOURNAL        Patent: WO 02074951-A 48 26-SEP-2002;
                KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
                KUNITAKA HIROSE,JUN SAKAI
COMMENT        OS Artificial Sequence
                PN WO 02074951-A/48
                PD 26-SEP-2002
                PR 13-MAR-2002 WO 2002JP002338
                PI 15-MAR-2001 JP 01P 073959
                PT MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
                C12N15/09,C12Q1/68
                CC Synthetic DNA
                FH Key Location/Qualifiers
                FT source 1..14 /organism='Artificial Sequence'.

FEATURES
  source
  1..14
  /organism="synthetic construct"
  /mol_type="genomic DNA"
  /db_xref="taxon:32630"

Query Match
Best Local Similarity 100.0%; Pred. No. 7e+02; Length 14;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1049
BD176802
LOCUS          BD176802          14 bp      DNA          linear      PAT 18-MAR-2003
DEFINITION     Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression.
ACCESSION      BD176802.1 GI:29122514
VERSION        WO 02074951-A/49.
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       artificial sequences.
REFERENCE      1 (bases 1 to 14)
AUTHORS        Yamamoto,M., Yamamoto,N., Hirose,K. and Sakai,J.
TITLE          Method of constructing cDNA tag for identifying expressed gene and
                method of analyzing gene expression
```


JOURNAL Patent: WO 02074951-A 49 26-SEP-2002;
KUREHA CHEMICAL INDUSTRY CO LTD,MIKIO YAMAMOTO,NAOKI YAMAMOTO,
KUNITAKA HIROSE,JUN SAKAI
COMMENT OS Artificial Sequence
PN WO 02074951-A/49
PD 26-SEP-2002
PF 13-MAR-2002 WO 2002JP002338
PR 15-MAR-2001 JP 01P 073959
PI MIKIO YAMAMOTO,NAOKI YAMAMOTO,KUNITAKA HIROSE,JUN SAKAI PC
C12N15/09,C12Q1/68
CC Synthetic DNA
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Artificial Sequence'.
FEATURES
source
1..14
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1050
BD209329 14 bp RNA linear PAT 17-JUL-2003
LOCUS Enzymatic nucleic acid treatment of diseases or conditions related
DEFINITION to hepatitis C virus infection.
ACCESSION BD209329
VERSION BD209329.1 GI:33019099
KEYWORDS JP 2002512791-A/2919.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 14)
AUTHORS Blatt,L., McSwiggen,J.A., Roberts,E., Pavco,P.A. and Macejak,D.
TITLE Enzymatic nucleic acid treatment of diseases or conditions related
to hepatitis C virus infection
JOURNAL Patent: JP 2002512791-A 2919 08-MAY-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Hepatitis virus (hepatitis C virus)
PN JP 2002512791-A/2919
PD 08-MAY-2002
PF 26-APR-1999 JP 2000545991
PR 27-APR-1998 US 60/083217,18-SEP-1998 US 60/100842 PR
25-FEB-1999 US 09/257608,23-MAR-1999 US 09/274553 PI
LAWRENCE BLATT, JAMES A MCSWIGGEN, ELISABETH ROBERTS, PAMELA A PI
PAVCO
PI DENNIS MACEJAK
PC C12N9/00,A61K31/7105,A61K38/21,A61K48/00,A61P31/12,C12N15/09,
PC A61K37/66,
PC C12N15/00
CC Enzymatic nucleic acid treatment of diseases or conditions CC
related to
CC hepatitis C virus infection.
FH Key Location/Qualifiers
FT source 1..14
FT /organism='Hepatitis virus (hepatitis C FT
virus)'.
FEATURES
source
1..14
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 13; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7e+02;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 700 TCGCGCCACCCA 712
Db 2 TCGCGCCACCCA 14
RESULT 1051
AR056155/c 15 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 359 from patent US 5837542.
DEFINITION AR056155
ACCESSION AR056155
VERSION AR056155.1 GI:5981732
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 359 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..15
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 15 AAAAAAAAAAAAAA 3
RESULT 1052
AR056160/c 15 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 364 from patent US 5837542.
DEFINITION AR056160
ACCESSION AR056160
VERSION AR056160.1 GI:5981737
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 364 17-NOV-1998;
FEATURES Location/Qualifiers
source 1..15
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1
RESULT 1053
AR113913/c 15 bp DNA linear PAT 16-MAY-2001
LOCUS Sequence 359 from patent US 6132967.
DEFINITION AR113913
ACCESSION AR113913
VERSION AR113913.1 GI:14094235
KEYWORDS Unknown.
SOURCE Unknown.

```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 359 17-OCT-2000;
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 15 AAAAAAAAAAAAAA 3

RESULT 1054
AR113918/c
LOCUS AR113918 15 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 364 from patent US 6132967.
ACCESSION AR113918
VERSION AR113918.1 GI:14094240
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 364 17-OCT-2000;
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1055
AR180774
LOCUS AR180774 15 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 842 from patent US 6331152.
ACCESSION AR180774
VERSION AR180774.1 GI:20222807
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Vogelstein,B., Kinzler,K.W., Zhang,L. and Zhou,W.
TITLE Gene expression profiles in normal and cancer cells
JOURNAL Patent: US 6331152-A 842 25-DEC-2001;
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="unassigned DNA"
Query Match
    Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1748
Db 13 AAAAAAAAAAAAAA 1

RESULT 1056
AR235555/c
LOCUS AR235555 15 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 54 from patent US 6461810.
ACCESSION AR235555
VERSION AR235555.1 GI:27278776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 15)
AUTHORS Fresco,J.R. and Johnson,M.D.
TITLE Triplex in-situ hybridization
JOURNAL Patent: US 6461810-A 54 08-OCT-2002;
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="unknown"
                /mol_type="genomic DNA"
Query Match
    Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 31 AGAGGAAAAAAAAA 43
Db 13 AGAGGAAAAAAAAA 1

RESULT 1057
AX377159
LOCUS AX377159 15 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 4 from Patent WO0212342.
ACCESSION AX377159
VERSION AX377159.1 GI:19573449
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kazemi,A., Koshy,B. and Sanchis,A.
TITLE Haplotypes of the edg4 gene
JOURNAL Patent: WO 0212342-A 4 14-FEB-2002;
GENE Genbank: U00000
FEATURES
    source
        Location/Qualifiers
            1..15
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"
Query Match
    Best Local Similarity 0.7%; Score 13; DB 1; Length 15;
    Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 271 CTCACACCCACCCC 285
Db 1 CTCACACCCACCCC 15

RESULT 1058
AX633193/c
LOCUS AX633193 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 332 from Patent EP1260586.
ACCESSION AX633193
VERSION AX633193.1 GI:28468807
KEYWORDS
```

SOURCE unidentified
ORGANISM unidentified
REFERENCE unclassified.

AUTHORS
1 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.

TITLE
Method and reagent for inhibiting the expression of disease related
genes

JOURNAL
Patent: EP 1260586-A 332 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
source
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||||

Db 15 AAAAAAAAAAAAAA 3

RESULT 1059
AX633203/c
LOCUS AX633203 15 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 342 from Patent EP1260586.
ACCESSION AX633203
VERSION AX633203.1 GI:28468817
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
1
AUTHORS
Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.

TITLE
Method and reagent for inhibiting the expression of disease related
genes

JOURNAL
Patent: EP 1260586-A 342 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
source
1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 13; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
|||||

Db 13 AAAAAAAAAAAAAA 1

RESULT 1060
AR049816
LOCUS AR049816 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 119 from patent US 5824770.
ACCESSION AR049816
VERSION AR049816.1 GI:5971808
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1
AUTHORS
Barascut,J.-L. and Imbach,J.-L.
TITLE
Oligothionucleotides
JOURNAL
Patent: US 5639873-A 4 17-JUN-1997;
FEATURES
source
1. .16
/organism="unassigned DNA"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1747
|||||

Db 2 CAAAAAAAAAAAAA 14

REFERENCE
1 (bases 1 to 16)
AUTHORS
Georgopoulos,K.
TITLE
IkaroS polypeptides
JOURNAL
Patent: US 5824770-A 119 20-OCT-1998;
FEATURES
Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 865 AGAGGAAGAGGAG 877
|||||

Db 3 AGAGGAAGAGGAG 15

RESULT 1061
AR149710
LOCUS AR149710 16 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 119 from patent US 6228611.
ACCESSION AR149710
VERSION AR149710.1 GI:15114301
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 16)
AUTHORS
Georgopoulos,K.
TITLE
IkaroS: A T cell pathway regulatory gene
JOURNAL
Patent: US 6228611-A 119 08-MAY-2001;
FEATURES
Location/Qualifiers
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 865 AGAGGAAGAGGAG 877
|||||

Db 3 AGAGGAAGAGGAG 15

RESULT 1062
I47692
LOCUS I47692 16 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 4 from patent US 5639873.
ACCESSION I47692
VERSION I47692.1 GI:2471657
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 16)
AUTHORS
Barascut,J.-L. and Imbach,J.-L.
TITLE
Oligothionucleotides
JOURNAL
Patent: US 5639873-A 4 17-JUN-1997;
FEATURES
source
1. .16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 865 AGAGGAAGAGGAG 877
|||||

Db 3 AGAGGAAGAGGAG 15

```
RESULT 1063
AR231305/c
LOCUS AR231305 16 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 42 from patent US 6451968.
ACCESSION AR231305
VERSION AR231305.1 GI:27272236
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Egholm,M., Nielsen,P., Buchardt,O., Dueholm,K.L., Christensen,L.,
Coull,J.M., Kiely,J. and Griffith,M.
TITLE Peptide nucleic acids
JOURNAL Patent: US 6451968-A 42 17-SEP-2002;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="genomic DNA"
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 30 AAGAGGAAAAA 45
Db 16 AAGAGGAAANNAA 1
RESULT 1064
AR404837
LOCUS AR404837 16 bp mRNA linear PAT 18-DEC-2003
DEFINITION Sequence 119 from patent US 6630141.
ACCESSION AR404837
VERSION AR404837.1 GI:40153564
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 16)
AUTHORS Georgopoulos,K.
TITLE Isolated antibody that binds to an Ikaros polypeptide
JOURNAL Patent: US 6630141-A 119 07-OCT-2003;
FEATURES
source
Location/Qualifiers
1..16
/organism="unknown"
/mol_type="mRNA"
Query Match 0.7%; Score 13; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 865 AGAGGAAGAGGAG 877
Db 3 AGAGGAAGAGGAG 15
RESULT 1065
AX708160
LOCUS AX708160 16 bp DNA linear PAT 04-APR-2003
DEFINITION Sequence 3 from Patent WO02072886.
ACCESSION AX708160
VERSION AX708160.1 GI:29564093
KEYWORDS
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1
AUTHORS Estibeiro,P.
TITLE Complex element micro-array and methods of use
JOURNAL Patent: WO 02072886-A 3 19-SEP-2002;
Expression Biosystems Limited (GB)
FEATURES
source
Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
RESULT 1066
AR057435/c
LOCUS AR057435 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1639 from patent US 5837542.
ACCESSION AR057435
VERSION AR057435.1 GI:5983012
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1639 17-NOV-1998;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
RESULT 1067
AR057586/c
LOCUS AR057586 17 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 1790 from patent US 5837542.
ACCESSION AR057586
VERSION AR057586.1 GI:5983163
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and
Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1790 17-NOV-1998;
FEATURES
source
Location/Qualifiers
1..17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
```

RESULT 1068
LOCUS AR057597 17 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 1801 from patent US 5837542.
ACCESSION AR057597
VERSION AR057597.1 GI:5983174
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1801 17-NOV-1998;
FEATURES
source Location/Qualifiers
1.17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 1069
LOCUS AR057619 17 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 1823 from patent US 5837542.
ACCESSION AR057619
VERSION AR057619.1 GI:5983196
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1823 17-NOV-1998;
FEATURES
source Location/Qualifiers
1.17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 1070
LOCUS AR057664 17 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 1868 from patent US 5837542.
ACCESSION AR057664
VERSION AR057664.1 GI:5983241
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Intercellular adhesion molecule-1 (ICAM-1) ribozymes
JOURNAL Patent: US 5837542-A 1868 17-NOV-1998;

FEATURES
source Location/Qualifiers
1.17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 1071
LOCUS AR115193 17 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 1639 from patent US 6132967.
ACCESSION AR115193
VERSION AR115193.1 GI:14095515
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1639 17-OCT-2000;
FEATURES
source Location/Qualifiers
1.17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 1072
LOCUS AR115344 17 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 1790 from patent US 6132967.
ACCESSION AR115344
VERSION AR115344.1 GI:14095666
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.
TITLE Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)
JOURNAL Patent: US 6132967-A 1790 17-OCT-2000;
FEATURES
source Location/Qualifiers
1.17
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5

RESULT 1073	ARL15355/c	LOCUS	17 bp	DNA	linear	PAT 16-MAY-2001	
DEFINITION	Sequence 1801 from patent US 6132967.						
ACCESSION	ARL15355						
VERSION	ARL15355.1	GI:14095677					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 17)						
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.						
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)						
JOURNAL	Patent: US 6132967-A 1801 17-OCT-2000;						
FEATURES	Location/Qualifiers						
source	1..17						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
Query Match	0.7%;	Score 13;	DB 1;	Length 17;			
Best Local Similarity	100.0%;	Pred. No. 8.5e+02;					
Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;
	Gaps	0;					
QY	765	CCGAGCCGAGGT	777				
Db	17	CCGAGCCGAGGT	5				
RESULT 1074	ARL15377/c	LOCUS	17 bp	DNA	linear	PAT 16-MAY-2001	
DEFINITION	Sequence 1823 from patent US 6132967.						
ACCESSION	ARL15377						
VERSION	ARL15377.1	GI:14095699					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 17)						
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.						
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)						
JOURNAL	Patent: US 6132967-A 1823 17-OCT-2000;						
FEATURES	Location/Qualifiers						
source	1..17						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
Query Match	0.7%;	Score 13;	DB 1;	Length 17;			
Best Local Similarity	100.0%;	Pred. No. 8.5e+02;					
Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;
	Gaps	0;					
QY	765	CCGAGCCGAGGT	777				
Db	17	CCGAGCCGAGGT	5				
RESULT 1075	ARL15422/c	LOCUS	17 bp	DNA	linear	PAT 16-MAY-2001	
DEFINITION	Sequence 1868 from patent US 6132967.						
ACCESSION	ARL15422						
VERSION	ARL15422.1	GI:14095744					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 17)						
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.						
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)						
JOURNAL	Patent: US 6132967-A 1868 17-OCT-2000;						
FEATURES	Location/Qualifiers						
source	1..17						
	/organism="unknown"						
	/mol_type="unassigned DNA"						
Query Match	0.7%;	Score 13;	DB 1;	Length 17;			
Best Local Similarity	100.0%;	Pred. No. 8.5e+02;					
Matches	13;	Conservative	0;	Mismatches	0;	Indels	0;
	Gaps	0;					
QY	765	CCGAGCCGAGGT	777				
Db	17	CCGAGCCGAGGT	5				
RESULT 1076	ARL15422/c	LOCUS	17 bp	DNA	linear	PAT 16-MAY-2001	
DEFINITION	Sequence 1868 from patent US 6132967.						
ACCESSION	ARL15422						
VERSION	ARL15422.1	GI:14095744					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 17)						
AUTHORS	Grimm,S., Stinchcomb,D.T., McSwiggen,J., Sullivan,S. and Draper,K.G.						
TITLE	Ribozyme treatment of diseases or conditions related to levels of intercellular adhesion molecule-1 (ICAM-1)						
JOURNAL	Patent: US 6132967-A 1868 17-OCT-2000;						
FEATURES	Location/Qualifiers						
source	1..17						

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.
TITLE        Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL      Patent: US 6346398-A 2547 12-FEB-2002;
FEATURES     Location/Qualifiers
              source
              1..17
              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 17 AAAAAAAAAAAAAA 5

RESULT 1078
AR323669/c AR323669 17 bp RNA linear PAT 17-AUG-2003
LOCUS      Sequence 1071 from patent US 6566127.
DEFINITION AR323669
ACCESSION  AR323669
VERSION    AR323669.1 GI:33709477
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 1071 20-MAY-2003;
FEATURES   Location/Qualifiers
              source
              1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 17 AAAAAAAAAAAAAA 5

RESULT 1079
AR327689 AR327689 17 bp RNA linear PAT 17-AUG-2003
LOCUS      Sequence 5091 from patent US 6566127.
DEFINITION AR327689
ACCESSION  AR327689
VERSION    AR327689.1 GI:33713497
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5091 20-MAY-2003;
FEATURES   Location/Qualifiers
              source
              1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1748
Db 17 AAAAAAAAAAAAAA 5

RESULT 1080
AR327690 AR327690 17 bp RNA linear PAT 17-AUG-2003
LOCUS      Sequence 5092 from patent US 6566127.
DEFINITION AR327690
ACCESSION  AR327690
VERSION    AR327690.1 GI:33713498
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 17)
AUTHORS    Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE      Method and reagent for the treatment of diseases or conditions
              related to levels of vascular endothelial growth factor receptor
JOURNAL    Patent: US 6566127-A 5092 20-MAY-2003;
FEATURES   Location/Qualifiers
              source
              1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 532 CCCCCGCCACCTC 544
Db 2 CCCCCGCCACCTC 14

RESULT 1081
AR3216924 AR3216924 17 bp RNA linear PAT 07-SEP-2001
LOCUS      Sequence 2366 from Patent WO0159103.
DEFINITION AR3216924
ACCESSION  AR3216924
VERSION    AR3216924.1 GI:15526985
KEYWORDS   .
SOURCE     synthetic construct
              synthetic construct
              artificial sequences.
ORGANISM   .
REFERENCE  1
AUTHORS    Blatt,L., McSwiggen,J. and Chowrira,B.M.
TITLE      Method and reagent for the modulation and diagnosis of cd20 and
              nogo gene expression
JOURNAL    Patent: WO 0159103-A 2366 16-AUG-2001;
              RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
              McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES   Location/Qualifiers
              source
              1..17
              /organism="synthetic construct"
              /mol_type="unassigned RNA"
              /db_xref="taxon:32630"
              /note="Nucleic Acid"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 866 GAGGAAGAGGAGG 878
Db 1 GAGGAAGAGGAGG 13

RESULT 1082
AX272583 AX272583 17 bp RNA linear PAT 29-OCT-2001
LOCUS      Sequence 152 from Patent WO0162911.
DEFINITION
```

```
ACCESSION AX272583
VERSION AX272583.1 GI:16545320
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 152 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1666 CTGTATGACTTTG 1678
Db 5 CTGTATGACTTTG 17
|||||
RESULT 1083
AX272970
LOCUS AX272970 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 539 from Patent WO0162911.
ACCESSION AX272970
VERSION AX272970.1 GI:16545707
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 539 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1666 CTGTATGACTTTG 1678
Db 5 CTGTATGACTTTG 17
|||||
RESULT 1084
AX273151
LOCUS AX273151 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 720 from Patent WO0162911.
ACCESSION AX273151
VERSION AX273151.1 GI:16545888
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 539 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1666 CTGTATGACTTTG 1678
Db 3 CTGTATGACTTTG 15
|||||
RESULT 1085
AX422887
LOCUS AX422887 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1223 from Patent WO0188124.
ACCESSION AX422887
VERSION AX422887.1 GI:21526269
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1223 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 524 CATATGAGCCCC 536
Db 4 CATATGAGCCCC 16
|||||
RESULT 1086
AX423096
LOCUS AX423096 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 1432 from Patent WO0188124.
ACCESSION AX423096
VERSION AX423096.1 GI:21526478
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., McLaughlin,F.G. and
Randi,A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 1432 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1..17
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"
```



```
Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 524 CATATGAGCCGCC 536
Db 2 CATATGAGCCGCC 14
|||||

RESULT 1087
AX531992/c
LOCUS AX531992 1501 from Patent EP1239051. 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1501 from Patent EP1239051.
ACCESSION AX531992
VERSION AX531992.1 GI:25255750
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon.M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1501 11-SEP-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 899 CCCTGAGCCGAGCC 911
Db 17 CCCTGAGCCGAGCC 5
|||||

RESULT 1088
AX634500/c
LOCUS AX634500 1639 from Patent EP1260586. 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1639 from Patent EP1260586.
ACCESSION AX634500
VERSION AX634500.1 GI:28470114
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelsky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1639 27-NOV-2002;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1..17
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
|||||

RESULT 1089
AX634623/c
LOCUS AX634623 1762 from Patent EP1260586. 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1762 from Patent EP1260586.
ACCESSION AX634623
VERSION AX634623.1 GI:28470237
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelsky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1762 27-NOV-2002;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1..17
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
|||||

RESULT 1090
AX634645/c
LOCUS AX634645 1784 from Patent EP1260586. 17 bp RNA linear PAT 21-FEB-2003
DEFINITION Sequence 1784 from Patent EP1260586.
ACCESSION AX634645
VERSION AX634645.1 GI:28470259
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpelsky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Woolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
genes
JOURNAL Patent: EP 1260586-A 1784 27-NOV-2002;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source 1..17
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"

Query Match      0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CCCAGGCCGAGGT 777
Db 17 CCCAGGCCGAGGT 5
|||||
```

```

RESULT 1091
AX634681/c
LOCUS
DEFINITION Sequence 1820 from Patent EP1260586.
ACCESSION AX634681
VERSION AX634681.1 GI:28470295
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 1820 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1..17
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGCCGAGGT 777
17 CCCAGCCGAGGT 5
Db

RESULT 1092
AX634688/c
LOCUS
DEFINITION Sequence 1827 from Patent EP1260586.
ACCESSION AX634688
VERSION AX634688.1 GI:28470302
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
Wolf,T.
TITLE Method and reagent for inhibiting the expression of disease related
Genes
JOURNAL Patent: EP 1260586-A 1827 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES
source
1..17
/organism="unidentified"
/mol_type="unassigned RNA"
/db_xref="taxon:32644"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 765 CCCAGCCGAGGT 777
17 CCCAGCCGAGGT 5
Db

RESULT 1093
AX671642
LOCUS

```

```

DEFINITION Sequence 87 from Patent WO03004526.
ACCESSION AX671642
VERSION AX671642.1 GI:29329990
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 87 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 572 CAATCCAGCCTC 584
4 CAATCCAGCCTC 16
Db

RESULT 1094
AX674812/c
LOCUS
DEFINITION Sequence 3257 from Patent WO03004526.
ACCESSION AX674812
VERSION AX674812.1 GI:29333160
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Telerman,A., Amson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 3257 16-JAN-2003;
Molecular Engines Laboratories (FR)
FEATURES
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 CGAAAAAAG 46
16 CGAAAAAAG 4
Db

RESULT 1095
AX690457
LOCUS
DEFINITION Sequence 3189 from Patent EP1281758.
ACCESSION AX690457
VERSION AX690457.1 GI:29413338
KEYWORDS
SOURCE
ORGANISM

```



```
QY 209 CCCTCAGGGGAG 221
Db 16 CCCTCAGGGGAG 4

RESULT 1100
AX739516
LOCUS AX739516 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 5106 from Patent WO03025177.
ACCESSION AX739516
VERSION AX739516.1 GI:30518813
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 5106 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1726 TCGAGTTTACAAA 1738
Db 3 TCGAGTTTACAAA 15

RESULT 1101
AX760808/c
LOCUS AX760808 17 bp DNA linear PAT 25-JUN-2003
DEFINITION Sequence 4129 from Patent WO03040369.
ACCESSION AX760808
VERSION AX760808.1 GI:32255424
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman,A., Anson,R. and Tuijnder,M.
TITLE Sequences involved in tumoral suppression, tumoral reversion,
apoptosis and/or viral resistance phenomena and their use as
medicines
JOURNAL Patent: WO 03040369-A 4129 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 13; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.5e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1398 GGAGACTGTGAGA 1410
Db 15 GGAGACTGTGAGA 3

RESULT 1102
AX7824/c
LOCUS AX7824 16 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 38 from Patent WO9533851.
ACCESSION AX7824
VERSION AX7824.1 GI:2301710
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS De,B.H., Portaeis,F., Machtelinckx,L., Jannes,G. and Rossau,R.
TITLE METHOD FOR THE DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF
MYCOBACTERIUM SPECIES
JOURNAL Patent: WO 9533851-A 38 14-DEC-1995;
COMMENT INNOGENETICS NV (BE)
FEATURES Other publication AU 2789695 960104.
source Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 242 CGGGGCCACACCGGC 257
Db 16 CGGGGCCACACCGGC 1

RESULT 1103
AX6860
LOCUS AX6860 16 bp DNA linear PAT 29-MAR-1999
DEFINITION Sequence 27 from Patent WO9740193.
ACCESSION AX6860
VERSION AX6860.1 GI:4538231
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 16)
AUTHORS Stuyver,L., Rossau,R. and Maertens,G.
TITLE METHOD FOR TYPING AND DETECTING HBV
JOURNAL Patent: WO 9740193-A 27 30-OCT-1997;
FEATURES INNOGENETICS NV (BE)
source Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 903 GAGCAGCCTCCAGAG 918
Db 1 GATCCAGCCTTCAGAG 16

RESULT 1104
AX051248/c
LOCUS AX051248 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 16 from patent US 5830658.
ACCESSION AR051248
VERSION AR051248.1 GI:5974612
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M.
```

TITLE Convergent synthesis of branched and multiply connected
macromolecular structures
JOURNAL Patent: US 5830658-A 16 03-NOV-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAAGGAAA 38
Db 16 AGGGGGGAAGAAA 1
|||||

RESULT 1105
AR066240/c
LOCUS 16 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5849900.
ACCESSION AR066240
VERSION AR066240.1 GI:5996456
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Moelling,K.
TITLE Inhibition of viruses by antisense oligomers capable of binding to
polypurine rich tract of single-stranded RNA or RNA-DNA hybrids
JOURNAL Patent: US 5849900-A 15-DEC-1998;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAAGGAAA 38
Db 16 AGGGGGGAAGAAA 1
|||||

RESULT 1106
AR074231
LOCUS 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 39 from patent US 5952490.
ACCESSION AR074231
VERSION AR074231.1 GI:10000986
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 39 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGGATGGG 1030
Db |||||||

RESULT 1107
AR074247
LOCUS 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 55 from patent US 5952490.
ACCESSION AR074247
VERSION AR074247.1 GI:10001002
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 55 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGGATGGG 1030
Db 1 GGGGTTGGGGTTGGG 16
|||||

RESULT 1108
AR074304
LOCUS 16 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 112 from patent US 5952490.
ACCESSION AR074304
VERSION AR074304.1 GI:10001059
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 112 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGGATGGG 1030
Db 1 GGGGTTGGGGTTGGG 16
|||||

RESULT 1109
AR077149/c
LOCUS 16 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 1 from patent US 5962225.
ACCESSION AR077149
VERSION AR077149.1 GI:10003895
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y.,
Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and
Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 39 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGGATGGG 1030
Db |||||||

REFERENCE 1 (bases 1 to 16)
AUTHORS Ramberg,E.R.
TITLE Methods and compositions for detection of specific nucleotide sequences
JOURNAL Patent: US 5962225-A 1 05-OCT-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 AGGGGGGAAGAGAA 38
|||||
Db 16 AGGGGGGAAGAGAAA 1

RESULT 1110
LOCUS AR082443 16 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 2 from patent US 5972901.
ACCESSION AR082443
VERSION AR082443.1 GI:10009169
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ferkol,T.W. Jr., Davis,P.B. and Ziady,A.-G.
TITLE Serpin enzyme complex receptor--mediated gene transfer
JOURNAL Patent: US 5972901-A 2 26-OCT-1999;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 AAGAGGAAAAA 45
|||||
Db 1 AAGAGGAAAAA 16

RESULT 1111
LOCUS AR138999 16 bp DNA linear PAT 16-JUN-2001
DEFINITION Sequence 2 from patent US 6200801.
ACCESSION AR138999
VERSION AR138999.1 GI:14481344
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Ferkol,T.W. Jr., Davis,P.B. and Ziady,A.-G.
TITLE Serpin enzyme complex receptor--mediated gene transfer
JOURNAL Patent: US 6200801-A 2 13-MAR-2001;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 AAGAGGAAAAA 45
|||||
Db 1 AAGAGGAAAAA 16

RESULT 1112
LOCUS I13390 16 bp DNA linear PAT 26-JUL-1995
DEFINITION Sequence 46 from patent US 5436150.
ACCESSION I13390
VERSION I13390.1 GI:910731
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Chandrasegaran,S.
TITLE Functional domains in flavobacterium okeanokoities (foki) restriction endonuclease
JOURNAL Patent: US 5436150-A 46 25-JUL-1995;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 19 AATTAGGGGGAAGAG 34
|||||
Db 1 AATTAGGGGGAAGAG 16

RESULT 1113
LOCUS I20477 16 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 56 from patent US 5514577.
ACCESSION I20477
VERSION I20477.1 GI:1600832
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Draper,K.G., Crooke,S.T., Mirabelli,C.K., Ecker,D.J., Hanecak,R.C., Anderson,K.P., Brown-Driver,V.L. and Wyatt,J.R.
TITLE Oligonucleotide therapies for modulating the effects of herpes viruses
JOURNAL Patent: US 5514577-A 56 07-MAY-1996;
FEATURES Location/Qualifiers
source 1..16
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1015 GTGGTTGGGGATGGG 1030
|||||
Db 1 GGGGTTGGGGTTGGG 16

RESULT 1114
LOCUS I28377 16 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 16 from patent US 5571677.
ACCESSION I28377
VERSION I28377.1 GI:1819153
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 16)
AUTHORS Gryaznov,S.M.

TITLE Convergent synthesis of branched and multiply connected

JOURNAL macromolecular structures

FEATURES Patent: US 5571677-A 16 05-NOV-1996;

source Location/Qualifiers

1..16

/organism="unknown"

/mol_type="unassigned DNA"

Query Match

Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAAGAGAAA 38

Db 16 AGGGGGGAAGAGAAA 1

RESULT 1115

LOCUS AR233918/c

DEFINITION Sequence 1 from patent US 6458540. linear DNA 16 bp PAT 20-DEC-2002

ACCESSION AR233918

VERSION AR233918.1 GI:27276545

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE 1 (bases 1 to 16)

AUTHORS Ramberg,E.R.

TITLE Methods and compositions for detection of specific nucleotide

sequences

JOURNAL Patent: US 6458540-A 1 01-OCT-2002;

FEATURES Location/Qualifiers

source 1..16

/organism="unknown"

/mol_type="genomic DNA"

Query Match

Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAAGAGAAA 38

Db 16 AGGGGGGAAGAGAAA 1

RESULT 1116

LOCUS AR281424

DEFINITION Sequence 37 from patent US 6518411. linear mRNA 16 bp PAT 10-APR-2003

ACCESSION AR281424

VERSION AR281424.1 GI:29717111

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE 1 (bases 1 to 16)

AUTHORS Murray,J.C. and Semina,E.

TITLE RGS compositions and therapeutic and diagnostic uses therefor

JOURNAL Patent: US 6518411-A 37 11-FEB-2003;

FEATURES Location/Qualifiers

source 1..16

/organism="unknown"

/mol_type="mRNA"

Query Match

Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1533 GGCCTGCAGCGCTGG 1548

Db 1 GGCCTGCAGCTCTGG 16

RESULT 1117

LOCUS AR285629

DEFINITION Sequence 1 from patent US 6528640. linear RNA 16 bp PAT 10-APR-2003

ACCESSION AR285629

VERSION AR285629.1 GI:29723223

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE 1 (bases 1 to 16)

AUTHORS Beigelman,L.; Burgin,A.; Beaudry,A.; Karpeisky,A.;

Matulic-Adamic,J.; Sweedler,D. and Zinnen,S.

TITLE Synthetic ribonucleic acids with RNase activity

JOURNAL Patent: US 6528640-A 1 04-MAR-2003;

FEATURES Location/Qualifiers

source 1..16

/organism="unknown"

/mol_type="unassigned RNA"

Query Match

Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 605 ATGGGGGCCCCACTCC 620

Db 1 ATGGGGGCGACACTCC 16

RESULT 1118

LOCUS AR285649

DEFINITION Sequence 21 from patent US 6528640. linear RNA 16 bp PAT 10-APR-2003

ACCESSION AR285649

VERSION AR285649.1 GI:29723243

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE 1 (bases 1 to 16)

AUTHORS Beigelman,L.; Burgin,A.; Beaudry,A.; Karpeisky,A.;

Matulic-Adamic,J.; Sweedler,D. and Zinnen,S.

TITLE Synthetic ribonucleic acids with RNase activity

JOURNAL Patent: US 6528640-A 21 04-MAR-2003;

FEATURES Location/Qualifiers

source 1..16

/organism="unknown"

/mol_type="unassigned RNA"

Query Match

Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 606 TGGGGGCCCCACTCCA 621

Db 1 TGGGGGCGACACTCCA 16

RESULT 1119

LOCUS AR366072/c

DEFINITION Sequence 38 from patent US 6329138. linear mRNA 16 bp PAT 12-SEP-2003

ACCESSION AR366072

VERSION AR366072.1 GI:34598429

KEYWORDS

SOURCE Unknown.

ORGANISM

REFERENCE 1 (bases 1 to 16)

AUTHORS De Beenhouwer,H.; Portaela,F.; nckx,L.M.; Jannes,G. and Rossau,R.

TITLE Method for detection of the antibiotic resistance spectrum of

Mycobacterium species


```
/organism="unknown"
/mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 242 CGGGCCACACCGGC 257
Db 16 CGGGCCACGACCGGC 1

RESULT 1125
AX032593
LOCUS AX032593 16 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 39 from Patent EP1016715.
ACCESSION AX032593
VERSION AX032593.1 GI:10279531
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 39 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
Db 1 GGGGTTGGGTTGGG 16

RESULT 1126
AX032609
LOCUS AX032609 16 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 55 from Patent EP1016715.
ACCESSION AX032609
VERSION AX032609.1 GI:10279547
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 55 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
Db 1 GGGGTTGGGTTGGG 16

RESULT 1127
AX032666
LOCUS AX032666 16 bp DNA linear PAT 20-SEP-2000
DEFINITION Sequence 112 from Patent EP1016715.
ACCESSION AX032666
VERSION AX032666.1 GI:10279604
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Imbach,J.L., Brown-Driver,V.L., Vickers,T.A., Ecker,D.J.,
Bennett,C.F., Chiang,M.Y., Anderson,K.P., Hanecak,R.C. and
Wyatt,J.R.
TITLE Oligonucleotides having a conserved g4 core sequence
JOURNAL Patent: EP 1016715-A 112 05-JUL-2000;
ISIS PHARMACEUTICALS INC (US)
FEATURES
source
Location/Qualifiers
1..16
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGG 1030
Db 1 GGGGTTGGGTTGGG 16

RESULT 1128
AX194485/c
LOCUS AX194485 16 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 85 from Patent WO0151500.
ACCESSION AX194485
VERSION AX194485.1 GI:15385141
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Klimman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 85 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
source
Location/Qualifiers
1..16
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/notes="Synthetic DNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 16;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 739 CCCCTCCCGGCGCCCC 754
Db 16 CCCCTCTCGAGCCCCC 1

RESULT 1129
AX281908/c
LOCUS AX281908 16 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 40 from Patent WO0177392.
ACCESSION AX281908
VERSION AX281908.1 GI:16609159
KEYWORDS
```


Qy 169 CCCACCTGGCTGCCCC 184
Db 1 CCCACCACTGGCTGCCCC 16

RESULT 1134
BD091347/c
LOCUS BD091347 16 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for detection of specific nucleotide sequences.
ACCESSION BD091347
VERSION BD091347.1 GI:22636958
KEYWORDS JP 2001522588-A/1.
SOURCE Human adenovirus type 1
ORGANISM Human adenovirus type 1
REFERENCE 1 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
AUTHORS 1 (bases 1 to 16)
TITLE Ramberg, E.R.
JOURNAL Methods and compositions for detection of specific nucleotide
CYGENE INC Patent: JP 2001522588-A 1 20-NOV-2001;
COMMENT OS Human adenovirus type 1
PN JP 2001522588-A/1
PD 20-NOV-2001
PF 12-NOV-1998 JP 2000519613
PR 12-NOV-1997 US 60/065378,24-FEB-1998 US 60/075812 PR
PI 05-MAR-1998 US 60/076872
PT ELLIOT R RAMBERG
PC CL2Q1/68,C12N15/09,C12N15/00
CC Methods and compositions for detection of specific nucleotide
sequences
FH Key 1. .16
FT source Location/Qualifiers
1. .16
/organism="Human adenovirus type 1"
/mol_type="genomic DNA"
/db_xref="taxon:10533"
/note="Human adenovirus type 1"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAGAGGAAA 38
Db 16 AGGGGGGAGAGGAAA 1

RESULT 1135
AX422500/c
LOCUS AX422500 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 836 from Patent WO0188124.
ACCESSION AX422500
VERSION AX422500.1 GI:21525882
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 836 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 16;
Best Local Similarity 87.5%; Pred. No. 8.5e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 23 AGGGGGGAGAGGAAA 38
Db 16 AGGGGGGAGAGGAAA 1

RESULT 1135
AX422500/c
LOCUS AX422500 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 836 from Patent WO0188124.
ACCESSION AX422500
VERSION AX422500.1 GI:21525882
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 836 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1021 GGGGATGGGCTGGG 1036
Db 17 GGGGATGGGCTGGG 2

RESULT 1136
AX422501/c
LOCUS AX422501 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 837 from Patent WO0188124.
ACCESSION AX422501
VERSION AX422501.1 GI:21525883
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Jarvis, T., von Carlowitz, I., McSwiggen, J.A., McLaughlin, F.G. and Randi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 837 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1021 GGGGATGGGCTGGG 1036
Db 16 GGGGATGGGCTGGG 1

RESULT 1137
AX46769/c
LOCUS AX46769 17 bp DNA linear PAT 07-MAR-1997
DEFINITION Sequence 6 from Patent EP0677585.
ACCESSION AX46769
VERSION AX46769.1 GI:2300864
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grifantini, R., Frascotti, G., Galli, G. and Grandi, G.
TITLE Process for the production of D-alpha-amino acids
JOURNAL Patent: EP 0677585-A 6 18-OCT-1995;
ENIRICERCH SPA (IT)
COMMENT Other publication JP 8051992 960227.
FEATURES
source
1. .17
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1506 CCCGCTGGATGGGCAC 1521
Db 16 CCCGCTGGATGGGCAC 1

source	1. .17	/organism="unknown"	/mol_type="unassigned DNA"
Query Match	0.7%; Score 12.8; DB 1; Length 17;		
Best Local Similarity	87.5%; Pred. No. 9e+02;		
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1442 GCTGTTACAAGTGCGA 1457		
Db	17 GCTGTTCCAAGTGCAA 2		
RESULT 1141			
AR040219/c			
LOCUS	AR040219	17 bp	DNA linear
DEFINITION	Sequence 1067 from patent US 5807743.		
ACCESSION	AR040219		
VERSION	AR040219.1	GI:5959582	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Stinchcomb, D.T. and McSwiggen, J.A.		
TITLE	Interleukin-2 receptor gamma-chain ribozymes		
JOURNAL	Patent: US 5807743-A 1067 15-SEP-1998;		
FEATURES	Location/Qualifiers		
source	1. .17		
Query Match	0.7%; Score 12.8; DB 1; Length 17;		
Best Local Similarity	87.5%; Pred. No. 9e+02;		
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1442 GCTGTTACAAGTGCGA 1457		
Db	17 GCTGTTCCAAGTGCAA 2		
RESULT 1142			
AR047356/c			
LOCUS	AR047356	17 bp	DNA linear
DEFINITION	Sequence 2149 from patent US 5817796.		
ACCESSION	AR047356		
VERSION	AR047356.1	GI:5968821	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 17)		
AUTHORS	Stinchcomb, D.T., Draper, K., McSwiggen, J. and Jarvis, T.		
TITLE	C-myc ribozymes having 2'-5'-linked adenylyate residues		
JOURNAL	Patent: US 5817796-A 2149 06-OCT-1998;		
FEATURES	Location/Qualifiers		
source	1. .17		
Query Match	0.7%; Score 12.8; DB 1; Length 17;		
Best Local Similarity	87.5%; Pred. No. 9e+02;		
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
QY	1733 TACAAAAAATAAAAAA 1748		
Db	16 TATATAAAAAATAAAAAA 1		
RESULT 1143			
AR057566/c			
LOCUS	AR057566	17 bp	DNA linear
DEFINITION	Sequence 1770 from patent US 5837542.		
FEATURES	Location/Qualifiers		
source	1. .17		

Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	862 GGAAGAGGAAGAGGAG 877	
Db	16 GCAAGAGGAAGAGCAG 1	
RESULT 1146		
LOCUS	AR097026	linear PAT 14-FEB-2001
DEFINITION	Sequence 89 from patent US 5071515.	
ACCESSION	AR097026	
VERSION	AR097026.1 GI:12805756	
KEYWORDS	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 17)	
TITLE	Mezes, P.S., Richard, R.A., Affholter, J.A. and Kotite, N.J.	
JOURNAL	Dimer and multimer forms of single chain polypeptides	
FEATURES	Patent: US 6071515-A 89 06-JUN-2000;	
source	Location/Qualifiers	
	1..17	
	/organism="unknown"	
	/mol_type="unassigned DNA"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	510 ACCAGACCCGACAGGCA 525	
Db	2 ACCAGACCCGACAGTCA 17	
RESULT 1147		
LOCUS	AR115324/c	linear PAT 16-MAY-2001
DEFINITION	Sequence 1770 from patent US 6132967.	
ACCESSION	AR115324	
VERSION	AR115324.1 GI:14095646	
KEYWORDS	Unknown.	
ORGANISM	Unknown.	
REFERENCE	Unclassified.	
AUTHORS	1 (bases 1 to 17)	
TITLE	Praper, K.G.	
JOURNAL	Ribozyme treatment of diseases or conditions related to levels of	
FEATURES	intercellular adhesion molecule-1 (ICAM-1)	
source	Patent: US 6132967-A 1770 17-OCT-2000;	
	Location/Qualifiers	
	1..17	
	/organism="unknown"	
	/mol_type="unassigned DNA"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
Qy	862 GGAAGAGGAAGAGGAG 877	
Db	17 GCAAGAGGAAGAGCAG 2	
RESULT 1148		
LOCUS	AR115448/c	linear PAT 16-MAY-2001
DEFINITION	Sequence 1894 from patent US 6132967.	
ACCESSION	AR115448	

```
VERSION AR115448.1 GI:14095770
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6132967-A 1894 17-OCT-2000;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 862 GGAAGAGGAGGAGGAG 877
Db 16 GCAAGAGGAGGAGCAG 1
RESULT 1149
AR115538/c
LOCUS AR115538 17 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1984 from patent US 6132967.
ACCESSION AR115538
VERSION AR115538.1 GI:14095860
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6132967-A 1984 17-OCT-2000;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 862 GGAAGAGGAGGAGGAG 877
Db 16 GCAAGAGGAGGAGCAG 1
RESULT 1150
AR158452/c
LOCUS AR158452 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 74 from patent US 6251588.
ACCESSION AR158452
VERSION AR158452.1 GI:16220492
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6251588-A 74 26-JUN-2001;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 862 GGAAGAGGAGGAGGAG 877
Db 16 GCAAGAGGAGGAGCAG 1
RESULT 1151
AR158453/c
LOCUS AR158453 17 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 75 from patent US 6251588.
ACCESSION AR158453
VERSION AR158453.1 GI:16220493
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6251588-A 75 26-JUN-2001;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 773 GAGGTGAAGTCTGGGG 788
Db 17 GAGGAGAAGTCTGGCG 2
RESULT 1152
AR173612
LOCUS AR173612 17 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 28 from patent US 6306586.
ACCESSION AR173612
VERSION AR173612.1 GI:17913932
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 17)
TITLE Ribozyme treatment of diseases or conditions related to levels of
JOURNAL intercellular adhesion molecule-1 (ICAM-1)
FEATURES Patent: US 6306586-A 28 23-OCT-2001;
source Location/Qualifiers
1. .17
/mol_type="unassigned DNA"
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 773 GAGGTGAAGTCTGGGG 788
Db 16 GAGGAGAAGTCTGGCG 1
RESULT 1153
BD241455/c
LOCUS BD241455 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
```

ACCESSION BD241455
VERSION BD241455.1 GI:33051225
KEYWORDS JP 2002525127-A/402.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 402 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/402
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
C12N15/09, C12Q1/68, G01N33/53, G01N33/56, G01N37/00, PC
G01N37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES source
1..17
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1750
Db 16 CAATAATAAAAAAAAAA 1
RESULT 1154
BD241481/C
LOCUS BD241481 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods and products related to genotyping and DNA analysis.
ACCESSION BD241481
VERSION BD241481.1 GI:33051251
KEYWORDS JP 2002525127-A/428.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 17)
AUTHORS Landers, J.E., Jordan, B., Housman, D.E. and Charest, A.
TITLE Methods and products related to genotyping and DNA analysis
JOURNAL Patent: JP 2002525127-A 428 13-AUG-2002;
MASSACHUSETTS INSTITUTE OF TECHNOLOGY
COMMENT OS Homo sapiens (human)
PN JP 2002525127-A/428
PD 13-AUG-2002
PF 24-SEP-1999 JP 2000572407
PR 25-SEP-1998 US 60/101757
PI JOHN E LANDERS, BARBARA JORDAN, DAVID E HOUSMAN, ALAIN CHAREST PC
C12N15/09, C12Q1/68, G01N33/53, G01N33/56, G01N37/00, PC
G01N37/00,
PC C12N15/00
CC Methods and products related to genotyping and DNA analysis FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Homo sapiens (human)'.
FEATURES source
1..17
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

/db_xref='taxon:9606'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1750
Db 16 CAATAATAAAAAAAAAA 1
RESULT 1155
BD254211
LOCUS BD254211 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254211
VERSION BD254211.1 GI:33063981
KEYWORDS JP 2002541795-A/2004.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2004 10-DEC-2002;
COMMENT RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/2004
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/123390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES source
1..17
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 612 CCCCACTCCAGCTCT 627
Db 2 CCCTCTCCAGCTCT 17
RESULT 1156
BD254586
LOCUS BD254586 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD254586
VERSION BD254586.1 GI:33064356
KEYWORDS JP 2002541795-A/2379.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2379 10-DEC-2002;

Query Match	0.7%;	Score 12.8;	DB 1;	Length 17;
Best Local Similarity	87.5%;	Pred. No. 9e+02;	Mismatches 0;	Indels 2;
Matches	14;	Conservative	0;	Gaps 0;
QY	23	AGGGGGGGAAGAGGAAA	38	
Db	16	AGGAGGGGAGAGGAAA	1	
RESULT 1158				
BD255011/c				
LOCUS	BD255011	17 bp	DNA	linear
DEFINITION	Regulation of repressor genes using nucleic acid molecules.			
ACCESSION	BD255011			
VERSION	BD255011.1	GI:33064781		
KEYWORDS	JP 2002541795-A/2804.			
SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.			
TITLE	Regulation of repressor genes using nucleic acid molecules			
JOURNAL	Patent: JP 2002541795-A 2804 10-DEC-2002;			
COMMENT	RIBOZYME PHARMACEUTICALS INC			
OS	Eukaryote			
PN	JP 2002541795-A/2804			
PD	10-DEC-2002			
PF	11-APR-2000	JP 2000611654		
PR	12-APR-1999	US 60/129390		
PI	LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN	PC		
C12N15/09, A61K38/00, A61P43/00, A61P43/00, C12N5/10, PC				
C12P21/02,				
PC				
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC				
C12R1:91),				
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,				
PC A61K37/02,				
PC (C12N5/00, C12R1:91)				
CC	Regulation of repressor genes using nucleic acid molecules			
Key	Location/Qualifiers			
FT	source	1..17		
FT	Location/Qualifiers	/organism='Eukaryote'.		
FEATURES				
source				
1..17				
/organism='unidentified'				
/mol_type='genomic DNA'				
/db_xref='taxon:32644'				
Query Match	0.7%;	Score 12.8;	DB 1;	Length 17;
Best Local Similarity	87.5%;	Pred. No. 9e+02;	Mismatches 0;	Indels 2;
Matches	14;	Conservative	0;	Gaps 0;
QY	1736	AAAAAAAAAAAAAAAAA	1751	
Db	1	AAGAAATAAAAAAAAAA	16	
RESULT 1157				
BD254877/c				
LOCUS	BD254877	17 bp	DNA	linear
DEFINITION	Regulation of repressor genes using nucleic acid molecules.			
ACCESSION	BD254877			
VERSION	BD254877.1	GI:33064647		
KEYWORDS	JP 2002541795-A/2670.			
SOURCE	unidentified			
ORGANISM	unclassified.			
REFERENCE	1 (bases 1 to 17)			
AUTHORS	Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.			
TITLE	Regulation of repressor genes using nucleic acid molecules			
JOURNAL	Patent: JP 2002541795-A 2670 10-DEC-2002;			
COMMENT	RIBOZYME PHARMACEUTICALS INC			
OS	Eukaryote			
PN	JP 2002541795-A/2670			
PD	10-DEC-2002			
PF	11-APR-2000	JP 2000611654		
PR	12-APR-1999	US 60/129390		
PI	LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN	PC		
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC				
C12P21/02,				
PC				
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC				
C12R1:91),				
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,				
PC A61K37/02,				
PC (C12N5/00, C12R1:91)				
CC	Regulation of repressor genes using nucleic acid molecules			
Key	Location/Qualifiers			
FT	source	1..17		
FT	Location/Qualifiers	/organism='Eukaryote'.		
FEATURES				
source				
1..17				
/organism='unidentified'				
/mol_type='genomic DNA'				
/db_xref='taxon:32644'				

PN JP 2002541795-A/2805
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;
Qy 861 AGGAGGAGGAGGAGGA 876
Db 17 AGGAGGAGGAGGAGGA 2

RESULT 1160
BD255013/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255013
VERSION BD255013.1 GI:33064783
KEYWORDS JP 2002541795-A/2806,
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2806 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2806
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;
Qy 861 AGGAGGAGGAGGAGGA 876
Db 17 AGGAGGAGGAGGAGGA 2

RESULT 1160
BD255013/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255013
VERSION BD255013.1 GI:33064783
KEYWORDS JP 2002541795-A/2806,
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2806 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2806
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;
Qy 861 AGGAGGAGGAGGAGGA 876
Db 17 AGGAGGAGGAGGAGGA 2

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 859 GCAGGAGGAGGAGAG 874
Db 16 GCAGGAGGAGGAGAG 1

RESULT 1161
BD255031
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255031
VERSION BD255031.1 GI:33064801
KEYWORDS JP 2002541795-A/2824,
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 2824 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/2824
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N15/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
Location/Qualifiers
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;
Qy 842 CTGGGGTCTCTGGGCC 857
Db 2 CTGGGGTCTGGGGGCC 17

RESULT 1162
BD255419/c
LOCUS
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255419
VERSION BD255419.1 GI:33065189
KEYWORDS JP 2002541795-A/3212,
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and McSwiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 3212 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/3212
PD 10-DEC-2002

PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA,PAVCO,JAMES,MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,

PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,C12R1:91)
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source

1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1735 CAAAAAAAAAAAAA 1750
|||||
Db 17 CAAAAAAAAAATTAA 2

RESULT 1163
BD255420/c
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255420
VERSION BD255420.1 GI:33065190
KEYWORDS JP 2002541795-A/3213.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3213 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/3213
PD 10-DEC-2002
PR 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA,PAVCO,JAMES,MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,

PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,C12R1:91)
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source

1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1735 CAAAAAAAAAAAAA 1750
|||||
Db 16 CAAAAAAAAAATTAA 1

RESULT 1164
BD255542/c

LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255542
VERSION BD255542.1 GI:33065312
KEYWORDS JP 2002541795-A/3335.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3335 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/3335
PD 10-DEC-2002
PR 11-APR-2000 JP 2000611654
PI LAWRENCE BLATT,MICHAEL,ZWICK,PAMELA,PAVCO,JAMES,MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
C12P21/02,

PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,C12R1:91)
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
KEY Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source

1..17
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 14; Conservative 0;

QY 1732 TTACAAAAAAAAAAAA 1747
|||||
Db 17 TCACAAAGAAAAAAAA 2

RESULT 1165
BD255581

LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD255581
VERSION BD255581.1 GI:33065351
KEYWORDS JP 2002541795-A/3374.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE
1 (bases 1 to 17)
Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
Regulation of repressor genes using nucleic acid molecules
Patent: JP 2002541795-A 3374 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/3374
PD 10-DEC-2002
PR 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390

PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1072 TTCTATGTTCTCAT 1087
|||||
Db 1 TTGTATTTCTTCAT 16
|||||
RESULT 1166
BD256533
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD256533
VERSION BD256533.1 GI:33066303
KEYWORDS JP 2002541795-A/4326.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt, L., Zwick, M., Pavco, P. and Mcswiggen, J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 4326 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Eukaryote
PN JP 2002541795-A/4326
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 AGTACTTGGCCAGTG 995
|||||
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

Db 2 AGTACTTGGCCATG 17
|||||
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 AGTACTTGGCCAGTG 995
|||||
Db 2 AGTACTTGGCCATG 17
|||||
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 980 AGTACTTGGCCAGTG 995
|||||
Db 2 AGTACTTGGCCATG 17
|||||
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09, A61K38/00, A61K48/00, A61P43/00, A61P43/00, C12N5/10, PC
C12P21/02,
PC
C12P21/02, C12P21/02//A61K31/711, (C12N5/10, C12R1:91), (C12P21/02, PC
C12R1:91),
PC (C12P21/02, C12R1:91), (C12P21/02, C12R1:91), C12N5/00, C12N5/00,
PC A61K37/02,
PC (C12N5/00, C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
Location/Qualifiers
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N5/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1732 TTACAAAAA 1747
Db |||||

RESULT 1169
BD257672/2
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD257672
VERSION BD257672.1 GI:33067442
KEYWORDS JP 2002541795-A/5465.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 5465 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/5465
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10,PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N5/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1731 TTACAAAAA 1746
Db |||||

RESULT 1170
BD258512/2
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258512
VERSION BD258512.1 GI:33068282
KEYWORDS JP 2002541795-A/6305.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6305 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/6305
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10,PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N5/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1731 TTACAAAAA 1746
Db |||||

RESULT 1170
BD258512/2
LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258512
VERSION BD258512.1 GI:33068282
KEYWORDS JP 2002541795-A/6305.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6305 10-DEC-2002;
RIBOZYME PHARMACEUTICALS INC
OS Eukaryote
PN JP 2002541795-A/6305
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10,PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,PC
C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N5/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key source Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote'.
FEATURES
source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1748
Db |||||

C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,PC C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote',
FEATURES source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1735 CAAAAAATAAAAAA 1750
Db 17 CAAAAAATAAAAAA 2
RESULT 1172
BD258581/c
LOCUS BD258581 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Regulation of repressor genes using nucleic acid molecules.
ACCESSION BD258581
VERSION BD258581.1 GI:33068351
KEYWORDS JP 2002541795-A/6374.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 17)
AUTHORS Blatt L., Zwick M., Pavco P. and Mcswiggen J.
TITLE Regulation of repressor genes using nucleic acid molecules
JOURNAL Patent: JP 2002541795-A 6374 10-DEC-2002;
COMMENT OS Eukaryote
PN JP 2002541795-A/6374
PD 10-DEC-2002
PF 11-APR-2000 JP 2000611654
PR 12-APR-1999 US 60/129390
PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC
C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10,PC
C12P21/02,
PC
C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02,PC C12R1:91),
PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
PC A61K37/02,
PC (C12N5/00,C12R1:91)
CC Regulation of repressor genes using nucleic acid molecules FH
Key Location/Qualifiers
FT source 1..17
FT /organism='Eukaryote',
FEATURES source
1..17
/organism='unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1731 TTTACAAAAAATAAAAA 1746
Db 16 TTTACAAAAAATAAAAA 1
RESULT 1173

E37369/c
LOCUS E37369 17 bp DNA linear PAT 31-JAN-2002
DEFINITION Swine serum lectin gene.
ACCESSION E37369
VERSION E37369.1 GI:18626673
KEYWORDS JP 2000166569-A/6.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Kawasaki,H.
TITLE Swine serum lectin gene
JOURNAL Patent: JP 2000166569-A 6 20-JUN-2000;
COMMENT OS Artificial Sequence
PN JP 2000166569-A/6
PD 20-JUN-2000
PR 09-DEC-1998 JP 1998350283
PI HARUYOSHI KAWASAKI
PC C12N15/09,C07K14/47,C12P21/02//C12N15/09,C12R1:91),C12N15/00,
PC (C12N15/00,C12R1:91)
CC
FT Key Location/Qualifiers
FT source 1..17
FT /organism='Artificial Sequence',
FEATURES source
1..17
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 806 AGAGAGAGCCAGGGCC 821
Db 16 AGGAGAGACCCAGGGCC 1
RESULT 1174
I26844/c
LOCUS I26844 17 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 67 from patent US 5561041.
ACCESSION I26844
VERSION I26844.1 GI:1606714
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Sidransky,D.
TITLE Nucleic acid mutation detection by analysis of.sputum
JOURNAL Patent: US 5561041-A 67 01-OCT-1996;
FEATURES source
1..17
/organism='unknown'
/mol_type='unassigned DNA'
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1023 GGATGGGGCTGGGGTT 1038
Db 16 GGATGGGGCTCCGGTT 1
RESULT 1175
I54408/c
LOCUS I54408 17 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 2149 from patent US 5646042.

[illegible]

Query Match 0.78: Score 12.8: DB 1: Length 17:

```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 526 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1398 GGAGACTGTGGAAT 1413
Db 2 GGAGAAATGTGAAAT 17
|||||
|||||

RESULT 1186
AR286186 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 558 from patent US 6528640.
DEFINITION AR286186
ACCESSION AR286186
VERSION AR286186.1 GI:29723782
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 558 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAACAAACAAACAAA 2
|||||
|||||

RESULT 1187
AR286187 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 559 from patent US 6528640.
DEFINITION AR286187
ACCESSION AR286187
VERSION AR286187.1 GI:29723783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 559 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAACAAACAAACAAA 2
|||||
|||||

RESULT 1187
AR286187 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 559 from patent US 6528640.
DEFINITION AR286187
ACCESSION AR286187
VERSION AR286187.1 GI:29723783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 559 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAACAAACAAACAAA 2
|||||
|||||

RESULT 1187
AR286187 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 559 from patent US 6528640.
DEFINITION AR286187
ACCESSION AR286187
VERSION AR286187.1 GI:29723783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 559 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAACAAACAAACAAA 2
|||||
|||||

RESULT 1187
AR286187 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 558 from patent US 6528640.
DEFINITION AR286187
ACCESSION AR286187
VERSION AR286187.1 GI:29723792
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 568 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 228 CCCCCGCGCACCCCG 243
Db 1 CCTCGCAGACCCCG 16
|||||
|||||

RESULT 1189
AR286453 17 bp RNA linear PAT 10-APR-2003
LOCUS Sequence 825 from patent US 6528640.
DEFINITION AR286453
ACCESSION AR286453
VERSION AR286453.1 GI:29724049
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A., Beaudry,A., Karpeisky,A.,
          Matulic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Synthetic ribonucleic acids with RNase activity
JOURNAL Patent: US 6528640-A 825 04-MAR-2003;
FEATURES Location/Qualifiers
          source
            1..17
              /organism="unknown"
              /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 CCACCTGGCTGCCCC 185
Db 17 CCCTTGGCTGCCCC 2
|||||
|||||

RESULT 1190
AR322498 17 bp DNA linear PAT 17-AUG-2003
LOCUS Sequence 6 from patent US 6566105.
DEFINITION AR322498
ACCESSION AR322498
VERSION AR322498.1 GI:33708267
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
```


Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Grifantini,R., Frascotti,G., Galli,G. and Grandi,G.
TITLE Process for the production of D- alpha.-amino acids
JOURNAL Patent: US 6566105-A 6 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy 1506 CCCGCTGGATGGGCAC 1521
|||||
Db 16 CCCGCTGGATCGGCC 1

RESULT 1191
AR323641/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 1043 from patent US 6566127.
ACCESSION AR323641
VERSION AR323641.1 GI:33709449
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1043 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy 29 GAAGAGGAGGAAAAA 44
|||||
Db 16 GAAGAGGAGGAGCAAA 1

RESULT 1192
AR323678/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 1080 from patent US 6566127.
ACCESSION AR323678
VERSION AR323678.1 GI:33709486
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1080 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy 1731 TTTACAAAAA 1746

Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 1264 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy 1704 CCAATCAAGAAATAAT 1719
|||||
Db 17 CCAATTAAAGAAATATT 2

RESULT 1194
AR3236204/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 3606 from patent US 6566127.
ACCESSION AR3236204
VERSION AR3236204.1 GI:33712012
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3606 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0;

Qy 1734 ACAAAAAA 1749
|||||
Db 16 ACAAAACAAAAACAA 1

RESULT 1195
AR3236206/c 17 bp RNA linear PAT 17-AUG-2003
LOCUS
DEFINITION Sequence 3608 from patent US 6566127.
ACCESSION AR3236206
VERSION AR3236206.1 GI:33712014
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 3608 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAACAAAAA 1749
||||| ||||| |||||
16 ACAACACAAACAAA 1

Db AR327941 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR327941
DEFINITION Sequence 5343 from patent US 6566127.
ACCESSION AR327941
VERSION AR327941.1 GI:33713749
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5343 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 721 GCCTCTCAGGCTTCG 736
||||| ||||| |||||
17 GCCTCTCAGGCTTCG 2

Db AR328074 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR328074
DEFINITION Sequence 5476 from patent US 6566127.
ACCESSION AR328074
VERSION AR328074.1 GI:33713882
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5476 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1631 CCATCCTTTGATGAT 1646
||||| ||||| |||||

Db AR328160 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR328160
DEFINITION Sequence 5562 from patent US 6566127.
ACCESSION AR328160
VERSION AR328160.1 GI:33713968
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 5562 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1704 CCAATCAAGAAATAT 1719
||||| ||||| |||||
16 CCAATTAAGAAATAT 1

Db AR329383 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR329383
DEFINITION Sequence 6785 from patent US 6566127.
ACCESSION AR329383
VERSION AR329383.1 GI:33715191
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6785 20-MAY-2003;
FEATURES Location/Qualifiers
source 1..17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1188 CCAGCCCATCTGGAC 1203
||||| ||||| |||||
2 CCAGACCATGCTGGAC 17

Db AR329554 17 bp RNA linear PAT 17-AUG-2003
LOCUS AR329554
DEFINITION Sequence 6956 from patent US 6566127.
ACCESSION AR329554
VERSION AR329554.1 GI:33715362
KEYWORDS
SOURCE Unknown.
ORGANISM Unassigned.
REFERENCE 1 (bases 1 to 17)
AUTHORS Pavco, P., McSwiggen, J.A., Stinchcomb, D.T. and Escobedo, J.

TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 6956 20-MAY-2003;
FEATURES Location/Qualifiers
source
1. 17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 398 GGCTCCCTGCACAG 413
Db 16 GGCTCCCTGCAGTCG 1

RESULT 1201
AR367363 AR367363 17 bp DNA linear PAT 12-SEP-2003
LOCUS Sequence 89 from patent US 6329507.
DEFINITION AR367363
ACCESSION AR367363
VERSION AR367363.1 GI:34600440
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Mezes P.S., Richard R.A., Affholter J.A. and Kotite, N.J.
TITLE Dimer and multimer forms of single chain polypeptides
JOURNAL Patent: US 6329507-A 89 11-DEC-2001;
FEATURES Location/Qualifiers
source
1. 17
/organism="unknown"
/mol_type="genomic DNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 510 ACCAGCCGACGAGCA 525
Db 2 ACCAGACCCACAGTCA 17

RESULT 1202
AR398144 AR398144 17 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 525 from patent US 6617438.
DEFINITION AR398144
ACCESSION AR398144
VERSION AR398144.1 GI:40135717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 525 09-SEP-2003;
FEATURES Location/Qualifiers
source
1. 17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1398 GGAGACTGTGAAT 1413
Db 2 GGAGAAATGTGAAT 17

RESULT 1203
AR398176 AR398176 17 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 557 from patent US 6617438.
DEFINITION AR398176
ACCESSION AR398176
VERSION AR398176.1 GI:40135774
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 557 09-SEP-2003;
FEATURES Location/Qualifiers
source
1. 17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
Db 17 AACACAAACAAACAAA 2

RESULT 1204
AR398177 AR398177 17 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 558 from patent US 6617438.
DEFINITION AR398177
ACCESSION AR398177
VERSION AR398177.1 GI:40135776
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 558 09-SEP-2003;
FEATURES Location/Qualifiers
source
1. 17
/organism="unknown"
/mol_type="unassigned RNA"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAACAAACAAA 1

RESULT 1205
AR398186 AR398186 17 bp RNA linear PAT 18-DEC-2003
LOCUS Sequence 567 from patent US 6617438.
DEFINITION AR398186
ACCESSION AR398186
VERSION AR398186.1 GI:40135795
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman, L., Burgin, A.B., Beaudry, A., Karpeisky, A., Matulic-Adamic, J., Sweedler, D. and Zinnen, S.
TITLE Oligoribonucleotides with enzymatic activity

```
JOURNAL Patent: US 6617438-A 567 09-SEP-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 228 CCCCCGGCGACCCCG 243
Db 1 CCCTCGAGCAGCCCG 16

RESULT 1206
AR398443/C AR398443 17 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 824 from patent US 6617438.
ACCESSION AR398443
VERSION AR398443.1 GI:40136260
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpelsky,A.,
          Matlic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 824 09-SEP-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 CCACCTGGCTGCCCC 185
Db 17 CCCTTGGCTGCCCC 2

RESULT 1207
AR433953
LOCUS
DEFINITION Sequence 376 from patent US 6656700.
ACCESSION AR433953
VERSION AR433953.1 GI:40196796
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 376 02-DEC-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1454 GCGAGGAGTGTGGCT 1469
Db 2 GCGAGGAGTGTGTGT 17

RESULT 1208
AR398443/C AR398443 17 bp RNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 824 from patent US 6617438.
ACCESSION AR398443
VERSION AR398443.1 GI:40136260
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Beigelman,L., Burgin,A.B., Beaudry,A., Karpelsky,A.,
          Matlic-Adamic,J., Sweedler,D. and Zinnen,S.
TITLE Oligoribonucleotides with enzymatic activity
JOURNAL Patent: US 6617438-A 824 09-SEP-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="unassigned RNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 170 CCACCTGGCTGCCCC 185
Db 17 CCCTTGGCTGCCCC 2

RESULT 1207
AR433953
LOCUS
DEFINITION Sequence 376 from patent US 6656700.
ACCESSION AR433953
VERSION AR433953.1 GI:40196796
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 376 02-DEC-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1454 GCGAGGAGTGTGGCT 1469
Db 2 GCGAGGAGTGTGTGT 17

RESULT 1208
AR433954
LOCUS
DEFINITION Sequence 377 from patent US 6656700.
ACCESSION AR433954
VERSION AR433954.1 GI:40196797
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 377 02-DEC-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1454 GCGAGGAGTGTGGCT 1469
Db 1 GCGAGGAGTGTGTGT 16

RESULT 1209
AR434060
LOCUS
DEFINITION Sequence 483 from patent US 6656700.
ACCESSION AR434060
VERSION AR434060.1 GI:40196903
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 483 02-DEC-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="genomic DNA"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 AAAAAAAGCCAGAA 52
Db 2 AAAAAAAGAAAGAA 17

RESULT 1210
AR434062
LOCUS
DEFINITION Sequence 485 from patent US 6656700.
ACCESSION AR434062
VERSION AR434062.1 GI:40196905
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 17)
AUTHORS Gu,Y. and Shannon,M.E.
TITLE Isoforms of human pregnancy-associated protein-E
JOURNAL Patent: US 6656700-A 485 02-DEC-2003;
FEATURES
  source
    1. .17
      /organism="unknown"
      /mol_type="genomic DNA"
```

```
Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 38 AAAAAAAAAAGCCAGAAA 53
Db 1 AAAAAAAAAAGAAAGAAA 16

RESULT 1211
AX214608/c
LOCUS AX214608 17 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 415 from Patent WO0122972.
ACCESSION AX214608
VERSION AX214608.1 GI:13920420
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Krieg, A.M., Schetter, C. and Vollmer, J.C.
TITLE Immunostimulatory nucleic acids
JOURNAL Patent: WO 0122972-A 415 05-APR-2001;
UNIVERSITY OF IOWA RESEARCH FOUNDATION (US) ; Coley Pharmaceutical
GmbH (DE)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 589 CTCCAGCGTCTCCCT 604
Db 2 CTCCAGCGTCCCAT 17

RESULT 1212
AX214608/c
LOCUS AX214608 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 50 from Patent WO0159103.
ACCESSION AX214608
VERSION AX214608.1 GI:15524651
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 50 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 888 GCCCAGGTCGCCCTG 903
Db 16 GCCCAGGAGGCCCTG 1

RESULT 1213
AX215070/c
LOCUS AX215070 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 512 from Patent WO0159103.
ACCESSION AX215070
VERSION AX215070.1 GI:15525113
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 512 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1330 TTTCACAGGAAGTTTG 1345
Db 17 TTTCACAGGAAGTTTG 2

RESULT 1214
AX215071/c
LOCUS AX215071 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 513 from Patent WO0159103.
ACCESSION AX215071
VERSION AX215071.1 GI:15525114
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 513 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source
1. .17
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1329 CTTTCACAGGAAGTTT 1344
Db 16 CTTTCACAGGAAGTTT 1

RESULT 1215
AX215501/c
LOCUS AX215501 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 943 from Patent WO0159103.
ACCESSION AX215501
VERSION AX215501.1 GI:15525544
```

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 943 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 388 CACAGCGAGGGCTCC 403
||| ||||| ||||| |||||
Db 2 CAAGCGAGGGCTCC 17

RESULT 1216
AX215502/c AX215502 17 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 944 from Patent WO0159103.
DEFINITION AX215502
ACCESSION AX215502
VERSION AX215502.1 GI:15525545
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 944 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 888 GCCCGAGGAGCCCTG 903
||||| ||||| ||||| |||||
Db 17 GCCCGAGGAGCCCTG 2

RESULT 1217
AX216917 AX216917 17 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 2359 from Patent WO0159103.
DEFINITION AX216917
ACCESSION AX216917
VERSION AX216917.1 GI:15526978
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 2361 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1. .17
/organism="synthetic construct"

JOURNAL Patent: WO 0159103-A 2359 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 AGGAGAGGAGAGGA 876
||||| ||||| ||||| |||||
Db 1 AAGAGAGGAGGAGGA 16

RESULT 1219
AX216919 AX216919 17 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 2361 from Patent WO0159103.
DEFINITION AX216919
ACCESSION AX216919
VERSION AX216919.1 GI:15526980
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression

JOURNAL Patent: WO 0159103-A 2361 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)

FEATURES
source 1. .17
/organism="synthetic construct"

```
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 863 GAAGAGGAGGAGGAGG 878
Db 1 GAAGAGGAGGAGGAGG 16

RESULT 1220
AX216926
LOCUS AX216926 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2368 from Patent WO0159103.
ACCESSION AX216926
VERSION AX216926.1 GI:15526987
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2368 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 863 GAAGAGGAGGAGGAGG 878
Db 1 GAAGAGGAGGAGGAGG 16

RESULT 1221
AX216975
LOCUS AX216975 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2417 from Patent WO0159103.
ACCESSION AX216975
VERSION AX216975.1 GI:15527036
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2417 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 863 GAAGAGGAGGAGGAGG 878
Db 1 GAAGAGGAGGAGGAGG 16

RESULT 1222
AX216975
LOCUS AX216975 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 2417 from Patent WO0159103.
ACCESSION AX216975
VERSION AX216975.1 GI:15527036
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 2417 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 863 GAAGAGGAGGAGGAGG 878
Db 1 GAAGAGGAGGAGGAGG 16

RESULT 1223
AX218303
LOCUS AX218303 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3745 from Patent WO0159103.
ACCESSION AX218303
VERSION AX218303.1 GI:15528364
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3745 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 858 TGCAGGAGGAGGAGGA 873
Db 1 TCCAGAGAGGAGGAGGA 16

RESULT 1224
AX218303
LOCUS AX218303 17 bp RNA linear PAT 07-SEP-2001
DEFINITION Sequence 3745 from Patent WO0159103.
ACCESSION AX218303
VERSION AX218303.1 GI:15528364
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B.M.
TITLE Method and reagent for the modulation and diagnosis of cd20 and
nogo gene expression
JOURNAL Patent: WO 0159103-A 3745 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US);
McSwiggen, James (US); Chowrira, Bharat M. (US)
FEATURES
source
1. .17
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 861 AGGAGAGGAGGAGGAGGA 876
Db 1 AAGAGAGGAGGAGGAGGA 16

RESULT 1224
```

AX227355	LOCUS	AX227355	17 bp	RNA	linear	PAT 10-SEP-2001
AX227355	DEFINITION	Sequence 727 from Patent WO0157206.				
AX227355	ACCESSION	AX227355				
AX227355.1	VERSION	AX227355.1	GI:15556496			
	KEYWORDS	synthetic construct				
	SOURCE	synthetic construct				
	ORGANISM	artificial sequences.				
REFERENCE		1				
AUTHORS		Fattaey A.R., Jarvis T., Mcswiggen J., Boohar R.N. and Holman P.S.				
TITLE		Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme				
JOURNAL		Patent: WO 0157206-A 727 '09-AUG-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="synthetic construct"				
		/mol_type="unassigned RNA"				
		/db_xref="taxon:32630"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	129	GACCGCTGCTGCAGT 144				
Db	2	GACAGCTGTCAGGAGT 17				
RESULT 1225						
AX226655/c	LOCUS	AX226655	17 bp	DNA	linear	PAT 26-OCT-2001
DEFINITION		Sequence 4046 from Patent WO0173002.				
ACCESSION		AX226655				
VERSION		AX226655.1	GI:16515454			
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1				
AUTHORS		Kniec E.B., Gamper H.B. and Rice M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4046 04-OCT-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCTGCAAGG 1534				
Db	17	CACATCTTCTGCAAG 2				
RESULT 1226						
AX226656	LOCUS	AX226656	17 bp	DNA	linear	PAT 26-OCT-2001
DEFINITION		Sequence 4047 from Patent WO0173002.				
ACCESSION		AX226656				
VERSION		AX226656.1	GI:16515455			
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1				
AUTHORS		Kniec E.B., Gamper H.B. and Rice M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4046 04-OCT-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCTGCAAGG 1534				
Db	17	CACATCTTCTGCAAG 2				
REFERENCE		1				
AUTHORS		Kniec E.B., Gamper H.B. and Rice M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4051 04-OCT-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCT				

AX227355	LOCUS	AX227355	17 bp	RNA	linear	PAT 10-SEP-2001
AX227355	DEFINITION	Sequence 727 from Patent WO0157206.				
AX227355	ACCESSION	AX227355				
AX227355.1	VERSION	AX227355.1	GI:15556496			
	KEYWORDS	synthetic construct				
	SOURCE	synthetic construct				
	ORGANISM	artificial sequences.				
REFERENCE		1				
AUTHORS		Fattaey A.R., Jarvis T., Mcswiggen J., Boohar R.N. and Holman P.S.				
TITLE		Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme				
JOURNAL		Patent: WO 0157206-A 727 '09-AUG-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="synthetic construct"				
		/mol_type="unassigned RNA"				
		/db_xref="taxon:32630"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	129	GACCGCTGCTGCAGT 144				
Db	2	GACAGCTGTCAGGAGT 17				
RESULT 1225						
AX226655/c	LOCUS	AX226655	17 bp	DNA	linear	PAT 26-OCT-2001
DEFINITION		Sequence 4046 from Patent WO0173002.				
ACCESSION		AX226655				
VERSION		AX226655.1	GI:16515454			
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1				
AUTHORS		Kniec E.B., Gamper H.B. and Rice M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4046 04-OCT-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCTGCAAGG 1534				
Db	17	CACATCTTCTGCAAG 2				
RESULT 1226						
AX226656	LOCUS	AX226656	17 bp	DNA	linear	PAT 26-OCT-2001
DEFINITION		Sequence 4047 from Patent WO0173002.				
ACCESSION		AX226656				
VERSION		AX226656.1	GI:16515455			
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1				
AUTHORS		Kniec E.B., Gamper H.B. and Rice M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4047 04-OCT-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCTGCAAGG 1534				
Db	17	CACATCTTCTGCAAG 2				
REFERENCE		1				
AUTHORS		Kniec E.B., Gamper H.B. and Rice M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4047 04-OCT-2001;				
FEATURES		1. .17				
source		Location/Qualifiers				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCT				

AX227355	LOCUS	AX227355	17 bp	RNA	linear	PAT 10-SEP-2001
AX227355	DEFINITION	Sequence 727 from Patent WO0157206.				
AX227355	ACCESSION	AX227355				
AX227355.1	VERSION	AX227355.1	GI:15556496			
	KEYWORDS	synthetic construct				
	SOURCE	synthetic construct				
	ORGANISM	artificial sequences.				
REFERENCE		1				
AUTHORS		Fattaey A.R., Jarvis T., Mcswiggen J., Boohar R.N. and Holman P.S.				
TITLE		Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme				
JOURNAL		Patent: WO 0157206-A 727 '09-AUG-2001;				
		RIBOZYME PHARMACEUTICALS, INC. (US); Fattaey, Ali R. (US)				
FEATURES		Location/Qualifiers				
source		1..17				
		/organism="synthetic construct"				
		/mol_type="unassigned RNA"				
		/db_xref="taxon:32630"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	129	GACCGCTGCTGCAGT 144				
Db	2	GACAGCTGTCAGGAGT 17				
RESULT 1225						
AX226655/c	LOCUS	AX226655	17 bp	DNA	linear	PAT 26-OCT-2001
DEFINITION		Sequence 4046 from Patent WO0173002.				
ACCESSION		AX226655				
VERSION		AX226655.1	GI:16515454			
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1				
AUTHORS		Kniec, E.B., Gamper, H.B. and Rice, M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4046 04-OCT-2001;				
		UNIVERSITY OF DELAWARE (US)				
FEATURES		Location/Qualifiers				
source		1..17				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCTGCAAGG 1534				
Db	17	CACATCTTCTGCAAG 2				
RESULT 1226						
AX226656	LOCUS	AX226656	17 bp	DNA	linear	PAT 26-OCT-2001
DEFINITION		Sequence 4047 from Patent WO0173002.				
ACCESSION		AX226656				
VERSION		AX226656.1	GI:16515455			
KEYWORDS		Homo sapiens (human)				
SOURCE		Homo sapiens				
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1				
AUTHORS		Kniec, E.B., Gamper, H.B. and Rice, M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4047 04-OCT-2001;				
		UNIVERSITY OF DELAWARE (US)				
FEATURES		Location/Qualifiers				
source		1..17				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				
Query Match		0.7%; Score 12.8; DB 1; Length 17;				
Best Local Similarity		87.5%; Pred. No. 9e+02;				
Matches		14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	1519	CACATCTTCTGCAAGG 1534				
Db	17	CACATCTTCTGCAAG 2				
REFERENCE		1				
AUTHORS		Kniec, E.B., Gamper, H.B. and Rice, M.C.				
TITLE		Targeted chromosomal genomic alterations with modified single stranded oligonucleotides				
JOURNAL		Patent: WO 0173002-A 4047 04-OCT-2001;				
		UNIVERSITY OF DELAWARE (US)				
FEATURES		Location/Qualifiers				
source		1..17				
		/organism="Homo sapiens"				
		/mol_type="unassigned DNA"				
		/db_xref="taxon:9606"				


```

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1519 CACATCTTGTGCAAGG 1534
||||| |||||
2 CACATCTTGTGCAAG 17

RESULT 1229
LOCUS AX272708 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 277 from Patent WO0162911.
ACCESSION AX272708
VERSION AX272708.1 GI:16545445
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 277 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 205 AGAGCCCTCAGGGGA 220
||||| |||||
1 AGAGCTCCCGAGGGA 16

RESULT 1230
AX272803/c
LOCUS AX272803 17 bp RNA linear PAT 29-OCT-2001
DEFINITION Sequence 372 from Patent WO0162911.
ACCESSION AX272803
VERSION AX272803.1 GI:16545540
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and
Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 372 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1136 CATATTGCGAGGCTG 1151
||||| |||||

```


Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 859 GCAGGAGGAGGAG 874
Db 2 GGAGGAGGAGGAG 17

RESULT 1238
AX423702

LOCUS AX423702 17 bp RNA linear PAT 18-JUN-2002
DEFINITION Sequence 2038 from Patent WO0188124.
ACCESSION AX423702
VERSION AX423702.1 GI:21527084
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Rardi, A.M.
TITLE Method and reagent for the inhibition of erg
JOURNAL Patent: WO 0188124-A 2038 22-NOV-2001;
RIBOZYME PHARMACEUTICALS, INC. (US); GLAXO GROUP LIMITED (GB)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 861 AGGAGAGGAGGAG 876
Db 2 AGGAGAGGAGGAG 17

RESULT 1239
AX475040/c

LOCUS AX475040 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 261 from Patent WO0224750.
ACCESSION AX475040
VERSION AX475040.1 GI:22214325
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 261 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 887 GCGCCAGGTCCT 902
Db 17 GCGCCAGGTCGAGCT 2

RESULT 1240
AX475041/c

LOCUS AX475041 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 262 from Patent WO0224750.
ACCESSION AX475041
VERSION AX475041.1 GI:22214326
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 262 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 887 GCGCCAGGTCCT 902
Db 16 GCGCCAGGTCGAGCT 1

RESULT 1241
AX475564/c

LOCUS AX475564 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 785 from Patent WO0224750.
ACCESSION AX475564
VERSION AX475564.1 GI:22214849
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL Patent: WO 0224750-A 785 28-MAR-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; Mismatches 0; Indels 2; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1676 TTGTCCCAATGCTG 1691
Db 17 TTGGCACCNAATGCG 2

RESULT 1242
AX475565/c

LOCUS AX475565 17 bp DNA linear PAT 12-AUG-2002
DEFINITION Sequence 786 from Patent WO0224750.
ACCESSION AX475565
VERSION AX475565.1 GI:22214850
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Zhang, J.

```

TITLE      Human kidney tumor overexpressed membrane protein 1
JOURNAL    Patent: WO 0224750-A 786 28-MAR-2002;
           Aeomica, Inc. (US)
FEATURES   source
           1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1676 TTGTCAACCAATGCTG 1691
DB 16 TTGGCACCNAATGCAG 1

RESULT 1243
AX499076
LOCUS      AX499076      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 383 from Patent EP1229046.
ACCESSION  AX499076
VERSION     AX499076.1 GI:23381369
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 383 07-AUG-2002;
           Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
           source
           1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 855 CCTGCAGGAAGAGGA 870
DB 2 CCTGCCGGAGGAGGA 17

RESULT 1244
AX499078
LOCUS      AX499078      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 385 from Patent EP1229046.
ACCESSION  AX499078
VERSION     AX499078.1 GI:23381371
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 385 07-AUG-2002;
           Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
           source
           1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 855 CCTGCAGGAAGAGGA 870
DB 2 CCTGCCGGAGGAGGA 17

RESULT 1244
AX499157
LOCUS      AX499157      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 464 from Patent EP1229046.
ACCESSION  AX499157
VERSION     AX499157.1 GI:23381450
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 464 07-AUG-2002;
           Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
           source
           1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 81 AGGTCCGGGACGAG 96
DB 17 AGGTCCGGGACGAG 2

RESULT 1246
AX499157
LOCUS      AX499157      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 464 from Patent EP1229046.
ACCESSION  AX499157
VERSION     AX499157.1 GI:23381450
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Zhan, J.
TITLE       Human testis expressed patched like protein
JOURNAL     Patent: EP 1229046-A 464 07-AUG-2002;
           Aeomica, Inc. (US)
FEATURES    Location/Qualifiers
           source
           1..17
           /organism="Homo sapiens"
           /mol_type="unassigned DNA"
           /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 81 AGGTCCGGGACGAG 96
DB 17 AGGTCCGGGACGAG 2

RESULT 1247
AX499339
LOCUS      AX499339      17 bp      DNA      linear      PAT 27-SEP-2002
DEFINITION Sequence 646 from Patent EP1229046.

```

ACCESSION AX499339	VERSION AX499339.1	GI:23381632
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	Zhan,J. Human testis expressed patched like protein Patent: EP 1229046-A 646 07-AUG-2002;	
AUTHORS	Aeomica, Inc. (US)	
TITLE	Human testis expressed patched like protein	
JOURNAL		
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	853 GGCCCTGCAGGAGCG 868	
Db	17 GGCCCTGCAGGAGCG 2	
RESULT 1248		
AX499685/c		
LOCUS	AX499685	17 bp DNA linear PAT 27-SEP-2002
DEFINITION	Sequence 992 from Patent EP1229046.	
ACCESSION	AX499685	
VERSION	AX499685.1	GI:23381978
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Zhan,J. Human testis expressed patched like protein Patent: EP 1229046-A 992 07-AUG-2002;	
AUTHORS	Aeomica, Inc. (US)	
TITLE	Human testis expressed patched like protein	
JOURNAL		
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	181 CCCCCGAAGCAGCGG 196	
Db	17 CCTCCGAAGAGCGCG 2	
RESULT 1249		
AX499686/c		
LOCUS	AX499686	17 bp DNA linear PAT 27-SEP-2002
DEFINITION	Sequence 993 from Patent EP1229046.	
ACCESSION	AX499686	
VERSION	AX499686.1	GI:23381979
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Zhan,J. Human testis expressed patched like protein Patent: EP 1229046-A 993 07-AUG-2002;	
AUTHORS	Aeomica, Inc. (US)	
TITLE	Human testis expressed patched like protein	
JOURNAL		
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	181 CCCCCGAAGCAGCGG 196	
Db	17 CCTCCGAAGAGCGCG 2	
RESULT 1250		
AX531314/c		
LOCUS	AX531314	17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 823 from Patent EP1239051.	
ACCESSION	AX531314	
VERSION	AX531314.1	GI:25254414
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Shannon,M. Human posh-like protein 1 Patent: EP 1239051-A 823 11-SEP-2002;	
AUTHORS	Aeomica, Inc. (US)	
TITLE	Human posh-like protein 1	
JOURNAL		
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	402 CCCTGCAGAGCGGGG 417	
Db	17 CCCTGCAGAGCGGGG 2	
RESULT 1251		
AX531315/c		
LOCUS	AX531315	17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 824 from Patent EP1239051.	
ACCESSION	AX531315	
VERSION	AX531315.1	GI:25254416
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Shannon,M. Human posh-like protein 1 Patent: EP 1239051-A 824 11-SEP-2002;	
AUTHORS	Aeomica, Inc. (US)	
TITLE	Human posh-like protein 1	
JOURNAL		
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	402 CCCTGCAGAGCGGGG 417	
Db	17 CCCTGCAGAGCGGGG 2	
RESULT 1252		
AX531316/c		
LOCUS	AX531316	17 bp DNA linear PAT 22-NOV-2002
DEFINITION	Sequence 824 from Patent EP1239051.	
ACCESSION	AX531316	
VERSION	AX531316.1	GI:25254416
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Shannon,M. Human posh-like protein 1 Patent: EP 1239051-A 824 11-SEP-2002;	
AUTHORS	Aeomica, Inc. (US)	
TITLE	Human posh-like protein 1	
JOURNAL		
FEATURES	Location/Qualifiers	
source	1..17	
	/organism="Homo sapiens"	
	/mol_type="unassigned DNA"	
	/db_xref="taxon:9606"	
Query Match	0.7%; Score 12.8; DB 1; Length 17;	
Best Local Similarity	87.5%; Pred. No. 9e+02;	
Matches	14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	402 CCCTGCAGAGCGGGG 417	
Db	17 CCCTGCAGAG	

[illegible][illegible]

QY 402 CCTGCAGACAGGGG 417
Db 16 CCTGCAGACGGGG 1

RESULT 1252
AX531999/c
LOCUS AX531999 17 bp DNA linear PAT 22-NOV-2002
DEFINITION Sequence 1508 from Patent EP1239051.
ACCESSION AX531999
VERSION AX531999.1 GI:25255764
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Shannon, M.
TITLE Human posh-like protein 1
JOURNAL Patent: EP 1239051-A 1508 11-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 893 AGTGCCCTGAGCCA 908
Db 16 AGAGCCCTGAGCCA 1

RESULT 1253
AX544714/c
LOCUS AX544714 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 227 from Patent EP1243660.
ACCESSION AX544714
VERSION AX544714.1 GI:25809925
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 227 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1026 TGGGGCTGGGTGTG 1041
Db 17 TGGGGCTGGGTGTG 2

RESULT 1254
AX544718/c
LOCUS AX544718 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 231 from Patent EP1243660.
ACCESSION AX544718
VERSION AX544718.1 GI:25809929

KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 231 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1023 GGATGGGCTGGGTT 1038
Db 16 GGATGGGCTGGGCT 1

RESULT 1255
AX544738/c
LOCUS AX544738 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 251 from Patent EP1243660.
ACCESSION AX544738
VERSION AX544738.1 GI:25809949
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 251 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 119 GGGCTTCAGACCGC 134
Db 17 GGGCTTCAGACCGC 2

RESULT 1256
AX544739/c
LOCUS AX544739 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 252 from Patent EP1243660.
ACCESSION AX544739
VERSION AX544739.1 GI:25809950
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 252 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 119 GGGGCTTCAAGACCGC 134
||| ||||| |||||
Db 16 GCGGCTTCAGGACCGC 1

RESULT 1257
AX544743
LOCUS AX544743 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 256 from Patent EP1243660.
ACCESSION AX544743
VERSION AX544743.1 GI:25809954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 256 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1535 CTGCAGCGCCTGGCG 1550
||| ||||| |||||
Db 2 CTGAAGCGCCTGTGCG 17

RESULT 1258
AX544745
LOCUS AX544745 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 258 from Patent EP1243660.
ACCESSION AX544745
VERSION AX544745.1 GI:25809956
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 258 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1536 CTGCAGCGCCTGGCG 1551
||| ||||| |||||
```

```
Db 1 CTGAAGCGCCTGTGCG 16

RESULT 1259
AX545140
LOCUS AX545140 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 653 from Patent EP1243660.
ACCESSION AX545140
VERSION AX545140.1 GI:25810351
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 653 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAAGAGGGGTGAAGG 108
||| ||||| |||||
Db 2 GAAGAGGAGCTGAAGG 17

RESULT 1260
AX545141
LOCUS AX545141 17 bp DNA linear PAT 26-NOV-2002
DEFINITION Sequence 654 from Patent EP1243660.
ACCESSION AX545141
VERSION AX545141.1 GI:25810352
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Zhang, J., Gu, Y. and Nguyen, C.T.
TITLE Human udp-galnac:polypeptide n-acetylgalatosaminyltransferase 10
JOURNAL Patent: EP 1243660-A 654 25-SEP-2002;
Aeomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 93 GAAGAGGGGTGAAGG 108
||| ||||| |||||
Db 1 GAAGAGGAGCTGAAGG 16

RESULT 1261
AX547276
LOCUS AX547276 17 bp DNA linear PAT 01-MAR-2003
DEFINITION Sequence 415 from Patent WO2053141.
ACCESSION AX547276
VERSION AX547276.1 GI:25812420
KEYWORDS
SOURCE synthetic construct
```

ORGANISM synthetic construct
artificial sequences.
1
AUTHORS Bratzler,R.L.
TITLE Inhibition of angiogenesis by nucleic acids
JOURNAL Patent: WO 02053141-A 415 11-JUL-2002;
Coley Pharmaceutical Group, Inc. (US)
FEATURES Location/Qualifiers
source
1..17
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic Sequence"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 589 CTCCCAGCGTCTCCCT 604
Db 2 CTCCCAGCGTCGCGCAT 17

RESULT 1262
AX579179
LOCUS AX579179 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1017 from Patent WO0211674.
ACCESSION AX579179
VERSION AX579179.1 GI:27648381
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1017 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1481 CTGAGGCGCAGTGTC 1496
Db 1 CTCAGGCGCAGTGTC 16

RESULT 1263
AX579725
LOCUS AX579725 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 1563 from Patent WO0211674.
ACCESSION AX579725
VERSION AX579725.1 GI:27648927
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Thompson,J., Mcswiggen,J., Mckenzie,T., Ayers,D., Szymkowski,D.E.
and Grupe,A.
TITLE Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)

JOURNAL Patent: WO 0211674-A 1563 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1480 TCTGAGGCGCAGTGTC 1495
Db 2 TCTCAGGCGCAGTGTC 17

RESULT 1264
AX615976
LOCUS AX615976 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 783 from Patent EP1262488.
ACCESSION AX615976
VERSION AX615976.1 GI:28447022
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Gu,Y. and Nguyen,C.T.
TITLE Human lcc1-domain containing protein
JOURNAL Patent: EP 1262488-A 783 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 CCAGTGCCCTGAGC 906
Db 2 CCAGTGCCACAGAC 17

RESULT 1265
AX615977
LOCUS AX615977 17 bp DNA linear PAT 20-FEB-2003
DEFINITION Sequence 784 from Patent EP1262488.
ACCESSION AX615977
VERSION AX615977.1 GI:28447023
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Gu,Y. and Nguyen,C.T.
TITLE Human lcc1-domain containing protein
JOURNAL Patent: EP 1262488-A 784 04-DEC-2002;
Aeomica, Inc. (US)
FEATURES Location/Qualifiers
source
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 891 CCAGTGCCCTGAGC 906
Db 2 CCAGTGCCACAGAC 17

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 891 CCAGTGCCTGAGC 906
 |||||
 Db 1 CCAGTGCACAGAGC 16

RESULT 1266
 AX634583/c
 LOCUS
 DEFINITION Sequence 1722 from Patent EP1260586.
 AX634583
 ACCESSION
 VERSION AX634583.1 GI:28470197
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified
 unclassified

REFERENCE 1
 AUTHORS
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
 Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
 Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
 Woolf,T.

TITLE
 Method and reagent for inhibiting the expression of disease related
 genes

JOURNAL
 Patent: EP 1260586-A 1722 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
 source
 1. 17
 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAGGAG 877
 |||||
 Db 17 GCAAGAGGAGGAGC 2

RESULT 1267
 AX634733/c
 LOCUS
 DEFINITION Sequence 1872 from Patent EP1260586.
 AX634733
 ACCESSION
 VERSION AX634733.1 GI:28470347
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified
 unclassified

REFERENCE 1
 AUTHORS
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
 Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
 Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
 Woolf,T.

TITLE
 Method and reagent for inhibiting the expression of disease related
 genes

JOURNAL
 Patent: EP 1260586-A 1872 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
 source
 1. 17
 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAGGAG 877
 |||||
 Db 17 GCAAGAGGAGGAGC 2

Db 16 GCAAGAGGAGGAGC 1
 |||||
 RESULT 1268
 AX634815/c
 LOCUS
 DEFINITION Sequence 1954 from Patent EP1260586.
 AX634815
 ACCESSION
 VERSION AX634815.1 GI:28470429
 KEYWORDS
 SOURCE
 ORGANISM
 unclassified
 unclassified

REFERENCE 1
 AUTHORS
 Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A.,
 Karpelisky,A., Draper,K.G., Kisch,K., Matulic-Adamic,J.,
 Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
 Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
 Woolf,T.

TITLE
 Method and reagent for inhibiting the expression of disease related
 genes

JOURNAL
 Patent: EP 1260586-A 1954 27-NOV-2002;
 RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
 source
 1. 17
 /organism="unidentified"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 862 GGAAGAGGAGGAG 877
 |||||
 Db 16 GCAAGAGGAGGAGC 1

RESULT 1269
 AX648952/c
 LOCUS
 DEFINITION Sequence 792 from Patent EP1273660.
 AX648952
 ACCESSION
 VERSION AX648952.1 GI:29151770
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens

REFERENCE 1
 AUTHORS
 Gu, Y.
 TITLE
 Human sodium-hydrogen exchanger like protein 1
 JOURNAL
 Patent: EP 1273660-A 792 08-JAN-2003;
 Asomica, Inc. (US)

FEATURES
 source
 1. 17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
 Best Local Similarity 87.5%; Pred. No. 9e+02;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1698 CTTCTCCATCAGA 1713
 |||||
 Db 17 CTTCTCCAAACAAGA 2

RESULT 1270
 AX648953/c
 LOCUS
 AX648953
 17 bp DNA linear PAT 22-MAR-2003

```

DEFINITION Sequence 793 from Patent EP1273660.
ACCESSION AX648953
VERSION AX648953.1 GI:29151771
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gu, Y.
TITLE Human sodium-hydrogen exchanger like protein 1
JOURNAL Patent: EP 1273660-A 793 08-JAN-2003;
FEATURES
source
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1698 CTTCTCTCCAATCAAGA 1713
Db 16 CTCTCTCCAACAAGA 1

RESULT 1271
AX672939/c
LOCUS AX672939 17 bp DNA linear PAT 27-MAR-2003
DEFINITION Sequence 1384 from Patent WO03004526.
ACCESSION AX672939
VERSION AX672939.1 GI:29331287
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1384 16-JAN-2003;
FEATURES
source
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 326 AGGCCCCAGGGGACC 341
Db 16 AGGCCCCAGTGGGATC 1

RESULT 1272
AX673204/c
LOCUS AX673204 17 bp DNA linear PAT 29-MAR-2003
DEFINITION Sequence 1649 from Patent WO03004526.
ACCESSION AX673204
VERSION AX673204.1 GI:29331552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and their use as
medicines
JOURNAL Patent: WO 03004526-A 1649 16-JAN-2003;
FEATURES
source
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 853 GGCCCTGCAGGAAGAG 868
Db 1 GGCCCTGCAGGCAGTG 16

RESULT 1273
AX688348
LOCUS AX688348 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1080 from Patent EP1281758.
ACCESSION AX688348
VERSION AX688348.1 GI:29411048
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 1080 05-FEB-2003;
FEATURES
source
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 184 CCGAAGCAGCCGGAGC 199
Db 16 CCGAAGCAGCGGATC 1

RESULT 1274
AX688601/c
LOCUS AX688601 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1333 from Patent EP1281758.
ACCESSION AX688601
VERSION AX688601.1 GI:29411303
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
mdz12
JOURNAL Patent: EP 1281758-A 1333 05-FEB-2003;
FEATURES
source

```

Db 2 ACAAGTGGCGGACTG 17

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 387 GCACACGCGGGCTC 402
Db 17 GCACACGTAGGCGCTC 2

RESULT 1275
AX688602/c
LOCUS AX688602 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1334 from Patent EP1281758.
ACCESSION AX688602
VERSION AX688602.1 GI:29411304
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1334 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 387 GCACACGCGGGCTC 402
Db 16 GCACACGTAGGCGCTC 1

RESULT 1276
AX688693
LOCUS AX688693 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1425 from Patent EP1281758.
ACCESSION AX688693
VERSION AX688693.1 GI:29411397
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1425 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1448 ACAAGTGGCGGACTG 1463
Db 1 ACAAGTGGCGGACTG 16

RESULT 1278
AX688740
LOCUS AX688740 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1472 from Patent EP1281758.
ACCESSION AX688740
VERSION AX688740.1 GI:29411444
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12
JOURNAL Patent: EP 1281758-A 1472 05-FEB-2003;
Aeomica, Inc. (US)
FEATURES
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match
Best Local Similarity 0.7%; Score 12.8; DB 1; Length 17;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 332 CAGGTGACCGGAGGA 347
Db 2 CAGGTGACCGGAGGA 17

RESULT 1279
AX688741
LOCUS AX688741 17 bp DNA linear PAT 31-MAR-2003
DEFINITION Sequence 1473 from Patent EP1281758.
ACCESSION AX688741
VERSION AX688741.1 GI:29411445

```
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 1473 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      332 CAGGGGACCGGAGGA 347
Db      1 CAGGTGACCGGAGGA 16

RESULT 1280
AX690554
LOCUS      AX690554
DEFINITION Sequence 3286 from Patent EP1281758.
ACCESSION  AX690554
VERSION     AX690554.1 GI:29413435
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 3286 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      133 GCTGTCGAGTCCCC 148
Db      2 GCTATCAGGAGTCCCC 17

RESULT 1281
AX690555
LOCUS      AX690555
DEFINITION Sequence 3287 from Patent EP1281758.
ACCESSION  AX690555
VERSION     AX690555.1 GI:29413436
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 4015 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

JOURNAL      Patent: EP 1281758-A 3287 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      657 AGCCTTCCCGTGCAA 672
Db      2 AGCCTTACCAGTGCAA 17

RESULT 1283
AX691283
LOCUS      AX691283
DEFINITION Sequence 4015 from Patent EP1281758.
ACCESSION  AX691283
VERSION     AX691283.1 GI:29414219
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 4015 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      657 AGCCTTCCCGTGCAA 672
Db      2 AGCCTTACCAGTGCAA 17

RESULT 1283
AX691283
LOCUS      AX691283
DEFINITION Sequence 4015 from Patent EP1281758.
ACCESSION  AX691283
VERSION     AX691283.1 GI:29414219
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS     Shannon,M., Gu,Y. and Nguyen,C.T.
TITLE       Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
JOURNAL      Patent: EP 1281758-A 4015 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES
source      1. .17
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 657 AGCCTTCCCCGCGCAA 672
|||||

Db 1 AGCCTTACCAGTCACA 16
|||||

RESULT 1284

AX692609 17 bp DNA linear PAT 31-MAR-2003

LOCUS AX692609 Sequence 5341 from Patent EP1281758.

DEFINITION AX692609

ACCESSION AX692609

VERSION AX692609.1 GI:29415567

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE Shannon, M., Gu, Y. and Nguyen, C.T.

JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

mdz12

Patent: EP 1281758-A 5341 05-FEB-2003;

Aeomica, Inc. (US)

FEATURES Location/Qualifiers

source 1..17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1605 ACCCTGCGGTTCTCA 1620
|||||

Db 2 ACCCTGCGGTTCTCA 17
|||||

RESULT 1285

AX692610 17 bp DNA linear PAT 31-MAR-2003

LOCUS AX692610 Sequence 5342 from Patent EP1281758.

DEFINITION AX692610

ACCESSION AX692610

VERSION AX692610.1 GI:29415568

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

TITLE Shannon, M., Gu, Y. and Nguyen, C.T.

JOURNAL Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and

mdz12

Patent: EP 1281758-A 5342 05-FEB-2003;

Aeomica, Inc. (US)

FEATURES Location/Qualifiers

source 1..17

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1605 ACCCTGCGGTTCTCA 1620
|||||

Db 1 ACCCTGCGGTTCTCA 16
|||||

RESULT 1286

AX698570/c 17 bp DNA linear PAT 02-APR-2003

LOCUS AX698570 Sequence 59 from Patent WO03010335.

DEFINITION AX698570

ACCESSION AX698570

VERSION AX698570.1 GI:29499398

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE artificial sequences.

AUTHORS 1 Mirel, D.B., Erlich, H.A., Bugawan, T.L., Noble, J.A. and Valdez, A.M.

TITLE IL-4 receptor sequence variation associated with type 1 diabetes

JOURNAL Patent: WO 03010335-A 59 06-FEB-2003;

Roche Diagnostics GmbH (DE); F. HOFMANN-LA ROCHE AG (CH)

FEATURES Location/Qualifiers

source 1..17

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="allele specific PCR primer"

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 899 CCCTGAGCCAGCCTCC 914
|||||

Db 16 CCCTGAGCCAGTCACC 1
|||||

RESULT 1287

AX723024 17 bp DNA linear PAT 08-MAY-2003

LOCUS AX723024 Sequence 711 from Patent WO03025176.

DEFINITION AX723024

ACCESSION AX723024

VERSION AX723024.1 GI:30423525

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Telesman, A., Amson, R. and Tuijinder, M.

JOURNAL Sequences involved in phenomena of tumour suppression, tumour

reversion, apoptosis and/or virus resistance and their use as

medicines

Patent: WO 03025176-A 711 27-MAR-2003;

Molecular Engines Laboratories (FR)

FEATURES Location/Qualifiers

source 1..17

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 9e+02;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 88 GGACGGAAGAGGGGT 103
|||||

Db 17 GGACGGAAGAGGGGAT 2
|||||

RESULT 1288

AX723728 17 bp DNA linear PAT 08-MAY-2003

LOCUS AX723728 Sequence 1415 from Patent WO03025176.

DEFINITION AX723728

ACCESSION AX723728

VERSION AX723728.1 GI:30503071

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE Telesman, A., Amson, R. and Tuijinder, M.

JOURNAL Sequences involved in phenomena of tumour suppression, tumour

reversion, apoptosis and/or virus resistance and their use as

medicines

Patent: WO 03025176-A 711 27-MAR-2003;

Molecular Engines Laboratories (FR)

FEATURES Location/Qualifiers

source 1..17

/organism="Mus musculus"

/mol_type="unassigned DNA"

/db_xref="taxon:10090"

REFERENCE 1 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 1415 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1206 GATCTCTCGGGGCTATG 1221
DB 1 GATCTCTCGGGGAGATG 16

RESULT 1289
LOCUS AX724111 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 1798 from Patent WO03025176.
ACCESSION AX724111
VERSION AX724111.1 GI:30503454
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE 1 Telerman, A., Amson, R. and Tuijnder, M.
AUTHORS 1
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 1798 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 326 AGGCCCGAGGGGACC 341
DB 16 AGGACCCAGGGGATC 1

RESULT 1290
LOCUS AX724397 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2084 from Patent WO03025176.
ACCESSION AX724397
VERSION AX724397.1 GI:30503740
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE 1 Telerman, A., Amson, R. and Tuijnder, M.
AUTHORS 1
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2084 27-MAR-2003;

FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1311 GATCCACTGTATTGAG 1326
DB 1 GATCTCTGTATTGAG 16

RESULT 1291
LOCUS AX724919 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2606 from Patent WO03025176.
ACCESSION AX724919
VERSION AX724919.1 GI:30504262
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE 1 Telerman, A., Amson, R. and Tuijnder, M.
AUTHORS 1
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2606 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1311 GATCCACTGTATTGAG 1326
DB 1 GATCTACTATTATTGAG 16

RESULT 1292
LOCUS AX725040 17 bp DNA linear PAT 08-MAY-2003
DEFINITION Sequence 2727 from Patent WO03025176.
ACCESSION AX725040
VERSION AX725040.1 GI:30504383
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE 1 Telerman, A., Amson, R. and Tuijnder, M.
AUTHORS 1
TITLE Sequences involved in phenomena of tumour suppression, tumour reversion, apoptosis and/or virus resistance and their use as medicines
JOURNAL Patent: WO 03025176-A 2727 27-MAR-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1. .17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 225 GATCCCCCGCGCACC 240
|||||
DB 1 GATCCCCGACGACC 16

RESULT 1293
AX725448 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3135 from Patent WO03025176.
ACCESSION AX725448
VERSION AX725448.1 GI:30504791
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3135 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1552 ATCCAGAGCTCTCAG 1567
|||||
DB 2 ATCCAGAACCTCTCAG 17

RESULT 1294
AX725848 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3535 from Patent WO03025176.
ACCESSION AX725848
VERSION AX725848.1 GI:30505191
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 3535 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 301 CCCCTTCATCTGAGC 316
|||||
DB 16 CCCCTTCAACTGATC 1

RESULT 1295
AX726840 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 4527 from Patent WO03025176.
ACCESSION AX726840
VERSION AX726840.1 GI:30506183
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 4527 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1681 ACCAATGCTGCTTC 1696
|||||
DB 2 ATCCATGCTGCTTC 17

RESULT 1296
AX727839 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 5526 from Patent WO03025176.
ACCESSION AX727839
VERSION AX727839.1 GI:30507182
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS 1 Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
JOURNAL Patent: WO 03025176-A 5526 27-MAR-2003;
Molecular Engines Laboratories (FR)
FEATURES
source Location/Qualifiers
1..17
/organism="Mus musculus"
/mol_type="unassigned DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1686 ATGCTGCTTCTCTT 1701
|||||
DB 2 ATCATGCTCTCTCTT 17

RESULT 1297
AX728077 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 5764 from Patent WO03025176.
ACCESSION AX728077

```

VERSION      AX728077.1  GI:30507420
KEYWORDS     Mus musculus (house mouse)
SOURCE       Mus musculus
ORGANISM     Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025176-A 5764 27-MAR-2003;
FEATURES     Molecular Engines Laboratories (FR)
SOURCE       Location/Qualifiers
              1. .17
              /organism="Mus musculus"
              /mol_type="unassigned DNA"
              /db_xref="taxon:10090"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      368  GGTCGATGGAGTACT 383
Db      1  GATCGATGGAGTACT 16

RESULT 1298
AX729967/c    17 bp  DNA  linear  PAT 08-MAY-2003
DEFINITION    Sequence 1601 from Patent WO03025175.
ACCESSION     AX729967
VERSION       AX729967.1  GI:30509310
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 1601 27-MAR-2003;
FEATURES     Molecular Engines Laboratories (FR)
SOURCE       Location/Qualifiers
              1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      326  AGGCCCGACGGGACG 341
Db      16  AGGCCCGACGGGATC 1

RESULT 1299
AX730062      17 bp  DNA  linear  PAT 08-MAY-2003
DEFINITION    Sequence 1696 from Patent WO03025175.
ACCESSION     AX730062
VERSION       AX730062.1  GI:30509405
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 1696 27-MAR-2003;
FEATURES     Molecular Engines Laboratories (FR)
SOURCE       Location/Qualifiers

```

```

AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 1696 27-MAR-2003;
FEATURES     Molecular Engines Laboratories (FR)
SOURCE       Location/Qualifiers
              1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1522  ATCTTGTCGAGGCGCT 1537
Db      2  ATCTTGTCGAGGCGCT 17

RESULT 1300
AX730114      17 bp  DNA  linear  PAT 08-MAY-2003
DEFINITION    Sequence 1748 from Patent WO03025175.
ACCESSION     AX730114
VERSION       AX730114.1  GI:30509457
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 1748 27-MAR-2003;
FEATURES     Molecular Engines Laboratories (FR)
SOURCE       Location/Qualifiers
              1. .17
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1644  GATCACTCTCCCTGAC 1659
Db      1  GATCTCTTCCCTGAC 16

RESULT 1301
AX730625/c    17 bp  DNA  linear  PAT 08-MAY-2003
DEFINITION    Sequence 2259 from Patent WO03025175.
ACCESSION     AX730625
VERSION       AX730625.1  GI:30509968
KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE    1
AUTHORS      Telerman,A., Amson,R. and Tuijnder,M.
TITLE        Sequences involved in phenomena of tumour suppression, tumour
              reversion, apoptosis and/or virus resistance and their use as
              medicines
JOURNAL      Patent: WO 03025175-A 2259 27-MAR-2003;
FEATURES     Molecular Engines Laboratories (FR)
SOURCE       Location/Qualifiers

```


source 1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1063 GTGGGCTGCTTGAT 1078
|||||
17 GTGGGCTGCTTGAT 2

RESULT 1302
AX731099/c 17 bp DNA linear PAT 08-MAY-2003

LOCUS AX731099
DEFINITION Sequence 2733 from Patent WO03025175.
ACCESSION AX731099
VERSION AX731099.1 GI:30510442
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
Teleman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 2733 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
AUTHORS
TITLE
LOCATION/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

JOURNAL
source

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 184 CCGAAGCAGCGGAC 199
|||||
16 CCGAAGCAGCGGATC 1

Db 16 CCGAAGCAGCGGATC 1

RESULT 1303
AX731554 17 bp DNA linear PAT 08-MAY-2003

LOCUS AX731554
DEFINITION Sequence 3188 from Patent WO03025175.
ACCESSION AX731554
VERSION AX731554.1 GI:30510897
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
Teleman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3188 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
AUTHORS
TITLE
LOCATION/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

JOURNAL
source

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1707 ATCAAGAAATATAAT 1722
|||||
2 ATCAAGAAATATAAT 17

Db 2 ATCAAGAAATATAAT 17

RESULT 1304
AX731857 17 bp DNA linear PAT 08-MAY-2003

LOCUS AX731857
DEFINITION Sequence 3491 from Patent WO03025175.
ACCESSION AX731857
VERSION AX731857.1 GI:30511200
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
Teleman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3491 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
AUTHORS
TITLE
LOCATION/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

JOURNAL
source

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1284 CCCCTTCACTGAT 1299
|||||
17 CCCCTTCACTGAT 2

Db 17 CCCCTTCACTGAT 2

RESULT 1305
AX731963 17 bp DNA linear PAT 08-MAY-2003

LOCUS AX731963
DEFINITION Sequence 3597 from Patent WO03025175.
ACCESSION AX731963
VERSION AX731963.1 GI:30511306
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1
Teleman, A., Amson, R. and Tuijnder, M.
Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or virus resistance and their use as
medicines
Patent: WO 03025175-A 3597 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
AUTHORS
TITLE
LOCATION/Qualifiers
1. .17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

JOURNAL
source

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 1306
AX735879 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 1469 from Patent WO03025177.
DEFINITION AX735879
ACCESSION AX735879
VERSION AX735879.1 GI:30515156
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 1469 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 801 GAGCCAGAGAGGCCA 816
Db 1 GATCCAGAGAGGCCA 16

RESULT 1307
AX736107 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 1697 from Patent WO03025177.
DEFINITION AX736107
ACCESSION AX736107
VERSION AX736107.1 GI:30515384
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 1697 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1011 AGATGTGTTGGGAT 1026
Db 17 AGATTGTGTGGGAT 2

RESULT 1308
AX737293 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 2883 from Patent WO03025177.
DEFINITION AX737293
ACCESSION AX737293
VERSION AX737293.1 GI:30516561
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 2883 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1311 GATCCACTGATTGAG 1326
Db 1 GATCTACTGTATGAG 16

RESULT 1309
AX737445 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 3035 from Patent WO03025177.
DEFINITION AX737445
ACCESSION AX737445
VERSION AX737445.1 GI:30516733
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour
reversion, apoptosis and/or resistance to viruses and the use
thereof as medicaments
JOURNAL Patent: WO 03025177-A 3035 27-MAR-2003;
Molecular Engines Laboratories (FR)

FEATURES
source Location/Qualifiers
1..17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 801 GAGCCAGAGAGGCCA 816
Db 1 GATCCAGAGAGGCCA 16

RESULT 1310
AX738613 17 bp DNA linear PAT 08-MAY-2003
LOCUS Sequence 4203 from Patent WO03025177.
DEFINITION AX738613
ACCESSION AX738613
VERSION AX738613.1 GI:30517903
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Telerman, A., Amson, R. and Tuijnder, M.
TITLE Sequences involved in phenomena of tumour suppression, tumour

DEFINITION Sequence 1261 from Patent WO03040369.
ACCESSION AX757940
VERSION AX757940.1 GI:32252556
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in tumoral suppression, tumor reversal, apoptosis and/or viral resistance phenomena and their use as medicines and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 1261 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 103 TGAAGGCCAGAGGCTC 118
16 TGAAGGCCAGAGGATC 1

RESULT 1316
AX759934 17 bp DNA PAT 25-JUN-2003
LOCUS AX759934 Sequence 3255 from Patent WO03040369.
DEFINITION AX759934
ACCESSION AX759934
VERSION AX759934.1 GI:32254550
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Telerman, A., Amson, R. and Tuijinder, M.
TITLE Sequences involved in tumoral suppression, tumor reversal, apoptosis and/or viral resistance phenomena and their use as medicines
JOURNAL Patent: WO 03040369-A 3255 15-MAY-2003;
FEATURES Molecular Engines Laboratories (FR)
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1552 ATCCAGAGCTTCAG 1567
2 ATCCAGAGCTTCAG 17

RESULT 1317
AX783890 17 bp DNA PAT 17-JUL-2003
LOCUS AX783890 Sequence 2221 from Patent WO03050284.
DEFINITION AX783890
ACCESSION AX783890
VERSION AX783890.1 GI:32951739
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2221 19-JUN-2003;
FEATURES Amersham Biosciences (SV) Corp. (US)
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 746 CGGGCCCCCAGCTTCC 761
2 CGGGCCCCCAGCTTCC 17

RESULT 1318
AX783891 17 bp DNA PAT 17-JUL-2003
LOCUS AX783891 Sequence 2222 from Patent WO03050284.
DEFINITION AX783891
ACCESSION AX783891
VERSION AX783891.1 GI:32951740
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2222 19-JUN-2003;
FEATURES Amersham Biosciences (SV) Corp. (US)
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 746 CGGGCCCCCAGCTTCC 761
1 CGGGCCCCCAGCTTCC 16

RESULT 1319
AX784080 17 bp DNA PAT 17-JUL-2003
LOCUS AX784080 Sequence 2411 from Patent WO03050284.
DEFINITION AX784080
ACCESSION AX784080
VERSION AX784080.1 GI:32951929
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2411 19-JUN-2003;
FEATURES Amersham Biosciences (SV) Corp. (US)
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1185 CTCCAGCCCATCTCG 1200
|||||
2 CTCCCTGCCCTCTCTG 17

RESULT 1320
AX784082 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Sequence 2413 from Patent WO03050284.
ACCESSION AX784082
VERSION AX784082.1 GI:32951931
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Guo, J.
TITLE Human prostate cancer candidate protein 1
JOURNAL Patent: WO 03050284-A 2413 19-JUN-2003;
Amersham Biosciences (SV) Corp. (US)
FEATURES
source 1.17
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1186 TCCAGCCCATCTCG 1201
|||||
1 TCCCTGCCCTCTCTG 16

RESULT 1321
BD104951 17 bp DNA linear PAT 27-AUG-2002
LOCUS BD104951
DEFINITION Kit and method for determining HLA type.
ACCESSION BD104951
VERSION BD104951.1 GI:22650525
KEYWORDS WO 0192572-A/1055.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
AUTHORS Inoko, H., Kagiya, T., Ichihara, T., Matsumura, Y., Moriya, S. and Nishida, M.
TITLE Kit and method for determining HLA type
JOURNAL Patent: WO 0192572-A 1055 06-DEC-2001;
NISHINO INDUSTRIES INC. SYSTEM RESEARCH INC. HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA, SHOGO MORIYA, MICHIO NISHIDA
COMMENT OS Artificial Sequence
PN WO 0192572-A/1055
PD 06-DEC-2001
PF 01-JUN-2001 WO 2001JP004662
PR 01-JUN-2000 JP 00P 164798
PI HIDEOTOSHI INOKO, TAEKO KAGIYA, TATSUO ICHIHARA, YOSHIYUKI MATSUMURA,
PI SHOGO MORIYA, MICHIO NISHIDA
PC C1201/68, C12M1/00, C12N15/09, G01N33/53
CC Description of Artificial Sequence: capture
FH key Location/Qualifiers
FT source 1.17
/organism="Artificial Sequence".
Location/Qualifiers

FEATURES
Location/Qualifiers

source 1.17
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 851 CTGGCCCTGCAGAG 866
|||||
17 CTGGCCCTGCAGAGT 2

RESULT 1322
BD134134 17 bp DNA linear PAT 18-SEP-2002
LOCUS BD134134
DEFINITION The helios gene.
ACCESSION BD134134
VERSION BD134134.1 GI:23229079
KEYWORDS JP 2002504357-A/4.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 17)
AUTHORS Georgopoulos, C., Morgan, B.A. and Kelly, C.
TITLE The helios gene
JOURNAL Patent: JP 2002504357-A 4 12-FEB-2002;
THE GENERAL HOSPITAL CORP
COMMENT PN Mus musculus (mouse)
PN JP 2002504357-A/4
PD 12-FEB-2002
PF 26-FEB-1999 JP 2000533017
PR 27-FEB-1998 US 60/076325
PI COTTEVA GEORGOPOULOS, BLUCE A MORGAN, CLARE KELLY PC
C12N15/09, A01K67/027, A61K31/711, A61K38/00, A61K48/00, A61P35/02, PC
A61P37/02,
PC C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10 PC
, C12P21/02, C12Q1/68,
PC C12N15/00, A61K37/02, C12N5/00
CC The helios gene
FH key Location/Qualifiers
FT source 1.17
/organism="Mus musculus (mouse)".
Location/Qualifiers

FEATURES
source 1.17
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 100 GGGTGAAGCCAGAG 115
|||||
1 GGGTGAAGCCCTCAG 16

RESULT 1323
BD200584 17 bp RNA linear PAT 17-JUL-2003
LOCUS BD200584
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD200584
VERSION BD200584.1 GI:33010354
KEYWORDS JP 2002509721-A/3610.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)

AUTHORS Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
TITLE Method and reagent for treating diseases or conditions concerning
JOURNAL molecule participating in vasculogenic response
PATENT: JP 2002509721-A 3610 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/3610
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT location/Qualifiers
/organism='Homo sapiens (human)'.
1..17
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 720 AGCCTCTGAGCTTCT 735
Db 1 AGCCTCTGCGCTTCT 16

RESULT 1324
LOCUS BD201657/c
DEFINITION 17 bp RNA linear PAT 17-JUL-2003
ACCESSION BD201657
VERSION BD201657.1 GI:33011427
KEYWORDS JP 2002509721-A/4683.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
PATENT: JP 2002509721-A 4683 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/4683
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17

FT location/Qualifiers
/organism='Homo sapiens (human)'.
1..17
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1704 CCAATCAGAAATTAAT 1719
Db 17 CTATATCATGAAATTAAT 2

RESULT 1325
LOCUS BD202792/c
DEFINITION 17 bp RNA linear PAT 17-JUL-2003
ACCESSION BD202792
VERSION BD202792.1 GI:33012562
KEYWORDS JP 2002509721-A/5818.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
PATENT: JP 2002509721-A 5818 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/5818
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO,ELISABETH ROBERTS,THALE JARVIS,CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,
PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source 1..17
FT location/Qualifiers
/organism='Homo sapiens (human)'.
1..17
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02; 2; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 30 AAGAGGAAAAA 45
Db 16 AAAAGGAAAAA 1

RESULT 1326
LOCUS BD202896/c
DEFINITION 17 bp RNA linear PAT 17-JUL-2003
ACCESSION BD202896
molecule participating in vasculogenic response.

VERSION BD202896.1 GI:33012666
KEYWORDS JP 2002509721-A/5922.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 5922 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/5922
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
FEATURES
source 1..17
Location/Qualifiers
1..17
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1706 AATCAAGAAATATATTA 1721
DB 17 AATAAATATATATTA 2
RESULT 1327
LOCUS BD202897/c 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD202897
VERSION BD202897.1 GI:33012667
KEYWORDS JP 2002509721-A/5923.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 5923 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/5923
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,

PC A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
FEATURES
source 1..17
Location/Qualifiers
1..17
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1706 AATCAAGAAATATATTA 1721
DB 16 AATAAATATATATTA 1
RESULT 1328
LOCUS BD203006/c 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response.
ACCESSION BD203006
VERSION BD203006.1 GI:33012776
KEYWORDS JP 2002509721-A/6032.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euteheria; Primates; Catarrhini; Homnidae; Homo.
TITLE 1 (bases 1 to 17)
Pavco,P.A., Roberts,E., Jarvis,T., Coeshott,C. and Mcswigen,J.A.
Method and reagent for treating diseases or conditions concerning
molecule participating in vasculogenic response
JOURNAL Patent: JP 2002509721-A 6032 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002509721-A/6032
PD 02-APR-2002
PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC C12N15/09,A61K31/7088,A61K31/7125,A61K48/00,A61P3/10,A61P17/06, PC
A61P29/00,A61P35/00,A61P43/00,C12N5/10,C12N9/00//A61K35/76,C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
FH Key Location/Qualifiers
FT source 1..17
/organism='Homo sapiens (human)'.
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'
FEATURES
source 1..17
Location/Qualifiers
1..17
Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACAAACAAACAAACAA 1749
DB 16 ACAAACAAACAAACAA 1

RESULT 1329
BD203175 LOCUS 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD203175.1 GI:33012945
VERSION BD203175.1
KEYWORDS JP 2002509721-A/6201.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
PAVCO,P.A., ROBERTS,E., JARVIS,T., COESHOTT,C. and MCSWIGGEN,J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
PATENT: JP 2002509721-A 6201 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
JOURNAL OS Homo sapiens (human)
COMMENT PN JP 2002509721-A/6201
OS Homo sapiens (human)
PN JP 2002509721-A/6201
PD 02-APR-2002

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 2 AAAAAAAAAAAAAA 17

RESULT 1330
BD203246 LOCUS 17 bp RNA linear PAT 17-JUL-2003
DEFINITION Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response.
ACCESSION BD203246.1 GI:33013016
VERSION BD203246.1
KEYWORDS JP 2002509721-A/6272.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 17)
PAVCO,P.A., ROBERTS,E., JARVIS,T., COESHOTT,C. and MCSWIGGEN,J.A. Method and reagent for treating diseases or conditions concerning molecule participating in vasculogenic response
PATENT: JP 2002509721-A 6272 02-APR-2002;
RIBOZYME PHARMACEUTICALS INC
JOURNAL OS Homo sapiens (human)
COMMENT PN JP 2002509721-A/6272
PD 02-APR-2002

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 2 AAAAAAAAAAAAAA 17

RESULT 1331
BD204781 LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel human chromosome 16 genes, compositions, methods of making and using same.
ACCESSION BD204781.1 GI:33014551
VERSION BD204781.1
KEYWORDS JP 2002514903-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
LANDER,G.M., BURN,T.C., CONNORS,T.D., DACKOWSKI,W.R., RAEY,T.J.V. and KLINGER,K.W. Novel human chromosome 16 genes, compositions, methods of making and using same
PATENT: JP 2002514903-A 12 21-MAY-2002;
GENZYME CORP
JOURNAL OS Synthetic construct
COMMENT PN JP 2002514903-A/12
PD 21-MAY-2002
PF 16-JUN-1997 JP 1998502904
PR 17-JUN-1996 US 08/655259, 01-OCT-1996 US 08/720614 PR
PI GREGORY M LANDES, TIMOTHY C BURN, TIMOTHY D CONNORS, WILLIAM R DACKOWSKI,
PI TERENCE J VAN RAEY, KATHERINE W KLINGER
PC C12N15/12, C12N15/85, C07K14/47, C07K14/475, C07K16/18, A01K67/027
CC Oligonucleotide Primer
FH Key
FT source
1. 17
Location/Qualifiers
/organism='Synthetic construct'.
1. 17
Location/Qualifiers
/organism='Synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1241 GCTGCTTACCTGCGT 1256

PF 24-MAR-1999 JP 2000541291
PR 27-MAR-1998 US 60/079678
PI PAMELA A PAVCO, ELISABETH ROBERTS, THALE JARVIS, CLAIRE COESHOTT,
PI JAMES A MCSWIGGEN
PC
C12N15/09, A61K31/7088, A61K48/00, A61P3/10, A61P17/06, PC
A61P29/00,
PC A61P35/00, A61P43/00, C12N5/10, C12N9/00//A61K35/76, C12N15/00, PC
C12N5/00
CC Method and reagent for treating diseases or conditions CC
concerning molecule
CC participating in vasculogenic response
FH Key Location/Qualifiers
FT source
1. 17
Location/Qualifiers
/organism='Homo sapiens (human)'.
1. 17
Location/Qualifiers
/organism='Homo sapiens'
/mol_type='genomic RNA'
/db_xref='taxon:9606'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAA 1748
DB 16 TACATTAATAAAAAA 1

RESULT 1331
BD204781 LOCUS 17 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel human chromosome 16 genes, compositions, methods of making and using same.
ACCESSION BD204781.1 GI:33014551
VERSION BD204781.1
KEYWORDS JP 2002514903-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 17)
LANDER,G.M., BURN,T.C., CONNORS,T.D., DACKOWSKI,W.R., RAEY,T.J.V. and KLINGER,K.W. Novel human chromosome 16 genes, compositions, methods of making and using same
PATENT: JP 2002514903-A 12 21-MAY-2002;
GENZYME CORP
JOURNAL OS Synthetic construct
COMMENT PN JP 2002514903-A/12
PD 21-MAY-2002
PF 16-JUN-1997 JP 1998502904
PR 17-JUN-1996 US 08/655259, 01-OCT-1996 US 08/720614 PR
PI GREGORY M LANDES, TIMOTHY C BURN, TIMOTHY D CONNORS, WILLIAM R DACKOWSKI,
PI TERENCE J VAN RAEY, KATHERINE W KLINGER
PC C12N15/12, C12N15/85, C07K14/47, C07K14/475, C07K16/18, A01K67/027
CC Oligonucleotide Primer
FH Key
FT source
1. 17
Location/Qualifiers
/organism='Synthetic construct'.
1. 17
Location/Qualifiers
/organism='Synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'

Query Match 0.7%; Score 12.8; DB 1; Length 17;
Best Local Similarity 87.5%; Pred. No. 9e+02;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1241 GCTGCTTACCTGCGT 1256

Db 17 GCTCCTCAGCAGCGT 2

RESULT 1332
BD204794/C 17 bp DNA linear PAT 17-JUL-2003

LOCUS Novel human chromosome 16 genes, compositions, methods of making

ACCESSION BD204794.1 GI:33014564

VERSION JP 2002514903-A/25.

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1 (bases 1 to 17)

AUTHORS Landes,G.M., Burr,T.C., Connors,T.D., Dackowski,W.R., Raay,T.J.V.

TITLE Novel human chromosome 16 genes, compositions, methods of making

JOURNAL Patent: JP 2002514903-A 25 21-MAY-2002;

COMMENT GENZYME CORP

PN JP 2002514903-A/25

PD 21-MAY-2002

PF 16-JAN-1997 JP 1998502904

PR 17-JUN-1996 US 08/665259,01-OCT-1996 US 08/720614 PR

PI 09-DEC-1996 US 08/762500

PI GREGORY M LANDES,TIMOTHY C BURR,TIMOTHY D CONNORS,WILLIAM R

PI DACKOWSKI,

PI TERENCE J VAN RAAY,KATHERINE W KLINGER

PC C12N15/12,C12N15/85,C07K14/47,C07K16/18,A01K67/027

CC Oligonucleotide primer

FT Key Location/Qualifiers

FEATURES 1.17 Location/Qualifiers

source /organism="synthetic construct"

/db_xref="taxon:32630"

Query Match 0.7%; Score 12.4; DB 1; Length 16;

Best Local Similarity 92.9%; Pred. No. 9.4e+02;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 850 TCTGGCCTGCAGC 863

Db 16 TCTGGCCTGCAGC 3

RESULT 1334

AX422502 17 bp RNA linear PAT 18-JUN-2002

LOCUS Sequence 838 from Patent WO0186124.

ACCESSION AX422502

VERSION AX422502.1 GI:21525884

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Jarvis,T., von Carlwiltz,I., Mcswiggen,J.A., McLaughlin,F.G. and

TITLE Method and reagent for the inhibition of erg

JOURNAL Patent: WO 0186124-A 838 22-NOV-2001;

FEATURES RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)

source 1.17 Location/Qualifiers

/organism="Homo sapiens"

/mol_type="unassigned RNA"

/db_xref="taxon:9606"

Query Match 0.7%; Score 12.4; DB 1; Length 17;

Best Local Similarity 92.9%; Pred. No. 1e+03;

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1021 GGGGATGGGGCTGG 1034

Db 15 GGGGATGGGGCTGG 2

Search completed: August 16, 2004, 15:19:39

Job time : 29 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2004, 15:23:23 ; Search time 27 Seconds
(without alignments)

3.725 Million cell updates/sec

Title: us-10-008-789-3

Perfect score: 1755

Sequence: 1 cgcccggcgaggtcccaaa.....aaaaaaaaaaaaaaaaaaaaa 1755

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 1487 seqs, 28657 residues

Total number of hits satisfying chosen parameters: 2974

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1489 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	27	1.5	27	1	Renilla luciferase
C 2	23	1.3	23	1	Human TRIP6 DNA sp
C 3	22.4	1.3	24	1	Oligo dt primer #2
C 4	22.4	1.3	24	1	Oligo dt primer #1
C 5	22.4	1.3	27	1	Anchored poly T RT
C 6	22.2	1.3	28	1	Deoxy-T22-tagged s
C 7	22.2	1.3	28	1	Minority genome me
C 8	21.4	1.2	24	1	PCR primer PGR32
C 9	21.4	1.2	25	1	Sequencing primer
C 10	21.4	1.2	25	1	PCR primer for hum
C 11	21.4	1.2	26	1	Human full length
C 12	21.4	1.2	26	1	Human zsig63 cDNA
C 13	21.4	1.2	26	1	Human secreted sal
C 14	21.4	1.2	26	1	ZC7764a primer use
C 15	21.4	1.2	26	1	Human zaphall lig
C 16	21.4	1.2	26	1	Human zsig63 PCR/s
C 17	21.4	1.2	27	1	EST polymorphic DN
C 18	21	1.2	21	1	Reverse transcript
C 19	21	1.2	21	1	Human TRIP6 DNA sp
C 20	21	1.2	25	1	PCR primer for hum
C 21	21	1.2	25	1	Human CYP2D6 gene
C 22	21	1.2	25	1	Bacterial PNP DNA
C 23	21	1.2	25	1	Oligo dt primer #3
C 24	21	1.2	26	1	Human BSI24 specif
C 25	21	1.2	26	1	Human pancreatic P
C 26	21	1.2	26	1	Bacterial PNP DNA
C 27	21	1.2	26	1	PolyPNP out-of-fra
C 28	21	1.2	27	1	Anchored poly T RT
C 29	21	1.2	28	1	Human haemoglobin
C 30	20.6	1.2	24	1	Aspergillus niger
C 31	20.6	1.2	26	1	Human zsig63 cDNA
C 32	20.6	1.2	26	1	Human secreted sal
C 33	20.6	1.2	26	1	ZC7231 primer used

C 34	20.6	1.2	26	1	AAD55692	Bovine viral diarr
C 35	20.6	1.2	26	1	ABX93598	Human zsig63 PCR/s
C 36	20.6	1.2	26	1	ACF36382	Nucleotide sequenc
C 37	20.6	1.2	27	1	ABQ76254	Murine SCE 5'-RAC
C 38	20.6	1.2	27	1	ABX12469	Coxsackie B virus
C 39	20.4	1.2	22	1	AAQ64724	2',5'-linked tetra
C 40	20.4	1.2	22	1	AAQ64724	L1 cleavage site r
C 41	20.4	1.2	23	1	AAQ30430	Oligomer IL6803 fo
C 42	20.4	1.2	23	1	AAQ30431	Oligomer IL6804 fo
C 43	20.4	1.2	23	1	AAQ62450	Cleavage of nuclei
C 44	20.4	1.2	23	1	AAQ62451	Cleavage of nuclei
C 45	20.4	1.2	23	1	ABL01773	Human MSH2 (hMSH2)
C 46	20.4	1.2	24	1	AAQ9286	POLYA, a competit
C 47	20.4	1.2	24	1	AAQ31743	Nucleotide sequenc
C 48	20.4	1.2	24	1	AAQ4086	Oligonucleotide PO
C 49	20.4	1.2	24	1	AAQ40359	pBluescriptSK+ pha
C 50	20.4	1.2	24	1	AAQ40353	pBluescriptSK+ pha
C 51	20.4	1.2	24	1	AAQ99756	Immunostimulatory
C 52	20.4	1.2	24	1	AAQ99304	Immunostimulatory
C 53	20.4	1.2	24	1	AAQ99757	Immunostimulatory
C 54	20.4	1.2	24	1	ABV14842	Human prostate exp
C 55	20.4	1.2	24	1	ABV14842	Angiogenesis inhib
C 56	20.4	1.2	24	1	ABV77949	Angiogenesis inhib
C 57	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 58	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 59	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 60	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 61	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 62	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 63	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 64	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 65	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 66	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 67	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 68	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 69	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 70	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 71	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 72	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 73	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 74	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 75	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 76	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 77	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 78	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 79	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 80	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 81	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 82	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 83	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 84	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 85	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 86	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 87	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 88	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 89	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 90	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 91	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 92	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 93	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 94	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 95	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 96	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 97	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 98	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 99	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 100	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 101	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 102	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 103	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 104	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 105	20.4	1.2	24	1	ABV78478	Angiogenesis inhib
C 106	20.4	1.2	24	1	ABV78478	Angiogenesis inhib

C 107	20.4	1.2	27	1	ACH03245	Immunostimulatory	180	20	1.1	20	1	ABZ89086	Human oligonucleot
C 108	20.4	1.2	27	1	AD337208	Immunostimulatory	181	20	1.1	20	1	ABZ85533	Human oligonucleot
C 109	20.2	1.2	22	1	AAL50570	Molecular array pr	182	20	1.1	20	1	ABZ89015	Human oligonucleot
C 110	20.2	1.2	22	1	ABX74887	Oligo-dT primer us	183	20	1.1	20	1	ABZ89441	Human oligonucleot
C 111	20.2	1.2	22	1	ACC48484	Locked nucleic aci	184	20	1.1	20	1	ABZ89016	Human oligonucleot
C 112	20.2	1.2	22	1	ACC48485	Locked nucleic aci	185	20	1.1	20	1	ABZ89120	Human oligonucleot
C 113	20.2	1.2	22	1	ACC48483	Locked nucleic aci	186	20	1.1	20	1	ABZ89704	Human oligonucleot
C 114	20.2	1.2	22	1	AAD51324	Anchored oligo dT	187	20	1.1	20	1	ACD27320	Nanotechnology nuc
C 115	20.2	1.2	23	1	ABX13916	3'-PCR primer used	188	20	1.1	20	1	ACC82890	Human TRIP6 antis
C 116	20.2	1.2	26	1	ABX94936	Renilla luciferase	189	20	1.1	20	1	ACC82896	Human TRIP6 antis
C 117	20	1.1	20	1	AAQ25565	Dye-coupled 3'-am	190	20	1.1	20	1	ACC82919	Human TRIP6 antis
C 118	20	1.1	20	1	AAQ33554	Microsatellite seq	191	20	1.1	20	1	ACC82889	Human TRIP6 antis
C 119	20	1.1	20	1	AAQ33554	Sequence of synthe	192	20	1.1	20	1	ACC82907	Human TRIP6 antis
C 120	20	1.1	20	1	AAQ94205	Alpha-anomeric oli	193	20	1.1	20	1	ACC82911	Human TRIP6 antis
C 121	20	1.1	20	1	AAQ75568	Reverse transcript	194	20	1.1	20	1	ACC82897	Human TRIP6 antis
C 122	20	1.1	20	1	AAQ90405	T2 (synthetic DNA	195	20	1.1	20	1	ACC82900	Human TRIP6 antis
C 123	20	1.1	20	1	AAQ763649	Anti-HIV antisens	196	20	1.1	20	1	ACC82905	Human TRIP6 antis
C 124	20	1.1	20	1	AAV34591	M. vaccae antigeni	197	20	1.1	20	1	ACC82909	Human TRIP6 antis
C 125	20	1.1	20	1	AAV86606	Oligonucleotide se	198	20	1.1	20	1	ACC82929	Human TRIP6 antis
C 126	20	1.1	20	1	AAZ27533	Synthetic RNA sequ	199	20	1.1	20	1	ACC82910	Human TRIP6 antis
C 127	20	1.1	20	1	AAZ11326	Mycobacterial 16S	200	20	1.1	20	1	ACC82921	Human TRIP6 antis
C 128	20	1.1	20	1	AAZ40449	Electrochemical det	201	20	1.1	20	1	ACC82899	Human TRIP6 antis
C 129	20	1.1	20	1	AAZ40448	Electrochemical det	202	20	1.1	20	1	ACC82920	Human TRIP6 antis
C 130	20	1.1	20	1	AAZ91117	Oligonucleotide #5	203	20	1.1	20	1	ACC82922	Human TRIP6 antis
C 131	20	1.1	20	1	AAZ50193	2'-Methoxyethoxy-m	204	20	1.1	20	1	ACC82951	Human TRIP6 antis
C 132	20	1.1	20	1	AAZ67238	Phosphorothioate p	205	20	1.1	20	1	ACC82952	Human TRIP6 antis
C 133	20	1.1	20	1	AAZ67230	Digoxigenin-label	206	20	1.1	20	1	ACC82953	Human TRIP6 antis
C 134	20	1.1	20	1	AAZ67241	Poly T oligonucleo	207	20	1.1	20	1	ACC82881	Human TRIP6 DNA sp
C 135	20	1.1	20	1	AAZ10402	DNA template for 3	208	20	1.1	20	1	ACC82901	Human TRIP6 antis
C 136	20	1.1	20	1	AAZ16997	Capture probe CP5	209	20	1.1	20	1	ACC82904	Human TRIP6 antis
C 137	20	1.1	20	1	AAZ60896	Conjugate forming	210	20	1.1	20	1	ACC82912	Human TRIP6 antis
C 138	20	1.1	20	1	AAZ63428	Oligonucleotide-na	211	20	1.1	20	1	ACC82939	Human TRIP6 antis
C 139	20	1.1	20	1	AAZ28481	Random oligonucleo	212	20	1.1	20	1	ACC82892	Human TRIP6 antis
C 140	20	1.1	20	1	AAZ10371	Oligonucleotide-cy	213	20	1.1	20	1	ACC82916	Human TRIP6 antis
C 141	20	1.1	20	1	AAZ99427	Immunostimulatory	214	20	1.1	20	1	ACC82925	Human TRIP6 antis
C 142	20	1.1	20	1	AAZ99099	Immunostimulatory	215	20	1.1	20	1	ACC82926	Human TRIP6 antis
C 143	20	1.1	20	1	AAZ99431	Immunostimulatory	216	20	1.1	20	1	ACC82938	Human TRIP6 antis
C 144	20	1.1	20	1	AAH46465	Oligonucleotide #1	217	20	1.1	20	1	ACC82941	Human TRIP6 antis
C 145	20	1.1	20	1	AAH78547	Nucleotide sequenc	218	20	1.1	20	1	ACC82945	Human TRIP6 antis
C 146	20	1.1	20	1	AAZ28351	DNA oligomer #1	219	20	1.1	20	1	ACC82948	Human TRIP6 antis
C 147	20	1.1	20	1	ABS77742	Angiogenesis inhib	220	20	1.1	20	1	ACC82928	Human TRIP6 antis
C 148	20	1.1	20	1	ABS78072	Angiogenesis inhib	221	20	1.1	20	1	ACC82935	Human TRIP6 antis
C 149	20	1.1	20	1	ABS78076	Angiogenesis inhib	222	20	1.1	20	1	ACC82906	Human TRIP6 antis
C 150	20	1.1	20	1	ABL39402	Immunostimulatory	223	20	1.1	20	1	ACC82924	Human TRIP6 antis
C 151	20	1.1	20	1	ABL38648	Immunostimulatory	224	20	1.1	20	1	ACC82931	Human TRIP6 antis
C 152	20	1.1	20	1	ABL39403	Immunostimulatory	225	20	1.1	20	1	ACC82932	Human TRIP6 antis
C 153	20	1.1	20	1	ABL54775	CD14 receptor PCR	226	20	1.1	20	1	ACC82937	Human TRIP6 antis
C 154	20	1.1	20	1	ABK65035	Nanoparticle-oligo	227	20	1.1	20	1	ACC82891	Human TRIP6 antis
C 155	20	1.1	20	1	ABK65050	Nanoparticle-oligo	228	20	1.1	20	1	ACC82923	Human TRIP6 antis
C 156	20	1.1	20	1	AAL45122	Oligonucleotide sy	229	20	1.1	20	1	ACC82940	Human TRIP6 antis
C 157	20	1.1	20	1	ABL36232	M tuberculosis rRN	230	20	1.1	20	1	ACC82944	Human TRIP6 antis
C 158	20	1.1	20	1	ABS64673	Nucleic acid detec	231	20	1.1	20	1	ACC82949	Human TRIP6 antis
C 159	20	1.1	20	1	ABS64688	Nucleic acid detec	232	20	1.1	20	1	ACC82918	Human TRIP6 antis
C 160	20	1.1	20	1	ABN87103	Capture probe CP5	233	20	1.1	20	1	ACC82940	Human TRIP6 antis
C 161	20	1.1	20	1	ABZ88267	Human oligonucleot	234	20	1.1	20	1	ACC82950	Human TRIP6 antis
C 162	20	1.1	20	1	ABZ88565	Human oligonucleot	235	20	1.1	20	1	ACC82895	Human TRIP6 antis
C 163	20	1.1	20	1	ABZ88619	Human oligonucleot	236	20	1.1	20	1	ACC82908	Human TRIP6 antis
C 164	20	1.1	20	1	ABZ89705	Human oligonucleot	237	20	1.1	20	1	ACC82927	Human TRIP6 antis
C 165	20	1.1	20	1	ABZ88816	Human oligonucleot	238	20	1.1	20	1	ACC82934	Human TRIP6 antis
C 166	20	1.1	20	1	ABZ88881	Human oligonucleot	239	20	1.1	20	1	ACC82954	Human TRIP6 antis
C 167	20	1.1	20	1	ABZ89706	Human oligonucleot	240	20	1.1	20	1	ACC82894	Human TRIP6 antis
C 168	20	1.1	20	1	ABZ88620	Human oligonucleot	241	20	1.1	20	1	ACC82914	Human TRIP6 antis
C 169	20	1.1	20	1	ABZ88814	Human oligonucleot	242	20	1.1	20	1	ACC82936	Human TRIP6 antis
C 170	20	1.1	20	1	ABZ89241	Human oligonucleot	243	20	1.1	20	1	ACC82946	Human TRIP6 antis
C 171	20	1.1	20	1	ABZ90650	Human oligonucleot	244	20	1.1	20	1	ACC82903	Human TRIP6 antis
C 172	20	1.1	20	1	ABZ88618	Human oligonucleot	245	20	1.1	20	1	ACC82917	Human TRIP6 antis
C 173	20	1.1	20	1	ABZ88815	Human oligonucleot	246	20	1.1	20	1	ACC82933	Human TRIP6 antis
C 174	20	1.1	20	1	ABZ85311	Human oligonucleot	247	20	1.1	20	1	ACC82943	Human TRIP6 antis
C 175	20	1.1	20	1	ABZ85435	Human oligonucleot	248	20	1.1	20	1	ACC82947	Human TRIP6 antis
C 176	20	1.1	20	1	ABZ88817	Human oligonucleot	249	20	1.1	20	1	ACC82955	Human TRIP6 antis
C 177	20	1.1	20	1	ABZ88939	Human oligonucleot	250	20	1.1	20	1	ACC82893	Human TRIP6 antis
C 178	20	1.1	20	1	ABZ89302	Human oligonucleot	251	20	1.1	20	1	ACC82898	Human TRIP6 antis
C 179	20	1.1	20	1	ABZ88566	Human oligonucleot	252	20	1.1	20	1	ACC82902	Human TRIP6 antis

C 253	20	1.1	20	1	ACB82913	Human TRIP6 antisense	C 326	19.2	1.1	21	1	ACC48482	Locked nucleic acid
C 254	20	1.1	20	1	ACC82915	Human TRIP6 antisense	C 327	19.2	1.1	21	1	ACC99729	Oligonucleotide.
C 255	20	1.1	20	1	ACC82942	Human TRIP6 antisense	C 328	19.2	1.1	21	1	AAQ73376	Anti-HSV-1 G4 olig
C 256	20	1.1	20	1	ACC59867	Doubly labelled DN	C 329	19.2	1.1	24	1	AAQ61902	HSV replication in
C 257	20	1.1	20	1	ABZ22916	Phosphorothioate 2	C 330	19.2	1.1	24	1	AAQ61990	Guanine quartet co
C 258	20	1.1	20	1	ALA61645	Thiol-modified oli	C 331	19.2	1.1	24	1	AAQ61894	HSV replication in
C 259	20	1.1	20	1	ABZ59815	Potato gene PCR pr	C 332	19.2	1.1	24	1	AAQ61997	Guanine quartet co
C 260	20	1.1	20	1	ABX79181	Thio-modified 20dA	C 333	19.2	1.1	24	1	AAQ97981	Peptide nucleic ac
C 261	20	1.1	20	1	ABX92177	Nanoparticle-assoc	C 334	19.2	1.1	24	1	ADB68048	G4 phosphorothioat
C 262	20	1.1	20	1	ACD27255	Nanotechnology nuc	C 335	19.2	1.1	25	1	AAQ61892	HSV replication in
C 263	20	1.1	20	1	ACD27125	Nanotechnology nuc	C 336	19.2	1.1	25	1	AAQ61893	HSV replication in
C 264	20	1.1	20	1	ACD27385	Nanotechnology nuc	C 337	19.2	1.1	25	1	AAQ97978	Peptide nucleic ac
C 265	20	1.1	20	1	ACD27190	Nanotechnology nuc	C 338	19.2	1.1	25	1	AAQ97978	Peptide nucleic ac
C 266	20	1.1	20	1	ACD27066	Nanotechnology nuc	C 339	19.2	1.1	25	1	AAQ97978	Peptide nucleic ac
C 267	20	1.1	20	1	ACH00064	Nanotechnology nuc	C 340	19.2	1.1	25	1	AAQ97978	Peptide nucleic ac
C 268	20	1.1	20	1	ACD99851	Immunostimulatory	C 341	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 269	20	1.1	20	1	ACD99847	Immunostimulatory	C 342	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 270	20	1.1	20	1	ACD99832	Immunostimulatory	C 343	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 271	20	1.1	20	1	ADA14838	Hairpin target seq	C 344	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 272	20	1.1	20	1	ADA06159	Nanoparticle label	C 345	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 273	20	1.1	20	1	ACD26995	Nanotechnology nuc	C 346	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 274	20	1.1	20	1	ADB36933	Immunostimulatory	C 347	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 275	20	1.1	20	1	ADB36601	Immunostimulatory	C 348	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 276	20	1.1	20	1	ADB36929	Immunostimulatory	C 349	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 277	20	1.1	21	1	AAQ75643	Reverse transcript	C 350	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 278	20	1.1	21	1	AAQ75646	Reverse transcript	C 351	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 279	20	1.1	21	1	AAQ75646	Reverse transcript	C 352	19.2	1.1	19	1	AAQ75549	Reverse transcript
C 280	20	1.1	21	1	AAQ90391	CP-1 (synthetic DN	C 353	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 281	20	1.1	21	1	AAQ10743	Oligonucleotide pr	C 354	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 282	20	1.1	21	1	AAQ53395	HIV-1 gag protein	C 355	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 283	20	1.1	21	1	AAQ81302	3' ribonucleoside	C 356	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 284	20	1.1	21	1	AAQ26973	Primer used to rev	C 357	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 285	20	1.1	21	1	AAZ44350	Protein kinase inh	C 358	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 286	20	1.1	21	1	AAQ99707	Immunostimulatory	C 359	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 287	20	1.1	21	1	ABH42480	Oligonucleotide us	C 360	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 288	20	1.1	21	1	ABH78428	Angiogenesis inhib	C 361	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 289	20	1.1	21	1	ABL39404	Immunostimulatory	C 362	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 290	20	1.1	21	1	ADH51323	Regular oligo dr p	C 363	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 291	20	1.1	21	1	ACH03246	Immunostimulatory	C 364	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 292	20	1.1	21	1	ADB37209	Immunostimulatory	C 365	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 293	20	1.1	23	1	AAQ30432	Oligomer IL6805 fo	C 366	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 294	20	1.1	23	1	AAQ16627	Gastric acid produ	C 367	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 295	20	1.1	24	1	AAI64873	Human serine/threo	C 368	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 296	20	1.1	24	1	ABL55130	Human gonadotropin	C 369	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 297	20	1.1	24	1	ABK86172	Oligo dr primer #4	C 370	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 298	19.8	1.1	24	1	ABS56855	Human PDZ protein	C 371	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 299	19.8	1.1	24	1	ALA7515	Human cyclophilin-	C 372	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 300	19.8	1.1	24	1	ADB68055	G4 phosphorothioat	C 373	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 301	19.6	1.1	26	1	AAQ01617	Human MINT31/CACNA	C 374	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 302	19.6	1.1	26	1	AAQ01577	Human T-type calci	C 375	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 303	19.6	1.1	26	1	AAQ01670	Human MINT31/CACNA	C 376	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 304	19.4	1.1	21	1	AAQ75648	Reverse transcript	C 377	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 305	19.4	1.1	21	1	AAQ75676	Reverse transcript	C 378	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 306	19.4	1.1	21	1	AAQ75660	Reverse transcript	C 379	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 307	19.4	1.1	21	1	AAQ75652	Reverse transcript	C 380	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 308	19.4	1.1	21	1	AAQ75612	Reverse transcript	C 381	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 309	19.4	1.1	21	1	AAQ75641	Reverse transcript	C 382	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 310	19.4	1.1	21	1	AAQ75769	Reverse transcript	C 383	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 311	19.4	1.1	21	1	AAQ75628	Reverse transcript	C 384	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 312	19.4	1.1	21	1	AAQ75726	Reverse transcript	C 385	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 313	19.4	1.1	21	1	AAQ75712	Reverse transcript	C 386	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 314	19.4	1.1	21	1	AAQ75775	Reverse transcript	C 387	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 315	19.4	1.1	21	1	AAQ75673	Reverse transcript	C 388	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 316	19.4	1.1	21	1	AAQ75640	Reverse transcript	C 389	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 317	19.4	1.1	21	1	AAQ75679	Reverse transcript	C 390	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 318	19.4	1.1	21	1	AAQ75616	Reverse transcript	C 391	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 319	19.4	1.1	21	1	AAQ75772	Reverse transcript	C 392	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 320	19.4	1.1	21	1	AAQ75647	Reverse transcript	C 393	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 321	19.4	1.1	21	1	AAQ75744	Reverse transcript	C 394	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 322	19.4	1.1	21	1	AAQ75615	DNA probe used in	C 395	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 323	19.4	1.1	24	1	ABZ22536	fragment of a plas	C 396	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 324	19.4	1.1	25	1	ABZ22535	fragment of a plas	C 397	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS
C 325	19.4	1.1	25	1	ACF79235	Calix(a)arene-olig	C 398	19.2	1.1	19	1	AAQ98952	Oligonucleotide IS

C 399	19	1.1	20	1	AA510447	Human stem cell fa	C 472	18.4	1.0	21	1	AAQ75627	Reverse transcript
C 400	19	1.1	20	1	AAQ35464	Rat SCF 5' cDNA am	C 473	18.4	1.0	21	1	AAQ75674	Reverse transcript
C 401	19	1.1	20	1	AB573848	SCF universal olig	C 474	18.4	1.0	21	1	AAQ75681	Reverse transcript
C 402	19	1.1	20	1	AB288880	Human oligonucleot	C 475	18.4	1.0	21	1	AAQ75778	Reverse transcript
C 403	19	1.1	20	1	AB289179	Human oligonucleot	C 476	18.4	1.0	21	1	AAQ75618	Reverse transcript
C 404	19	1.1	20	1	AB299050	Human PDE4C oligon	C 477	18.4	1.0	21	1	AAQ75629	Reverse transcript
C 405	19	1.1	20	1	AB289678	Human oligonucleot	C 478	18.4	1.0	21	1	AAQ75725	Reverse transcript
C 406	19	1.1	20	1	AB287681	Human oligonucleot	C 479	18.4	1.0	21	1	AAQ75773	Reverse transcript
C 407	19	1.1	20	1	AB289677	Human oligonucleot	C 480	18.4	1.0	21	1	AAQ75614	Reverse transcript
C 408	19	1.1	20	1	AB282460	Stem cell factor (C 481	18.4	1.0	21	1	AAQ75682	Reverse transcript
C 409	19	1.1	21	1	AD525651	Reverse transcript	C 482	18.4	1.0	21	1	AAQ75682	Reverse transcript
C 410	19	1.1	21	1	AAQ75639	Reverse transcript	C 483	18.4	1.0	21	1	AAQ75678	Reverse transcript
C 411	19	1.1	21	1	AAQ75650	Reverse transcript	C 484	18.4	1.0	21	1	AAQ75713	Reverse transcript
C 412	19	1.1	21	1	AAQ75642	Reverse transcript	C 485	18.4	1.0	21	1	AAQ75615	Reverse transcript
C 413	19	1.1	21	1	AAQ75649	Reverse transcript	C 486	18.4	1.0	21	1	AAQ75659	Reverse transcript
C 414	19	1.1	21	1	AAQ75653	Reverse transcript	C 487	18.4	1.0	21	1	AAQ75680	Reverse transcript
C 415	19	1.1	21	1	AAQ75654	Reverse transcript	C 488	18.4	1.0	21	1	AAQ75743	Reverse transcript
C 416	19	1.1	22	1	ABA93238	PolyA adaptor olig	C 489	18.4	1.0	21	1	AAQ75714	Reverse transcript
C 417	19	1.1	23	1	AAQ75028	LCR oligo 2. Synt	C 490	18.4	1.0	21	1	AAQ75723	Reverse transcript
C 418	19	1.1	23	1	AAQ75029	LCR oligo 3. Synt	C 491	18.4	1.0	21	1	AAQ75776	Reverse transcript
C 419	19	1.1	24	1	AAH43079	Nucleotide sequenc	C 492	18.4	1.0	21	1	AAQ75672	Reverse transcript
C 420	19	1.1	24	1	ABQ79878	Nucleotide sequenc	C 493	18.4	1.0	21	1	AAQ75746	Reverse transcript
C 421	19	1.1	24	1	ADC75073	Biosensor related	C 494	18.4	1.0	21	1	AAQ75617	Reverse transcript
C 422	19	1.1	25	1	AA162055	Soybean 318013 reg	C 495	18.4	1.0	21	1	AAQ75768	Reverse transcript
C 423	18.8	1.1	24	1	ABQ73254	Human macro protei	C 496	18.4	1.0	21	1	AAQ75777	Reverse transcript
C 424	18.8	1.1	25	1	AAQ96256	HLA DPA1 gene PCR	C 497	18.4	1.0	21	1	AAQ75662	Reverse transcript
C 425	18.4	1.0	20	1	AAQ75584	Reverse transcript	C 498	18.4	1.0	21	1	AAQ75774	Reverse transcript
C 426	18.4	1.0	20	1	AAQ75585	Reverse transcript	C 499	18.4	1.0	21	1	AAQ75613	Reverse transcript
C 427	18.4	1.0	20	1	AAQ75572	Reverse transcript	C 500	18.4	1.0	21	1	AAQ75677	Reverse transcript
C 428	18.4	1.0	20	1	AAQ75560	Reverse transcript	C 501	18.4	1.0	21	1	AAQ75745	Reverse transcript
C 429	18.4	1.0	20	1	AAQ75577	Reverse transcript	C 502	18.4	1.0	21	1	AAQ75770	Reverse transcript
C 430	18.4	1.0	20	1	AAQ75593	Reverse transcript	C 503	18.4	1.0	21	1	AAQ75711	Reverse transcript
C 431	18.4	1.0	20	1	AAQ75561	Reverse transcript	C 504	18.4	1.0	21	1	AAZ26563	Human polymorphic
C 432	18.4	1.0	20	1	AAQ75601	Reverse transcript	C 505	18.4	1.0	21	1	AAQ75716	Human gene single
C 433	18.4	1.0	20	1	AAQ75564	Reverse transcript	C 506	18.4	1.0	21	1	AAZ24290	Complementary nucl
C 434	18.4	1.0	20	1	AAQ75600	Reverse transcript	C 507	18.4	1.0	21	1	AAZ79794	EST polymorphic DN
C 435	18.4	1.0	20	1	AAQ75583	Reverse transcript	C 508	18.4	1.0	22	1	ABX192356	Amino modified oli
C 436	18.4	1.0	20	1	AAQ75580	Reverse transcript	C 509	18.4	1.0	22	1	ABQ73084	Human zcytor19 PCR
C 437	18.4	1.0	20	1	AAQ75599	Reverse transcript	C 510	18.4	1.0	23	1	AAA29753	Synthetic oligonuc
C 438	18.4	1.0	20	1	AAQ74916	Reverse transcript	C 511	18.4	1.0	24	1	AAH24266	Human phosphatase
C 439	18.4	1.0	20	1	AAQ74918	Mammalian stem cel	C 512	18.4	1.0	24	1	AAH44623	Human PD 17 PCR pr
C 440	18.4	1.0	20	1	AAQ13753	Mammalian stem cel	C 513	18.4	1.0	24	1	ABK13715	RT-PCR primer #2 f
C 441	18.4	1.0	20	1	AAQ13754	Stem cell factor u	C 514	18.4	1.0	24	1	ABK12409	RT-PCR primer #1 f
C 442	18.4	1.0	20	1	AAH41332	Stem cell factor u	C 515	18.2	1.0	19	1	AAZ06572	(-)-limonene-6-hyd
C 443	18.4	1.0	20	1	AAH41333	Universal stem cel	C 516	18.2	1.0	19	1	AZ299489	primer HOOK for cD
C 444	18.4	1.0	20	1	AAQ41133	Universal stem cel	C 517	18.2	1.0	19	1	AAZ15201	3' sequencing prim
C 445	18.4	1.0	20	1	AAQ41112	Human SCF (stem ce	C 518	18.2	1.0	19	1	AAH21968	Mouse total gene e
C 446	18.4	1.0	20	1	AAQ41113	Human SCF (stem ce	C 519	18.2	1.0	19	1	AAZ76617	Spearmint (-)-limo
C 447	18.4	1.0	20	1	AAZ89092	Mammalian stem cel	C 520	18.2	1.0	19	1	AAZ06525	Mouse microglia an
C 448	18.4	1.0	20	1	AAZ83959	BAP28 gene fragmen	C 521	18.2	1.0	19	1	ABK71509	CNS related 3' seq
C 449	18.4	1.0	20	1	AAH23891	Human SCF (stem ce	C 522	18.2	1.0	19	1	ABQ73231	Rabbit atheroscler
C 450	18.4	1.0	20	1	AAH23890	Human SCF (stem ce	C 523	18.2	1.0	19	1	AAZ34663	PCR primer #4 used
C 451	18.4	1.0	20	1	AAQ41213	Human SCF (stem ce	C 524	18.2	1.0	19	1	AAZ40279	HOOK PCR primer us
C 452	18.4	1.0	20	1	AAQ41214	Human SCF (stem ce	C 525	18.2	1.0	19	1	ABZ68389	Reverse transcript
C 453	18.4	1.0	20	1	AAQ10448	Human stem cell fa	C 526	18.2	1.0	19	1	ACC79402	M13 sequencing pri
C 454	18.4	1.0	20	1	AAQ10448	Human stem cell fa	C 527	18.2	1.0	19	1	AAZ49149	3' sequencing prim
C 455	18.4	1.0	20	1	AAQ35465	Rat SCF 5' cDNA am	C 528	18.2	1.0	19	1	AAZ50267	3' sequencing prim
C 456	18.4	1.0	20	1	AAQ35466	Rat SCF 5' cDNA am	C 529	18.2	1.0	19	1	ADC21495	Human PRDI-BP1 RT-
C 457	18.4	1.0	20	1	AB573849	SCF universal olig	C 530	18.2	1.0	20	1	AAZ09197	Oligonucleotide 9
C 458	18.4	1.0	20	1	AB573850	SCF universal olig	C 531	18	1.0	18	1	AAQ34110	Sequence of a micr
C 459	18.4	1.0	20	1	ABZ89546	Human oligonucleot	C 532	18	1.0	18	1	AAQ75025	PCR primer. Synth
C 460	18.4	1.0	20	1	ABZ89085	Human oligonucleot	C 533	18	1.0	18	1	AAZ94669	Anchored poly(T) o
C 461	18.4	1.0	20	1	ABZ88694	Human oligonucleot	C 534	18	1.0	18	1	AAV21970	Nuclease resistant
C 462	18.4	1.0	20	1	ABZ89240	Human oligonucleot	C 535	18	1.0	18	1	AAZ19943	Primer SEQ ID NO:3
C 463	18.4	1.0	20	1	AD525462	Stem cell factor (C 536	18	1.0	18	1	AAZ19942	Primer SEQ ID NO:2
C 464	18.4	1.0	20	1	AD525461	Stem cell factor (C 537	18	1.0	18	1	AAZ87161	Oligoarabinonucleo
C 465	18.4	1.0	21	1	AAQ75611	Reverse transcript	C 538	18	1.0	18	1	AAZ87162	Oligoarabinonucleo
C 466	18.4	1.0	21	1	AAQ75630	Reverse transcript	C 539	18	1.0	18	1	AAZ87166	Deoxyarabinonucleo
C 467	18.4	1.0	21	1	AAQ75724	Reverse transcript	C 540	18	1.0	18	1	AAZ87167	Deoxyarabinonucleo
C 468	18.4	1.0	21	1	AAQ75661	Reverse transcript	C 541	18	1.0	18	1	AAQ35665	Oligonucleotide #6
C 469	18.4	1.0	21	1	AAQ75671	Reverse transcript	C 542	18	1.0	18	1	AAZ17014	Oligonucleotide A1
C 470	18.4	1.0	21	1	AAQ75675	Reverse transcript	C 543	18	1.0	18	1	AAQ75597	Binary encoded seq
C 471	18.4	1.0	21	1	AAQ75771	Reverse transcript	C 544	18	1.0	18	1	AAZ99708	Immunostimulatory

C 545	18	1.0	18	1	AAF99734	Immunostimulatory	C 618	18	1.0	24	1	ABN85073	Human S4 ribosomal
C 546	18	1.0	18	1	AAF82472	Phagemid vector pC	C 619	18	1.0	24	1	AAQ33505	T7Tl8Apad PS12-24-
C 547	18	1.0	18	1	AAS94743	Rat secreted facto	C 620	17.8	1.0	21	1	AAQ75748	Reverse transcript
C 548	18	1.0	18	1	ABS78455	Angiogenesis inhib	C 621	17.8	1.0	21	1	AAQ75733	Reverse transcript
C 549	18	1.0	18	1	ABS78429	Angiogenesis inhib	C 622	17.8	1.0	21	1	AAQ75736	Reverse transcript
C 550	18	1.0	18	1	ABL39401	Immunostimulatory	C 623	17.8	1.0	21	1	AAQ75730	Reverse transcript
C 551	18	1.0	18	1	AD441497	Oligonucleotide us	C 624	17.8	1.0	21	1	AAQ75780	Reverse transcript
C 552	18	1.0	18	1	ABS54337	Poly d(T) primer,	C 625	17.8	1.0	21	1	AAQ75781	Reverse transcript
C 553	18	1.0	18	1	ABA93239	Adaptor oligonucle	C 626	17.8	1.0	21	1	AAQ75684	Reverse transcript
C 554	18	1.0	18	1	AAD56466	Target RNA #1 used	C 627	17.8	1.0	21	1	AAQ75695	Reverse transcript
C 555	18	1.0	18	1	AAD56440	Antisense oligo #1	C 628	17.8	1.0	21	1	AAQ75753	Reverse transcript
C 556	18	1.0	18	1	AAD56446	2'P-ANA antisense	C 629	17.8	1.0	21	1	AAQ75694	Reverse transcript
C 557	18	1.0	18	1	ACH03247	Immunostimulatory	C 630	17.8	1.0	21	1	AAQ75728	Reverse transcript
C 558	18	1.0	18	1	AAD57871	Antisense oligo #1	C 631	17.8	1.0	21	1	AAQ75758	Reverse transcript
C 559	18	1.0	18	1	AAD57878	Antisense DNA-RNA	C 632	17.8	1.0	21	1	AAQ75788	Reverse transcript
C 560	18	1.0	18	1	AAD57879	Antisense DNA-RNA	C 633	17.8	1.0	21	1	AAQ75791	Reverse transcript
C 561	18	1.0	18	1	AAD57877	Antisense DNA-RNA	C 634	17.8	1.0	21	1	AAQ75716	Reverse transcript
C 562	18	1.0	18	1	AAD57890	Target RNA #1 used	C 635	17.8	1.0	21	1	AAQ75727	Reverse transcript
C 563	18	1.0	18	1	AB372120	Immunostimulatory	C 636	17.8	1.0	21	1	AAQ75740	Reverse transcript
C 564	18	1.0	18	1	ADB37236	Immunostimulatory	C 637	17.8	1.0	21	1	AAQ75779	Reverse transcript
C 565	18	1.0	18	1	ADE77617	Human probe NEG fo	C 638	17.8	1.0	21	1	AAQ75689	Reverse transcript
C 566	18	1.0	19	1	AAQ75548	Reverse transcript	C 639	17.8	1.0	21	1	AAQ75722	Reverse transcript
C 567	18	1.0	19	1	AAQ75550	Reverse transcript	C 640	17.8	1.0	21	1	AAQ75760	Reverse transcript
C 568	18	1.0	19	1	AAQ75547	Reverse transcript	C 641	17.8	1.0	21	1	AAQ75692	Reverse transcript
C 569	18	1.0	19	1	ABE5521	Tailing reaction r	C 642	17.8	1.0	21	1	AAQ75705	Reverse transcript
C 570	18	1.0	19	1	ABZ75398	Synthetic nuclease	C 643	17.8	1.0	21	1	AAQ75737	Reverse transcript
C 571	18	1.0	19	1	ABZ75399	Reverse transcript	C 644	17.8	1.0	21	1	AAQ75756	Reverse transcript
C 572	18	1.0	20	1	AAQ75566	Reverse transcript	C 645	17.8	1.0	21	1	AAQ75785	Reverse transcript
C 573	18	1.0	20	1	AAQ75574	Reverse transcript	C 646	17.8	1.0	21	1	AAQ75685	Reverse transcript
C 574	18	1.0	20	1	AAQ75559	Reverse transcript	C 647	17.8	1.0	21	1	AAQ75704	Reverse transcript
C 575	18	1.0	20	1	AAQ75563	Reverse transcript	C 648	17.8	1.0	21	1	AAQ75708	Reverse transcript
C 576	18	1.0	20	1	AAQ75565	Reverse transcript	C 649	17.8	1.0	21	1	AAQ75759	Reverse transcript
C 577	18	1.0	20	1	AAQ75562	Reverse transcript	C 650	17.8	1.0	21	1	AAQ75734	Reverse transcript
C 578	18	1.0	20	1	AAQ75573	Reverse transcript	C 651	17.8	1.0	21	1	AAQ75683	Reverse transcript
C 579	18	1.0	20	1	AAQ75571	Reverse transcript	C 652	17.8	1.0	21	1	AAQ75696	Reverse transcript
C 580	18	1.0	20	1	ABZ83312	Human oligonucleot	C 653	17.8	1.0	21	1	AAQ75710	Reverse transcript
C 581	18	1.0	20	1	ABZ89338	Human oligonucleot	C 654	17.8	1.0	21	1	AAQ75721	Reverse transcript
C 582	18	1.0	20	1	ABZ89301	Reverse transcript	C 655	17.8	1.0	21	1	AAQ75792	Reverse transcript
C 583	18	1.0	21	1	AAQ75622	Reverse transcript	C 656	17.8	1.0	21	1	AAZ26584	Human polymorphic
C 584	18	1.0	21	1	AAQ75633	Reverse transcript	C 657	17.4	1.0	19	1	AAQ75552	Reverse transcript
C 585	18	1.0	21	1	AAQ75670	Reverse transcript	C 658	17.4	1.0	19	1	AAQ75553	Reverse transcript
C 586	18	1.0	21	1	AAQ75609	Reverse transcript	C 659	17.4	1.0	19	1	AAQ75551	Reverse transcript
C 587	18	1.0	21	1	AAQ75620	Reverse transcript	C 660	17.4	1.0	19	1	AAQ75555	Reverse transcript
C 588	18	1.0	21	1	AAQ75626	Reverse transcript	C 661	17.4	1.0	19	1	AAQ75557	Reverse transcript
C 589	18	1.0	21	1	AAQ75657	Reverse transcript	C 662	17.4	1.0	19	1	AAQ75557	Reverse transcript
C 590	18	1.0	21	1	AAQ75664	Reverse transcript	C 663	17.4	1.0	19	1	ADE29541	Mitogen activated
C 591	18	1.0	21	1	AAQ75669	Reverse transcript	C 664	17.4	1.0	19	1	ADE29704	Cytochrome P450 se
C 592	18	1.0	21	1	AAQ75631	Reverse transcript	C 665	17.4	1.0	20	1	AAQ49436	Reverse transcript
C 593	18	1.0	21	1	AAQ75668	Reverse transcript	C 666	17.4	1.0	20	1	AAQ75559	Reverse transcript
C 594	18	1.0	21	1	AAQ75607	Reverse transcript	C 667	17.4	1.0	20	1	AAQ75575	Reverse transcript
C 595	18	1.0	21	1	AAQ75625	Reverse transcript	C 668	17.4	1.0	20	1	AAQ75586	Reverse transcript
C 596	18	1.0	21	1	AAQ75634	Reverse transcript	C 669	17.4	1.0	20	1	AAQ75594	Reverse transcript
C 597	18	1.0	21	1	AAQ75665	Reverse transcript	C 670	17.4	1.0	20	1	AAQ75581	Reverse transcript
C 598	18	1.0	21	1	AAQ75667	Reverse transcript	C 671	17.4	1.0	20	1	AAQ75578	Reverse transcript
C 599	18	1.0	21	1	AAQ75608	Reverse transcript	C 672	17.4	1.0	20	1	AAQ75602	Reverse transcript
C 600	18	1.0	21	1	AAQ75655	Reverse transcript	C 673	17.4	1.0	20	1	AAQ75582	Reverse transcript
C 601	18	1.0	21	1	AAQ75663	Reverse transcript	C 674	17.4	1.0	20	1	AAQ75592	Reverse transcript
C 602	18	1.0	21	1	AAQ75636	Reverse transcript	C 675	17.4	1.0	20	1	AAQ75576	Reverse transcript
C 603	18	1.0	21	1	AAQ75610	Reverse transcript	C 676	17.4	1.0	20	1	ABZ88266	Human oligonucleot
C 604	18	1.0	21	1	AAQ75632	Reverse transcript	C 677	17.4	1.0	20	1	ABZ85534	Human oligonucleot
C 605	18	1.0	21	1	AAQ75619	Reverse transcript	C 678	17.4	1.0	20	1	ABZ89487	Human oligonucleot
C 606	18	1.0	21	1	AAQ75621	Reverse transcript	C 679	17.4	1.0	20	1	ABZ88564	Human oligonucleot
C 607	18	1.0	21	1	AAQ75656	Reverse transcript	C 680	17.4	1.0	20	1	ABZ89703	Reverse transcript
C 608	18	1.0	21	1	AAQ75624	Reverse transcript	C 681	17.4	1.0	21	1	AAQ75735	Reverse transcript
C 609	18	1.0	21	1	AAQ75637	Reverse transcript	C 682	17.4	1.0	21	1	AAQ75738	Reverse transcript
C 610	18	1.0	21	1	AAQ75666	Reverse transcript	C 683	17.4	1.0	21	1	AAQ75719	Reverse transcript
C 611	18	1.0	21	1	AAQ75623	Reverse transcript	C 684	17.4	1.0	21	1	AAQ75739	Reverse transcript
C 612	18	1.0	21	1	AAQ75635	Reverse transcript	C 685	17.4	1.0	21	1	AAQ75729	Reverse transcript
C 613	18	1.0	21	1	AAQ75658	Reverse transcript	C 686	17.4	1.0	21	1	AAQ75732	Reverse transcript
C 614	18	1.0	21	1	AAQ75638	Reverse transcript	C 687	17.4	1.0	21	1	AAQ75718	Reverse transcript
C 615	18	1.0	22	1	AAQ64706	2',5'-linked tetra	C 688	17.4	1.0	21	1	AAQ75741	Reverse transcript
C 616	18	1.0	22	1	ABX94933	Renilla luciferase	C 689	17.4	1.0	21	1	AAQ75742	Reverse transcript
C 617	18	1.0	23	1	AAD37503	T7Tl8Apad PS13-23-	C 690	17.4	1.0	21	1	AAQ75747	Reverse transcript

C 691	17.4	1.0	21	1	AAQ75715	Reverse transcript	C 764	17	1.0	21	1	AAQ75798	Reverse transcript
C 692	17.4	1.0	21	1	AAQ75686	Reverse transcript	C 765	17	1.0	21	1	AAQ75687	Reverse transcript
C 693	17.4	1.0	21	1	AAQ75703	Reverse transcript	C 766	17	1.0	21	1	AAQ75693	Reverse transcript
C 694	17.4	1.0	21	1	AAQ75706	Reverse transcript	C 767	17	1.0	21	1	AAQ75787	Reverse transcript
C 695	17.4	1.0	21	1	AAQ75717	Reverse transcript	C 768	17	1.0	21	1	AAQ75793	Reverse transcript
C 696	17.4	1.0	21	1	AAQ75731	Reverse transcript	C 769	17	1.0	21	1	AAQ75794	Reverse transcript
C 697	17.4	1.0	21	1	AAQ75782	Reverse transcript	C 770	17	1.0	21	1	AAQ75690	Reverse transcript
C 698	17.4	1.0	21	1	AAQ75707	Reverse transcript	C 771	17	1.0	21	1	AAQ75763	Reverse transcript
C 699	17.4	1.0	21	1	AAQ75750	Reverse transcript	C 772	17	1.0	21	1	AAQ75688	Reverse transcript
C 700	17.4	1.0	21	1	AAQ75749	Reverse transcript	C 773	17	1.0	21	1	AAQ75700	Reverse transcript
C 701	17.4	1.0	21	1	AAQ75709	Reverse transcript	C 774	17	1.0	21	1	AAQ75786	Reverse transcript
C 702	17.4	1.0	21	1	AAQ75720	Reverse transcript	C 775	17	1.0	21	1	AAQ75764	Reverse transcript
C 703	17.4	1.0	23	1	ABQ96219	Tumour suppression	C 776	17	1.0	21	1	AAQ75796	Reverse transcript
C 704	17.2	1.0	19	1	AAQ75431	Template mRNA poly	C 777	17	1.0	21	1	AAQ75797	Reverse transcript
C 705	17.2	1.0	19	1	AAQ75431	RT-PCR primer of t	C 778	17	1.0	21	1	AAQ75757	Reverse transcript
C 706	17.2	1.0	22	1	AAQ75431	Guanine quartet co	C 779	17	1.0	21	1	AAQ75790	Reverse transcript
C 707	17.2	1.0	22	1	AAQ75431	Guanine quartet co	C 780	17	1.0	21	1	AAQ75697	Reverse transcript
C 708	17.2	1.0	22	1	AAQ75431	HSV replication in	C 781	17	1.0	21	1	AAQ75784	Reverse transcript
C 709	17.2	1.0	22	1	AAQ75431	HSV replication in	C 782	17	1.0	21	1	AAQ75698	Reverse transcript
C 710	17.2	1.0	22	1	AAQ75431	Peptide nucleic ac	C 783	17	1.0	21	1	AAQ75699	Reverse transcript
C 711	17.2	1.0	22	1	AAQ75431	Immunostimulatory	C 784	17	1.0	21	1	AAQ75751	Reverse transcript
C 712	17.2	1.0	22	1	AAQ75431	Angiogenesis inhib	C 785	17	1.0	21	1	AAQ75691	Reverse transcript
C 713	17.2	1.0	22	1	AAQ75431	Immunostimulatory	C 786	17	1.0	21	1	AAQ75754	Reverse transcript
C 714	17.2	1.0	22	1	AAQ75431	Immunostimulatory	C 787	17	1.0	21	1	AAQ75755	Reverse transcript
C 715	17	1.0	17	1	AAQ75431	Oestrogen receptor	C 788	17	1.0	21	1	AAQ75761	Reverse transcript
C 716	17	1.0	17	1	AAQ75431	Oestrogen receptor	C 789	17	1.0	21	1	AAQ75765	Reverse transcript
C 717	17	1.0	17	1	AAQ75431	Oestrogen receptor	C 790	17	1.0	21	1	AAQ75789	Reverse transcript
C 718	17	1.0	17	1	AAQ75431	Oestrogen receptor	C 791	17	1.0	21	1	AAQ75701	Reverse transcript
C 719	17	1.0	17	1	AAQ75431	Human retrovirus H	C 792	17	1.0	21	1	AAQ75766	Reverse transcript
C 720	17	1.0	17	1	AAQ75431	2'-Methoxyethoxy-m	C 793	17	1.0	21	1	AAQ75783	Reverse transcript
C 721	17	1.0	17	1	AAQ75431	Tumour suppression	C 794	17	1.0	22	1	AAQ75761	Human mismatch rep
C 722	17	1.0	17	1	AAQ75431	Human MDZ7 scannin	C 795	16.8	1.0	20	1	AAQ73379	Anti-HSV-1 G4 olig
C 723	17	1.0	17	1	AAQ75644	Antisense oligo #2	C 796	16.8	1.0	20	1	AAQ61999	Guanine quartet co
C 724	17	1.0	17	1	AAQ75644	2'-P-ANA antisense	C 797	16.8	1.0	20	1	AAQ61896	HSV replication in
C 725	17	1.0	17	1	AAQ75644	2'-F-ANA antisense	C 798	16.8	1.0	20	1	AAQ61995	Guanine quartet co
C 726	17	1.0	17	1	AAQ75644	2'-F-ANA antisense	C 799	16.8	1.0	20	1	AAQ61904	HSV replication in
C 727	17	1.0	17	1	AAQ75645	2'-F-ANA antisense	C 800	16.8	1.0	20	1	AAQ75982	Peptide nucleic ac
C 728	17	1.0	17	1	AAQ75558	Tumour suppression	C 801	16.8	1.0	20	1	AAQ75712	Oligonucleotide 7
C 729	17	1.0	18	1	AAQ75558	Sequence derived f	C 802	16.8	1.0	20	1	AAQ75712	Antisense IGFBP-5
C 730	17	1.0	18	1	AAQ75558	Anchored poly(T) o	C 803	16.8	1.0	20	1	AAQ75712	Human daxx inhibit
C 731	17	1.0	18	1	AAQ75558	Anchored poly(T) o	C 804	16.8	1.0	20	1	AAQ75712	Polyprimidine Cri
C 732	17	1.0	18	1	AAQ75558	Nucleotide sequenc	C 805	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 733	17	1.0	18	1	AAQ75558	Human protein AQ2	C 806	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 734	17	1.0	18	1	AAQ75558	Phosphorothioate o	C 807	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 735	17	1.0	18	1	AAQ75558	Human adult ovary	C 808	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 736	17	1.0	18	1	AAQ75558	Human adipose tiss	C 809	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 737	17	1.0	18	1	AAQ75558	Binary encoded seq	C 810	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 738	17	1.0	18	1	AAQ75558	mRNA fragment used	C 811	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 739	17	1.0	19	1	AAQ75558	Reverse transcript	C 812	16.8	1.0	20	1	AAQ75712	Human oligonucleot
C 740	17	1.0	19	1	AAQ75558	Reverse transcript	C 813	16.8	1.0	21	1	AAQ75712	Human gene single
C 741	17	1.0	19	1	AAQ75558	Reverse transcript	C 814	16.8	1.0	21	1	AAQ75712	Aryl hydrocarbon n
C 742	17	1.0	19	1	AAQ75558	Telomerase Oligo-d	C 815	16.8	1.0	21	1	AAQ75712	Primer of the inve
C 743	17	1.0	20	1	AAQ75558	Reverse transcript	C 816	16.8	1.0	22	1	AAQ75712	Primer of the inve
C 744	17	1.0	20	1	AAQ75558	Reverse transcript	C 817	16.4	0.9	18	1	AAQ75712	RT-PCR primer of t
C 745	17	1.0	20	1	AAQ75558	Reverse transcript	C 818	16.4	0.9	18	1	AAQ75712	RT-PCR primer of t
C 746	17	1.0	20	1	AAQ75558	Reverse transcript	C 819	16.4	0.9	18	1	AAQ75712	5'-PCR primer used
C 747	17	1.0	20	1	AAQ75597	Reverse transcript	C 820	16.4	0.9	18	1	AAQ75712	Nucleotide sequenc
C 748	17	1.0	20	1	AAQ75604	Reverse transcript	C 821	16.4	0.9	18	1	AAQ75712	Nucleotide sequenc
C 749	17	1.0	20	1	AAQ75588	Reverse transcript	C 822	16.4	0.9	19	1	AAQ75712	Mitogen activated
C 750	17	1.0	20	1	AAQ75590	Reverse transcript	C 823	16.4	0.9	19	1	AAQ75712	Mitogen activated
C 751	17	1.0	20	1	AAQ75590	Reverse transcript	C 824	16.4	0.9	20	1	AAQ75712	Ribonucleotide red
C 752	17	1.0	20	1	AAQ75606	Reverse transcript	C 825	16.4	0.9	20	1	AAQ75712	PCR primer used to
C 753	17	1.0	20	1	AAQ75606	Reverse transcript	C 826	16.4	0.9	20	1	AAQ75712	Synthetic oligonuc
C 754	17	1.0	20	1	AAQ75587	Reverse transcript	C 827	16.4	0.9	20	1	AAQ75712	Hepatitis B virus
C 755	17	1.0	20	1	AAQ75871	Nucleotide sequenc	C 828	16.4	0.9	20	1	AAQ75712	Hepatitis B virus
C 756	17	1.0	20	1	AAQ75896	Human oligonucleot	C 829	16.4	0.9	20	1	AAQ75712	Human oligonucleot
C 757	17	1.0	20	1	AAQ75853	Human oligonucleot	C 830	16.4	0.9	20	1	AAQ75712	Human oligonucleot
C 758	17	1.0	20	1	AAQ75897	Human oligonucleot	C 831	16.4	0.9	20	1	AAQ75712	Human oligonucleot
C 759	17	1.0	20	1	AAQ75897	Human oligonucleot	C 832	16.4	0.9	21	1	AAQ75712	Baculovirus C2 com
C 760	17	1.0	21	1	AAQ75702	Reverse transcript	C 833	16.4	0.9	21	1	AAQ75712	Human polymorphic
C 761	17	1.0	21	1	AAQ75752	Reverse transcript	C 834	16.4	0.9	21	1	AAQ75712	Human polymorphic
C 762	17	1.0	21	1	AAQ75762	Reverse transcript	C 835	16.4	0.9	21	1	AAQ75712	Human polymorphic
C 763	17	1.0	21	1	AAQ75795	Reverse transcript	C 836	16.4	0.9	21	1	AAQ75712	PCR primer used to

C 837	16.2	0.9	18	1	AA18389	RT-PCR primer of t	C 910	15.8	0.9	20	1	AB282707	Human HSL chimeric
C 838	16.2	0.9	21	1	AAV48674	JunB gene antisense	C 911	15.8	0.9	20	1	AB222800	Human heparanase p
C 839	16.2	0.9	21	1	ADB74186	Rice transposon ge	C 912	15.8	0.9	20	1	ADC39031	Human ELAM-1 taige
C 840	16	0.9	16	1	AA18367	RT-PCR primer of t	C 913	15.8	0.9	21	1	ADC35554	Human CD81/TAPA-1
C 841	16	0.9	16	1	AA07568	Homo sapiens fetal	C 914	15.8	0.9	21	1	AA226004	Human polymorphic
C 842	16	0.9	16	1	AA066068	DNA chip primer #4	C 915	15.8	0.9	21	1	AA276115	Human biallelic ma
C 843	16	0.9	16	1	ABA00585	Oligonucleotide #5	C 916	15.8	0.9	21	1	AA280155	Forward primer #26
C 844	16	0.9	16	1	AAF30895	Oligonucleotide-mi	C 917	15.6	0.9	17	1	AAV19118	Anchor oligo (T)
C 845	16	0.9	16	1	AA030880	Oligonucleotide po	C 918	15.4	0.9	17	1	AA18371	RT-PCR primer of t
C 846	16	0.9	16	1	AAH42481	Oligonucleotide us	C 919	15.4	0.9	17	1	AA18370	RT-PCR primer of t
C 847	16	0.9	16	1	ABA97402	Nucleotide sequenc	C 920	15.4	0.9	17	1	AA25456	Oestrogen receptor
C 848	16	0.9	16	1	AA056451	2'-F-ANA antisense	C 921	15.4	0.9	17	1	AA25455	Oestrogen receptor
C 849	16	0.9	16	1	AA154078	Oligo-homodeoxyrib	C 922	15.4	0.9	17	1	AA25457	Oestrogen receptor
C 850	16	0.9	16	1	AB068519	DNA hybridisation	C 923	15.4	0.9	17	1	ABK02364	Human NOD2 Ambery
C 851	16	0.9	17	1	AA069800	Human flt1 VEGF re	C 924	15.4	0.9	17	1	ABA91530	Human ERG DNzyme
C 852	16	0.9	17	1	AA069801	Human flt1 VEGF re	C 925	15.4	0.9	17	1	ABK18820	Oligo-AT PCR prime
C 853	16	0.9	17	1	AA030181	PCR primer GT15G u	C 926	15.4	0.9	17	1	AA044151	Human MD27 scannin
C 854	16	0.9	17	1	AA235714	Murine gene anchor	C 927	15.4	0.9	17	1	ADB04269	Human MD27 scannin
C 855	16	0.9	17	1	AA082721	Human IGA nephropa	C 928	15.4	0.9	17	1	ADB04270	Murine oligonucleo
C 856	16	0.9	17	1	AA036740	Anchor oligo (GT)	C 929	15.4	0.9	17	1	ACC63788	Cross-linking olig
C 857	16	0.9	17	1	AA025449	Oestrogen receptor	C 930	15.4	0.9	18	1	AAQ20109	Cross-linking olig
C 858	16	0.9	17	1	AA025454	Oestrogen receptor	C 931	15.4	0.9	18	1	AAQ20108	Cross-linking olig
C 859	16	0.9	17	1	AA064204	PCR anchor primer,	C 932	15.4	0.9	18	1	AAQ30446	Oligomer TNFR941 f
C 860	16	0.9	17	1	AA064183	PCR anchor primer,	C 933	15.4	0.9	18	1	AAQ35501	Purine rich HUMNFR
C 861	16	0.9	17	1	AA064173	PCR anchor primer,	C 934	15.4	0.9	18	1	AAQ30448	Oligomer TNFR943 f
C 862	16	0.9	17	1	AA064163	PCR anchor primer,	C 935	15.4	0.9	18	1	AAQ30447	Oligomer TNFR942 f
C 863	16	0.9	17	1	AA064215	PCR anchor primer,	C 936	15.4	0.9	18	1	AAV54170	Nucleotide sequenc
C 864	16	0.9	17	1	AA064232	PCR anchor primer,	C 937	15.4	0.9	18	1	AAV54164	Nucleotide sequenc
C 865	16	0.9	17	1	AA092294	Human pollinosis-a	C 938	15.4	0.9	18	1	AAV54169	Nucleotide sequenc
C 866	16	0.9	17	1	AA092294	PCR anchor primer,	C 939	15.4	0.9	18	1	AAV54172	Nucleotide sequenc
C 867	16	0.9	17	1	AA084876	Human pollinosis-a	C 940	15.4	0.9	18	1	AAV54167	Nucleotide sequenc
C 868	16	0.9	17	1	AAH47128	Nucleotide sequenc	C 941	15.4	0.9	18	1	AAV22960	Probe used to isol
C 869	16	0.9	17	1	ABK13941	5'-PCR primer used	C 942	15.4	0.9	18	1	AA290642	Human adipose tiss
C 870	16	0.9	17	1	ABK49636	Human Acetyltransf	C 943	15.4	0.9	18	1	AA290646	Human adipose tiss
C 871	16	0.9	17	1	ABL59040	Nucleotide sequenc	C 944	15.4	0.9	18	1	AA290640	Human adipose tiss
C 872	16	0.9	17	1	ABN99831	Human allergic dis	C 945	15.4	0.9	18	1	AA290645	Human adipose tiss
C 873	16	0.9	17	1	AA049950	Human B153 expres	C 946	15.4	0.9	18	1	AA290643	Human adipose tiss
C 874	16	0.9	17	1	AA047236	Allergic disease e	C 947	15.4	0.9	19	1	AA060415	Primer eGFP2 used
C 875	16	0.9	17	1	ABK49758	Human atopic derma	C 948	15.4	0.9	20	1	AA073293	Primer for pUC19 D
C 876	16	0.9	17	1	ABK404273	Human MD27 scannin	C 949	15.4	0.9	20	1	AA073291	Primer 1 for pUC19
C 877	16	0.9	17	1	ABK404271	Human MD27 scannin	C 950	15.4	0.9	20	1	AA073292	Primer 2 for pUC19
C 878	16	0.9	17	1	AB270578	Primer. Synthetic	C 951	15.4	0.9	20	1	AA072164	Humanised anti-Fas
C 879	16	0.9	17	1	ACF36345	Nucleotide sequenc	C 952	15.4	0.9	20	1	AA072168	Humanised anti-Fas
C 880	16	0.9	17	1	ACF36370	Nucleotide sequenc	C 953	15.4	0.9	20	1	AA072168	Humanised anti-Fas
C 881	16	0.9	17	1	ADC84470	PCR primer for amp	C 954	15.4	0.9	20	1	AA072168	Murine melanocorti
C 882	16	0.9	18	1	AAV54174	Nucleotide sequenc	C 955	15.4	0.9	20	1	AA072168	Humanised HFE7A de
C 883	16	0.9	18	1	AAV54165	Nucleotide sequenc	C 956	15.4	0.9	20	1	AA072168	Humanised HFE7A de
C 884	16	0.9	18	1	AAV54171	Nucleotide sequenc	C 957	15.4	0.9	20	1	ABL48724	Humanised anti-Fas
C 885	16	0.9	18	1	AAV54165	Nucleotide sequenc	C 958	15.4	0.9	20	1	ABL48728	Humanised anti-Fas
C 886	16	0.9	18	1	AAV54165	Human adipose tiss	C 959	15.4	0.9	20	1	ABA05917	Hepatitis B virus
C 887	16	0.9	18	1	AAV54165	Human adipose tiss	C 960	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 888	16	0.9	18	1	AAV54165	Human adipose tiss	C 961	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 889	16	0.9	18	1	AAV54165	Human adipose tiss	C 962	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 890	16	0.9	18	1	AAV54165	Human adipose tiss	C 963	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 891	16	0.9	18	1	AAV54165	Human adipose tiss	C 964	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 892	16	0.9	18	1	AAV54165	Human adipose tiss	C 965	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 893	16	0.9	18	1	AAV54165	Human adipose tiss	C 966	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 894	16	0.9	18	1	AAV54165	Human adipose tiss	C 967	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 895	16	0.9	18	1	AAV54165	Human adipose tiss	C 968	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 896	16	0.9	18	1	AAV54165	Human adipose tiss	C 969	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 897	16	0.9	18	1	AAV54165	Human adipose tiss	C 970	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 898	16	0.9	18	1	AAV54165	Human adipose tiss	C 971	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 899	16	0.9	18	1	AAV54165	Human adipose tiss	C 972	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 900	16	0.9	18	1	AAV54165	Human adipose tiss	C 973	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 901	16	0.9	18	1	AAV54165	Human adipose tiss	C 974	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 902	16	0.9	18	1	AAV54165	Human adipose tiss	C 975	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 903	16	0.9	18	1	AAV54165	Human adipose tiss	C 976	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 904	16	0.9	18	1	AAV54165	Human adipose tiss	C 977	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 905	16	0.9	18	1	AAV54165	Human adipose tiss	C 978	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 906	16	0.9	18	1	AAV54165	Human adipose tiss	C 979	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 907	16	0.9	18	1	AAV54165	Human adipose tiss	C 980	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 908	16	0.9	18	1	AAV54165	Human adipose tiss	C 981	15.4	0.9	20	1	ABL45981	Humanised anti-Fas
C 909	16	0.9	18	1	AAV54165	Human adipose tiss	C 982	15.4	0.9	20	1	ABL45981	Humanised anti-Fas

c1129	15	0.9	17	1	ADB04274	Human MD27 scannin	1202	14.4	0.8	19	1	AAC69249	Human ABC1 gene ex
c1130	15	0.9	17	1	ADC84468	PCR primer for amp	c1203	14.4	0.8	19	1	AAC94997	Oligonucleotide KC
c1131	15	0.9	17	1	ADC84468	PCR primer for amp	1204	14.4	0.8	19	1	AAH94353	Cyclin D2 ribozyme
c1132	15	0.9	17	1	ADE77745	DNA oligo (SeqID 5	1205	14.4	0.8	19	1	AAH95915	Cyclin D2 ribozyme
c1133	15	0.9	17	1	AAV54175	Nucleotide sequenc	1206	14.4	0.8	19	1	ABX94535	23S/16S rRNA detec
c1134	15	0.9	18	1	AAV54173	Nucleotide sequenc	1207	14.4	0.8	20	1	ACC82908	Human TRIP6 antis
c1135	15	0.9	18	1	AAV54166	Nucleotide sequenc	1208	14.4	0.8	20	1	ACC82908	Human TRIP6 antis
c1136	15	0.9	18	1	AAV33391	HIV-1 gag protein	1209	14.2	0.8	15	1	AAA47676	Oligo d(T) primer
c1137	15	0.9	18	1	AAZ90649	Human adipose tiss	1209	14.2	0.8	15	1	AAA47676	Oligo d(T) primer
c1138	15	0.9	18	1	AAZ90648	Human adipose tiss	c1210	14.2	0.8	15	1	AAH44150	RT-PCR primer of t
c1139	15	0.9	18	1	AAZ90651	Human adipose tiss	c1211	14.2	0.8	16	1	AAH18387	Human TSA7005 gene
c1140	15	0.9	18	1	AAZ90651	Human adipose tiss	c1212	14.2	0.8	16	1	AAH27758	Primer used in hum
c1141	15	0.9	18	1	AAZ58385	Polynucleotide # 1	1213	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1142	15	0.9	18	1	AAZ58386	Polynucleotide # 2	c1214	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1143	15	0.9	20	1	AAZ01703	Oligonucleotide ba	c1215	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1144	15	0.9	20	1	AAZ01703	PCR primer used to	c1216	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1145	15	0.9	20	1	AAZ36602	Human Her-1 antis	c1217	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1146	15	0.9	20	1	ABL57070	Molecular beacon t	c1218	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1147	15	0.9	20	1	ADZ35095	HT15-C downstream	1219	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1148	15	0.9	20	1	ABZ87313	Human oligonucleot	c1220	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1149	15	0.9	20	1	ABZ98535	Human ICAM oligonu	c1221	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1150	15	0.9	20	1	ABZ89440	Human oligonucleot	c1222	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1151	15	0.9	20	1	ABZ90649	Human oligonucleot	c1223	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1152	15	0.9	20	1	ABZ25524	Human p53 exon 5 p	1224	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1153	14.8	0.8	18	1	ADZ57844	Target oligonucleo	c1225	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1154	14.8	0.8	18	1	AAQ73381	Anti-HSV-1 G4 olig	c1226	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1155	14.8	0.8	18	1	AAQ61992	Guanine quartet co	c1227	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1156	14.8	0.8	18	1	AAQ61897	HSV replication in	1228	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1157	14.8	0.8	18	1	AAQ61913	HIV replication in	c1229	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1158	14.8	0.8	18	1	AAQ97983	Peptide nucleic ac	c1230	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1159	14.8	0.8	18	1	AAZ25595	Human flt1 VEGF re	c1231	14.4	0.8	14	1	AAQ33508	Sequence of micros
c1160	14.8	0.8	18	1	AAZ52631	Human rhog antisen	1232	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1161	14.8	0.8	18	1	AAZ52631	Human secreted pro	c1233	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1162	14.8	0.8	18	1	AAZ52631	Rho G antisense ph	c1234	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1163	14.8	0.8	18	1	ABA91529	DNA-RNA-DNA oligon	c1235	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1164	14.8	0.8	18	1	ABK27450	Colon cancer assoc	c1236	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1165	14.8	0.8	18	1	ABL43463	Human chromosome 1	1237	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1166	14.8	0.8	18	1	ABN89400	Rice acetolactate a	c1238	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1167	14.8	0.8	18	1	ADA27360	Human microsatelli	c1239	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1168	14.8	0.8	18	1	ADA27360	Rice acetolactate	c1240	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1169	14.8	0.8	19	1	AAZ82914	cdk4 ribozyme bind	c1241	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1170	14.8	0.8	19	1	AAZ57557	Mouse CD7 gene fra	c1242	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1171	14.8	0.8	19	1	AAH58076	Cell-cycle depende	c1243	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1172	14.8	0.8	19	1	ABK93655	Human inhibitor of	c1244	14.4	0.8	15	1	AAQ33508	Sequence of micros
c1173	14.6	0.8	15	1	ABK32799	Rhesus rotavirus (c1245	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1174	14.4	0.8	16	1	AAV08586	Human APPBP1 gene,	c1246	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1175	14.4	0.8	16	1	AAV18360	Primer ACE/118FT f	1247	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1176	14.4	0.8	16	1	AAV18360	RT-PCR primer of t	1248	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1177	14.4	0.8	16	1	AAV18360	RT-PCR primer of t	1249	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1178	14.4	0.8	16	1	AAV18360	RT-PCR primer of t	1250	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1179	14.4	0.8	16	1	AAV18360	Human angiotensin-	1251	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1180	14.4	0.8	16	1	AAV18360	Human ACE, AGT and	c1252	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1181	14.4	0.8	16	1	AAV18360	Oligo-dT PCR prime	c1253	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1182	14.4	0.8	17	1	AAZ5458	Oestrogen receptor	c1254	14.4	0.8	16	1	AAQ33508	Sequence of micros
c1183	14.4	0.8	17	1	ABK03501	Human CD20 Zinzyne	c1255	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1184	14.4	0.8	17	1	ABK03501	Human NODG Amberzy	c1256	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1185	14.4	0.8	17	1	ABK03501	Human GDMPL-1 17-m	c1257	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1186	14.4	0.8	17	1	ABK03501	Human GDMPL-1 17-m	c1258	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1187	14.4	0.8	17	1	ABK03501	Human ERG hamme	1259	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1188	14.4	0.8	17	1	ACA06469	NFKB sub-unit modu	c1260	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1189	14.4	0.8	17	1	ACA06469	NFKB sub-unit modu	c1261	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1190	14.4	0.8	17	1	ACA06469	NFKB sub-unit modu	c1262	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1191	14.4	0.8	17	1	ABZ65136	Human MD27 scannin	c1263	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1192	14.4	0.8	17	1	ABZ65136	Human HER2 DNzyme	c1264	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1193	14.4	0.8	17	1	ABZ65136	Human H-Ras DNzyme	c1265	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1194	14.4	0.8	17	1	ABZ65136	Human K-Ras DNzyme	1266	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1195	14.4	0.8	18	1	AAZ94794	Human leukocyte an	1267	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1196	14.4	0.8	18	1	AAZ94794	Human CD71 phospho	1268	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1197	14.4	0.8	18	1	AAZ94794	Single nucleotide	1269	14.4	0.8	17	1	AAQ33508	Sequence of micros
c1198	14.4	0.8	18	1	AAZ94794	SNP specific lower	c1270	14.4	0.8	18	1	AAQ33508	Sequence of micros
c1199	14.4	0.8	18	1	AAZ94794	Human Her-2 antis	c1271	14.4	0.8	18	1	AAQ33508	Sequence of micros
c1200	14.4	0.8	18	1	AAZ94794	Antisense inhibiti	1272	14.4	0.8	18	1	AAQ33508	Sequence of micros
c1201	14.4	0.8	19	1	AAV65956	Downstream PCR pri	c1273	13.8	0.8	17	1	AAQ33508	Sequence of micros

Human ABC1 gene ex
Oligonucleotide KC
Cyclin D2 ribozyme
Cyclin D2 ribozyme
23S/16S rRNA detec
Human TRIP6 antis
Oligo d(T) primer
Oligo-dT PCR prime
RT-PCR primer of t
Human TSA7005 gene
Primer used in hum
Sequence of micros
3' primer for DUB-
3' poly(T) primer
Poly(T) oligonucle
Barley HPPD primer
Triple helix third
Triple helix formi
Triple helix formi
WO9223258 oligonuc
Human senescence f
Oligonucleotide #1
Oligonucleotide #2
RNA oligonucleotid
EG1 cDNA tag relat
EG1 cDNA tag relat
EG1 cDNA tag relat
Retinoid-regulated
Light responsive o
Mouse ICAM hammerh
Mouse reia hammerh
Human ICAM hammerh
Human ICAM hammerh
Human ICAM hammerh
RT-PCR primer of t
Gastric acid produ
IGF-1 oligonucleot
Triple helix formi
Triple helix formi
Triple helix formi
Triple helix formi
Triple helix formi
EST polymorphic DN
RT-PCR primer of t
RT-PCR primer of t
Primer for sequenc
Primer for sequenc
CC83 heavy chain o
CC83 heavy chain o
Mouse immunoglobul
Oligo-dT PCR prime
Oligo-dT PCR prime
Oligo-dT PCR prime
Oligo-dT PCR prime
Human flt1 VEGF re
Human flt1 VEGF re
Human TIB-2 subatr
Oestrogen receptor
Human ERG hamme
Human POSHL1 scann
Human POSHL1 scann
Human MD27 scannin
Murine oligonucleo
Murine oligonucleo
Murine oligonucleo
Tumour suppression
Tumour suppression
Plant growth assoc
DNA sequence of ca
SNP specific lower
Drosophila ubx gen
Human chromosome 1
Camellia sinensis
Human c-myb hammer

c1275	13.8	0.8	17	1	AAAX75068	Mouse flt-1 VEGF r	c1348	13.8	0.8	18	1	AAAT31547	Vaccinia virus thymine kinase
c1276	13.8	0.8	17	1	AAAX75073	Mouse flt-1 VEGF r	c1349	13.8	0.8	18	1	AAAZ31397	TK gene specific factor
c1277	13.8	0.8	17	1	AAAX69804	Human flt1 VEGF re	c1350	13.8	0.8	18	1	AAAT96696	Hereditary haemochromatosis
c1278	13.8	0.8	17	1	AAAX75070	Mouse flt-1 VEGF r	c1351	13.8	0.8	18	1	AAAV01515	Antisense primer for VEGF
c1279	13.8	0.8	17	1	AAAX75069	Mouse flt-1 VEGF re	c1352	13.8	0.8	18	1	AAAT5622	Mouse flt-1 VEGF r
c1280	13.8	0.8	17	1	AAAX69380	Human flt1 VEGF re	c1353	13.8	0.8	18	1	AAAT85157	Vaccinia virus thymine kinase
c1281	13.8	0.8	17	1	AAAX75071	Mouse flt-1 VEGF re	c1354	13.8	0.8	18	1	AAAV12805	Clonotypic IGH CDR
c1282	13.8	0.8	17	1	AAAX69805	Human flt1 VEGF re	c1355	13.8	0.8	18	1	AAAX89560	Forward PCR primer
c1283	13.8	0.8	17	1	AAAX63006	Delta-9 desaturase	c1356	13.8	0.8	18	1	AAAX06978	Secretory peptide
c1284	13.8	0.8	17	1	AAAX20382	Integrin alpha 6 s	c1357	13.8	0.8	18	1	AAAX08679	Oligonucleotide de
c1285	13.8	0.8	17	1	AAAX20383	Integrin alpha 6 s	c1358	13.8	0.8	18	1	AAAZ08292	Antisense PCR prim
c1286	13.8	0.8	17	1	AAAX18807	Human TIE-2 subtr	c1359	13.8	0.8	18	1	AAAZ30195	PCR primer Mki7 us
c1287	13.8	0.8	17	1	AAAX36380	Human genomic SNP	c1360	13.8	0.8	18	1	AAAX25292	Antisense oligonuc
c1288	13.8	0.8	17	1	AAAX36382	Human genomic SNP	c1361	13.8	0.8	18	1	AAAX25213	Antisense oligonuc
c1289	13.8	0.8	17	1	AAAZ40668	L. delbruekii inae	c1362	13.8	0.8	18	1	AAAZ27102	Helicase cleavage
c1290	13.8	0.8	17	1	AAAZ25445	Oestrogen receptor	c1363	13.8	0.8	18	1	AAAZ62882	Shrimp white spot
c1291	13.8	0.8	17	1	AAAZ25182	Oestrogen receptor	c1364	13.8	0.8	18	1	AAAF73407	Grand fir monoterp
c1292	13.8	0.8	17	1	AAAZ25180	Oestrogen receptor	c1365	13.8	0.8	18	1	AAAF45239	Human fibronectin
c1293	13.8	0.8	17	1	AAAZ25446	Oestrogen receptor	c1366	13.8	0.8	18	1	ABK72460	Sample orionucleo
c1294	13.8	0.8	17	1	AAAZ25181	Oestrogen receptor	c1367	13.8	0.8	18	1	ABL54126	Cleavage product o
c1295	13.8	0.8	17	1	AAAF02549	Hammerhead ribozym	c1368	13.8	0.8	18	1	ABN99768	DNA probe #22 for
c1296	13.8	0.8	17	1	AAAF06382	Hammerhead ribozym	c1369	13.8	0.8	18	1	ABL54922	Human tumour suppr
c1297	13.8	0.8	17	1	AAAF06381	Hammerhead ribozym	c1370	13.8	0.8	18	1	ABT04715	End-labelled probe
c1298	13.8	0.8	17	1	AAAF03345	Hammerhead ribozym	c1371	13.8	0.8	18	1	ABK43380	Siglec-BMS, PCR pr
c1299	13.8	0.8	17	1	AAAF03342	Hammerhead ribozym	c1372	13.8	0.8	18	1	ABK43392	Siglec-BMS, PCR pr
c1300	13.8	0.8	17	1	AAAF05473	Hammerhead ribozym	c1373	13.8	0.8	18	1	ABQ78689	Cleavage product o
c1301	13.8	0.8	17	1	AAAF02205	Hammerhead ribozym	c1374	13.8	0.8	18	1	ABL59657	Oligonucleotide pr
c1302	13.8	0.8	17	1	AAAC67367	Alzheimer's disease	c1375	13.8	0.8	18	1	ABT06236	Synthetic DNA sell
c1303	13.8	0.8	17	1	ABK01375	Human NOGO Inozyme	c1376	13.8	0.8	18	1	ABK87302	FEN 1 nuclease cle
c1304	13.8	0.8	17	1	ABK02358	Human NOGO Ambery	c1377	13.8	0.8	18	1	ADAL4814	Vaccinia virus TK
c1305	13.8	0.8	17	1	ABK02357	Human NOGO Ambery	c1378	13.8	0.8	18	1	ABZ59706	Humanin-like prote
c1306	13.8	0.8	17	1	ABK03744	Human CD20 Ambery	c1379	13.8	0.8	18	1	AAAL61062	Human humanin cDNA
c1307	13.8	0.8	17	1	ABK02367	Human NOGO Ambery	c1380	13.8	0.8	18	1	ADC35343	Vaccinia virus thymine kinase
c1308	13.8	0.8	17	1	ABLA46642	Human GRID NCH rib	c1381	13.8	0.8	18	1	ABE15136	Beer spoilage-asso
c1309	13.8	0.8	17	1	ABLA46640	Human GRID NCH rib	c1382	13.6	0.8	15	1	AAAD32456	Human ORG1 gene p
c1310	13.8	0.8	17	1	ABLA46643	Human GRID NCH rib	c1383	13.6	0.8	15	1	ABN87920	Human GSR allele s
c1311	13.8	0.8	17	1	ABLA46459	Human GRID hammerh	c1384	13.6	0.8	15	1	ABK92606	ASO primer #4 to d
c1312	13.8	0.8	17	1	ABLA46888	Human GRID G-cleav	c1385	13.6	0.8	15	1	AAAD25688	Human CDK4 gene po
c1313	13.8	0.8	17	1	ACAC89333	First conventional	c1386	13.4	0.8	15	1	AAAS6927	HIV-1 proviral DNA
c1314	13.8	0.8	17	1	ABN10512	Human GDMPLP-1 17-m	c1387	13.4	0.8	15	1	AAAT86603	Oligonucleotide se
c1315	13.8	0.8	17	1	ABN07887	Human GDMPLP-1 17-m	c1388	13.4	0.8	15	1	AAAL1718	Human MIF gene Dsk
c1316	13.8	0.8	17	1	ABN00904	Human GDMPLP-1 17-m	c1389	13.4	0.8	15	1	AAAF46740	IGFBP3 oligonucleo
c1317	13.8	0.8	17	1	ABN10513	Human GDMPLP-1 17-m	c1390	13.4	0.8	15	1	AAAF49276	IGF-1 oligonucleot
c1318	13.8	0.8	17	1	ABN10514	Human GDMPLP-1 17-m	c1391	13.4	0.8	15	1	AAAF45532	IGFBP2 oligonucleo
c1319	13.8	0.8	17	1	ABN10030	Human GDMPLP-1 17-m	c1392	13.4	0.8	15	1	AAAF46883	IGFBP3 oligonucleo
c1320	13.8	0.8	17	1	ABN10510	Human GDMPLP-1 17-m	c1393	13.4	0.8	15	1	AAAF46741	IGFBP3 oligonucleo
c1321	13.8	0.8	17	1	AAAD33383	LDLR cDNA amplifi	c1394	13.4	0.8	15	1	AAAF46738	IGFBP3 oligonucleo
c1322	13.8	0.8	17	1	ABV85236	Human pp-GaNTase 1	c1395	13.4	0.8	15	1	AAAF46739	IGFBP3 oligonucleo
c1323	13.8	0.8	17	1	ABV85235	Human pp-GaNTase 1	c1396	13.4	0.8	15	1	AAAF80919	PTGS2 allele speci
c1324	13.8	0.8	17	1	ABV85237	Human pp-GaNTase 1	c1397	13.4	0.8	15	1	ABAA97405	Nucleotide sequenc
c1325	13.8	0.8	17	1	ABV85264	Human pp-GaNTase 1	c1398	13.4	0.8	15	1	ABK98166	Triple helix formi
c1326	13.8	0.8	17	1	ABV79401	Human HTPL scannin	c1399	13.4	0.8	15	1	ABK98185	Triple helix formi
c1327	13.8	0.8	17	1	ABV79138	Human HTPL scannin	c1400	13.4	0.8	15	1	ABX798339	EST polymorphic DN
c1328	13.8	0.8	17	1	ABK18613	Human ERG G-cleave	c1401	13.4	0.8	15	1	ACD82442	Nucleic acid cloni
c1329	13.8	0.8	17	1	ABK18870	Human ERG DNazyme	c1402	13.4	0.8	15	1	ACD82604	Nucleic acid cloni
c1330	13.8	0.8	17	1	ABK18192	Human ERG hammerge	c1403	13.4	0.8	15	1	ADB68522	Single-base mismat
c1331	13.8	0.8	17	1	ABSV74958	Human PAPP-Ea asso	c1404	13.4	0.8	16	1	AAQ25457	Purine rich HIV ta
c1332	13.8	0.8	17	1	ABV90794	Human PSH11 scann	c1405	13.4	0.8	16	1	AAAT44591	Cryptosporidium pa
c1333	13.8	0.8	17	1	ACCS9531	Human HOS-2 gene p	c1406	13.4	0.8	16	1	AAAT73333	Forward primer #66
c1334	13.8	0.8	17	1	ABQ80178	Variant primer DBM	c1407	13.4	0.8	16	1	ABF57076	Molecular beacon t
c1335	13.8	0.8	17	1	ABT36841	Tumour suppression	c1408	13.4	0.8	16	1	ACF63316	Human Ghrelin anti
c1336	13.8	0.8	17	1	ACA08326	Necrosis factor ka	c1409	13.4	0.8	16	1	AAAD57846	Target oligonucleo
c1337	13.8	0.8	17	1	ADB00093	Human MDZ3 scannin	c1410	13.4	0.8	17	1	AAQ94364	Septoria tritici I
c1338	13.8	0.8	17	1	ABZ64549	Human HER2 DNazyme	c1411	13.4	0.8	17	1	AAQ81619	Plasmodium falci
c1339	13.8	0.8	17	1	ABZ61439	Human H-Ras DNazym	c1412	13.4	0.8	17	1	AAAT81052	Human c-myc hamme
c1340	13.8	0.8	17	1	ABZ61374	Human H-Ras DNazym	c1413	13.4	0.8	17	1	AAAT88942	Bumper primer 2 fo
c1341	13.8	0.8	17	1	ACB265369	Human HER2 DNazyme	c1414	13.4	0.8	17	1	AAAX70026	Human flt1 VEGF re
c1342	13.8	0.8	17	1	ACB262029	HCV minus strand D	c1415	13.4	0.8	17	1	AAAX70027	Human flt1 VEGF re
c1343	13.8	0.8	17	1	ACD62960	HCV minus strand D	c1416	13.4	0.8	17	1	AAAX70028	Human flt1 VEGF re
c1344	13.8	0.8	17	1	ACD56960	HCV DNazyme subtr	c1417	13.4	0.8	17	1	AAV62512	Septoria tritici s
c1345	13.8	0.8	17	1	ACB68140	Murine oligonucleo	c1418	13.4	0.8	17	1	AAAZ30889	Integrin subunit b
c1346	13.8	0.8	17	1	ADD42044	Rice acetolactate	c1419	13.4	0.8	17	1	AAAZ30088	Integrin subunit b
c1347	13.8	0.8	17	1	AAAN97167	Mutagenic oligonuc	c1420	13.4	0.8	17	1	AAAX30261	HIV gag bumper pri

c1421	13.4	0.8	17	1	AAC72533	Single nucleotide
c1422	13.4	0.8	17	1	AAC72524	Single nucleotide
c1423	13.4	0.8	17	1	AAC72521	Single nucleotide
c1424	13.4	0.8	17	1	AAA70335	DNA synthesis adap
c1425	13.4	0.8	17	1	AAF81949	MSA1 N-terminal fr
c1426	13.4	0.8	17	1	ABK03736	Human CD20 Ambery
c1427	13.4	0.8	17	1	ABK03265	Human NOGO Ambery
c1428	13.4	0.8	17	1	ABA80561	APOE mutation corr
c1429	13.4	0.8	17	1	ABA80560	APOE mutation corr
c1430	13.4	0.8	17	1	ABA80567	Human cDNA syntheis
c1431	13.4	0.8	17	1	AAI71138	Detection probe SE
c1432	13.4	0.8	17	1	HAN10029	Human GDMLP-1 17-m
c1433	13.4	0.8	17	1	ABN10511	Human GDMLP-1 17-m
c1434	13.4	0.8	17	1	ABN06400	Human GDMLP-1 17-m
c1435	13.4	0.8	17	1	ABN07888	Human GDMLP-1 17-m
c1436	13.4	0.8	17	1	ABN10289	Human GDMLP-1 17-m
c1437	13.4	0.8	17	1	ABN10291	Human GDMLP-1 17-m
c1438	13.4	0.8	17	1	ABN10508	Human GDMLP-1 17-m
c1439	13.4	0.8	17	1	ABN06399	Human GDMLP-1 17-m
c1440	13.4	0.8	17	1	ABN07889	Human GDMLP-1 17-m
c1441	13.4	0.8	17	1	ABN06398	Human GDMLP-1 17-m
c1442	13.4	0.8	17	1	ABN07884	Human GDMLP-1 17-m
c1443	13.4	0.8	17	1	ABN10509	Human GDMLP-1 17-m
c1444	13.4	0.8	17	1	ABN10028	Human GDMLP-1 17-m
c1445	13.4	0.8	17	1	ABN10290	Human GDMLP-1 17-m
c1446	13.4	0.8	17	1	ABV79402	Human HTPL scannin
c1447	13.4	0.8	17	1	ABV79403	Human HTPPL scannin
c1448	13.4	0.8	17	1	ABK19204	Human ERG Ambery
c1449	13.4	0.8	17	1	ABK18235	Human ERG hammerhe
c1450	13.4	0.8	17	1	ABK17536	Human ERG hammerhe
c1451	13.4	0.8	17	1	ABK19388	Human ERG Ambery
c1452	13.4	0.8	17	1	ABK19205	Human ERG Ambery
c1453	13.4	0.8	17	1	ABK19389	Human ERG Ambery
c1454	13.4	0.8	17	1	ABK17999	Human ERG hammerhe
c1455	13.4	0.8	17	1	ABK18187	Human ERG hammerhe
c1456	13.4	0.8	17	1	ABK18234	Human ERG hammerhe
c1457	13.4	0.8	17	1	ABK57766	Human CLCA1 gene e
c1458	13.4	0.8	17	1	ABK56032	Human CLCA1 gene e
c1459	13.4	0.8	17	1	ABK57765	Human CLCA1 gene e
c1460	13.4	0.8	17	1	ACC53048	Human tumour suppr
c1461	13.4	0.8	17	1	ACC52311	Human tumour suppr
c1462	13.4	0.8	17	1	ACA06577	NFKB sub-unit modu
c1463	13.4	0.8	17	1	ACA07733	NFKB sub-unit modu
c1464	13.4	0.8	17	1	ACA06470	NFKB sub-unit modu
c1465	13.4	0.8	17	1	ACA09009	NFKB sub-unit modu
c1466	13.4	0.8	17	1	ACA06875	NFKB sub-unit modu
c1467	13.4	0.8	17	1	ACA07620	NFKB sub-unit modu
c1468	13.4	0.8	17	1	ACA07621	NFKB sub-unit modu
c1469	13.4	0.8	17	1	ADB00091	Human MD23 scannin
c1470	13.4	0.8	17	1	ADB02201	Human MD24 scannin
c1471	13.4	0.8	17	1	ADB02200	Human MD24 scannin
c1472	13.4	0.8	17	1	ADB00092	Human MD23 scannin
c1473	13.4	0.8	17	1	ADB04267	Human MD27 scannin
c1474	13.4	0.8	17	1	ADB02202	Human MD24 scannin
c1475	13.4	0.8	17	1	ABZ59906	Human K-Ras DNazym
c1476	13.4	0.8	17	1	ABZ61980	Human H-Kas DNazym
c1477	13.4	0.8	17	1	ABZ61544	Human H-Kas DNazym
c1478	13.4	0.8	17	1	ACD65653	HCV minus strand D
c1479	13.4	0.8	17	1	ACC65252	Murine oligonucleo
c1480	13.4	0.8	17	1	ACC62770	Murine oligonucleo
c1481	13.4	0.8	17	1	ADB42204	Tumour suppression</

ALIGNMENTS

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1567 GCCACCGTCAACCACTGACTGCTGAGTC 1593
|||
Db 27 GCCACCGTCAACCACTGACTGCTGAGTC 1

RESULT. T 2

ACC82883
ID ACC82883 standard; DNA; 23 BP.

AC ACC82883:

DT 27-AUG-2003 (first entry)

Human TRIP6 DNA specific PCR probe.

Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour; OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis; inflammation; therapy; hyperproliferative disorder; infection; cancer; chromosome 7q22; ZRP-1; PCR; probe; ss.

OS Homo sapiens.

Key	Location/Qualifiers
-----	---------------------

```
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "FAM labelled"
```

```

FT modified_base 23
FT /*tag= b
FT /mod_base= OTHER
FT /note= "TAMRA labelled"

```

AA
PN
WO2003040328-A2.

15-MAY-2003

XX
PF 05-NOV-2002; 2002WO-US035479.

PR 08-NOV-2001; 2001US-00008789.

PA (ISIS-) ISIS PHARM INC.

PI Bennett CF, Dobie K;

DR WPI; 2003-430662/40.

PT New antisense oligonucleotides targeted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.

PS Example 13: Page 74: 111pp: English.

The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. The are also useful in antisense therapy. The present sequence is human TRIP6 DNA specific PCR probe, used in the exemplification of the invention

Sequence 23 BP; 2 A; 6 C; 7 G; 8 T; 0 U; 0 Other;

Query Match 1.3%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 23; Conservative 0; Mismatches 0; Indels

Qy 1046 TTGATCGCGTCTTTTACGTGGC 1068
|||||
Db 1 TTGATCGCGTCTTTTACGTGGC 23

RESULT 3

ABK86169
ID ABK86169 standard; DNA; 24 BP.

AC ABK86169;

DT 24-SEP-2002 (first entry)

DE Oligo dT primer #2 used in method to study gene expression.

KW Oligo dT primer; gene expression analysis; primer; ss.

OS Synthetic.

XX
PN
WO200236828-A2.

PD 10-MAY-2002.

01-NOV-2001: 2001WO-US045401.

01-NOV-2000: 2000US-02449333P.

XX PA (GENO-) GENOMIC SOLUTIONS INC.

PI Kane MD, Dombkowski AA, Nagel AC:

WPI: 2002-508123/54.

AA Identifying and characterizing gene expression in samples, for
PT PT
PT identifying mRNAs expressed at different levels, comprises emp
PT PT
PT identifier having a oligo-dT primer of a specific sequence and
PT PT
PT detectable marker at its 5' end.

PS Disclosure; Page 11; 45pp; English.

The invention relates to systems for identification and characterisation of gene expression in one or more samples, comprising an identifier having a specific oligo-dT primer sequence, where the identifier comprises a detectable marker at its 5' end. The system is useful for identifying any or all genes expressed in a given *in vivo* or *in vitro* RNA sample, as well as the relative differences in mRNA between 2 or more samples, where desired, for supporting discovery of new genes, and for identifying mRNAs that are expressed at different levels between 2 or more samples. The new system or method addresses limitations of prior methods by comprising compositions and systems that incorporate new strategies where molecular or biochemical assay compositions and systems are linked to DNA or RNA sequence databases for optimal resource efficiency in assaying gene expression. The system has the following advantages over existing methods: (a) prior sequence information or clone library construction is not needed to enable the assay; (b) provides immediate sequence information in addition to information concerning changes or differences in mRNA level, to determine mRNA expression level and mRNA identification in one assay; (c) generates cDNA fragments from all mRNAs present in the sample for subsequent investigation by common molecular biology techniques; and (d) does not require prior knowledge of the sequence of the genome of the organism under investigation and can be employed in organisms lacking significant genomic sequence information. The present sequence represents an oligo dT primer used in the method of the invention.

Sequence 24 BP: 20 A: 0 C: 1 G: 3 T: 0 U: 0 Other: 0

Query Match 1.3%; Score 22.4; DB 1; Length 24;

QV 1730 GTTTACAAAAAAAAAAAAAAAAAAAA 1753
 Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 BSC local similarity 95.0%; Fied. NO: 87;

Db 1 GTTTAAAAA 24

RESULT 4

ABK86168/C
ID ABK86168 standard; DNA; 24 BP.

XX AC ABK86168;

XX DT 24-SEP-2002 (first entry)

XX DE Oligo dT primer #1 used in method to study gene expression.

XX KW Oligo dT primer; gene expression analysis; primer; ss.

XX OS Synthetic.

XX PN WO200236828-A2.

XX PD 10-MAY-2002.

XX PF 01-NOV-2001; 2001WO-US045401.

XX PR 01-NOV-2000; 2000US-0244933P.

XX PA (GENO-) GENOMIC SOLUTIONS INC.

XX PI Kane MD, Dombkowski AA, Nagel AC;

XX DR WPI; 2002-508123/54.

XX PT Identifying and characterizing gene expression in samples, for
XX PT identifying mRNAs expressed at different levels, comprises employing an
XX PT identifier having an oligo-dT primer of a specific sequence and a
XX PT detectable marker at its 5' end.

XX PS Disclosure; Page 11; 45pp; English.

XX CC The invention relates to systems for identification and characterisation
XX CC of gene expression in one or more samples, comprising an identifier having
XX CC a specific oligo-dT primer sequence, where the identifier comprises a
XX CC detectable marker at its 5' end. The system is useful for identifying any
XX CC or all genes expressed in a given *in vivo* or *in vitro* RNA sample, as well
XX CC as the relative differences in mRNA between 2 or more samples, where
XX CC desired, for supporting discovery of new genes, and for identifying mRNAs
XX CC that are expressed at different levels between 2 or more samples. The new
XX CC system or method addresses limitations of prior methods by comprising
XX CC compositions and systems that incorporate new strategies where molecular
XX CC or biochemical assay compositions and systems are linked to DNA or RNA
XX CC sequence databases for optimal resource efficiency in assaying gene
XX CC expression. The system has the following advantages over existing
XX CC methods: (a) prior sequence information or clone library construction is
XX CC not needed to enable the assay; (b) provides immediate sequence
XX CC information in addition to information concerning changes or differences
XX CC in mRNA level, to determine mRNA expression level and mRNA identification
XX CC in one assay; (c) generates cDNA fragments from all mRNAs present in the
XX CC sample for subsequent investigation by common molecular biology
XX CC techniques; and (d) does not require prior knowledge of the sequence of
XX CC the genome of the organism under investigation and can be employed in
XX CC organisms lacking significant genomic sequence information. The present
XX CC invention represents an oligo dT primer used in the method of the
XX CC invention

XX SQ Sequence 24 BP; 3 A; 1 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.3%; Score 22.4; DB 1; Length 24;
Best Local Similarity 95.8%; Pred. No. 87;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1730 GTTTAAAAA 1753

Db 24 GTTTAAAAA 1

RESULT 5

AAV71935/C

XX ID AAV71935 standard; DNA; 27 BP.

XX AC AAV71935;

XX DT 18-FEB-1999 (first entry)

XX DE Anchored poly T RT-PCR primer.

XX KW Normalised; cDNA library; mRNA cloning; reverse transcription;
XX KW immobilise; screening; hybridisation; nucleic acid amplification;
XX KW expression pattern; drug development; PCR primer; RT-PCR; ss.

XX OS Synthetic.

XX PN WO9851789-A2.

XX PD 19-NOV-1998.

XX PF 13-MAY-1998; 98WO-DK000186.

XX PR 13-MAY-1997; 97DK-00000547.

XX PR 19-MAY-1997; 97US-00871030.

XX PR 27-MAR-1998; 98DK-00000432.

XX PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.

XX PI Warthoe PR;

XX DR WPI; 1999-009772/01.

XX PT Preparation of normalised, subdivided cDNA libraries from mRNA - by
XX PT reverse transcription and amplification, used to screen for new genes and
XX PT interacting proteins, potential drugs, and for diagnosis.

XX PS Example 1; Page 29; 71pp; English.

XX CC The invention relates to preparation of a normalised, subdivided library
XX CC of amplified cDNA from the coding regions of mRNA in a sample. The method
XX CC involves reverse transcription, with at least one cDNA primer of formula
XX CC 5'-Con1-dTn2-Vn3-Nn4 to form first strand cDNA where Con1 = any sequence
XX CC of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3 and n4
XX CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
XX CC cDNA synthesis using the first strand as template and a second cDNA
XX CC primer of a similar formula, in the presence of DNA polymerase I (or its
XX CC Klenow fragment) and amplification of double-stranded cDNA with a set of
XX CC amplification primers. Comparison of cDNA in the prepared library with a
XX CC database (a computer-generated list of molecular weights of restricted
XX CC DNA fragments of known sequence) is used to determine presence of an
XX CC expressed protein in a cell, also to detect changes in such expression
XX CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
XX CC cDNA stably immobilised on it, obtained by a similar method, are used to
XX CC screen for genes of a particular family, by hybridisation with nucleic
XX CC acid from the family (to identify new genes) and to detect differences in
XX CC expression patterns between cells. The polypeptides expressed by the
XX CC libraries can be used for drug development. Sequences AAV71935 to
XX CC AAV71946 represent primers used to exemplify the method of the invention

XX SQ Sequence 27 BP; 2 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 1.3%; Score 22.4; DB 1; Length 27;
Best Local Similarity 95.8%; Pred. No. 96;
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1755

Db 27 TTTAAAAA 4

RESULT 6

RESULT 10
AA84259/c

ID AA84259 standard; DNA; 25 BP.

XX AAX84259;

AC AC

XX XX

DT 08-SEP-1999 (first entry)

XX XX

DE PCR primer for human Nck associated protein 1 coding sequence.

XX Nck associated protein 1; Nap1; human; apoptosis; Alzheimer's disease;

KW therapy; PCR primer; ss.

KW Synthetic.

OS Homo sapiens.

XX XX

PN WO9931239-A1.

XX XX

PD 24-JUN-1999.

XX XX

PF 14-DEC-1998; 98WO-JP005646.

XX XX

PR 15-DEC-1997; 97JP-00363183.

XX XX

PA (KYOW) KYOWA HAKKO KOGYO KK.

PA (SAKA/) SAKAKI Y.

XX XX

PI Sakaki Y;

XX XX

DR WFI; 1999-395181/33.

XX XX

PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of

PT Alzheimer's disease.

XX XX

PS Disclosure; Page 76; 90pp; Japanese.

XX XX

CC This sequence represents a PCR primer used to isolate DNA encoding the

CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits

CC apoptosis. The protein can be used in the investigation, diagnosis and

CC treatment (e.g. by gene therapy) of Alzheimer's disease

XX XX

SQ Sequence 25 BP; 1 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.2%; Score 21.4; DB 1; Length 25;
Best Local Similarity 95.7%; Pred. No. 1.2e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1733 TACAAAAA.....AAAAAAAAA 1755
||| |||||||||
Db 25 TAAAAA.....AAAAAAAAA 3

RESULT 11
AAD03682/c

ID AAD03682 standard; DNA; 26 BP.

XX AAD03682;

AC AC

XX XX

DT 19-JUN-2001 (first entry)

XX XX

DE Human full length zcytorl3 cDNA isolating polyA PCR primer, ZC7764b.

XX XX

KW Human; phosphodiesterase; PDE; zcytorl3; antiasthmatic; antiarthritic;

KW antipsoriatic; cytostatic; antiatherosclerotic; antiinfertility;

KW cardant; antiinflammatory; dermatological; wound healing; antiviral;

KW antibacterial; therapy; inflammatory bowel disease; diverticulitis;

KW spermatogenesis; sperm capacitation; immunoncontraceptive; vaccine;

KW cancer; reperfusion ischaemia; psoriasis; melanoma; myocarditis; PID;

KW pelvic inflammatory disease; eczema; scleroderma; vasoconstriction;

KW heart arrhythmia; congestive heart disease; muscle spasm; fatigue;

KW chromosomal abnormality; gene therapy; PCR primer; ss.

XX OS

OS Homo sapiens.

XX	WO200125444-A2.
XX	PN
XX	XX
XX	PD
XX	12-APR-2001.
XX	PF
XX	06-OCT-2000; 2000WO-US027734.
XX	PR
XX	07-OCT-1999; 99US-00414025.
XX	PA
XX	(ZYMO) ZYMOGENETICS INC.
XX	PI
XX	Praenell SR, Novak JE, Gao Z;
XX	DR
XX	WPI; 2001-266312/27.
XX	PS
XX	Example 1C; Page 118; 122pp; English.
XX	The patent discloses novel human phosphodiesterase (PDE), zcytorl3 cDNA
CC	and its corresponding protein. Zcytorl3 protein is used to promote wound
CC	healing in tissues, to exhibit anti-bacterial and anti-viral effects and
CC	to identify modulators (e.g. agonists or antagonists). Zcytorl3, its
CC	agonists or antagonists are useful in the treatment of inflammatory heart
CC	or cardiovascular conditions, muscle inflammation, inflammation during
CC	and after surgery, arthritis, asthma, inflammatory bowel disease or
CC	diverticulitis, for modulating spermatogenesis, sperm capacitation, as
CC	immun contraceptive or anti-fertility vaccine and for treating male
CC	infertility. Zcytorl3 protein and its antibodies are used to diagnose
CC	cancer, reperfusion ischemia, asthma, psoriasis and melanoma. Zcytorl3
CC	proteins are used to enhance fertilisation. Zcytorl3 antagonists are used
CC	to treat myocarditis, atherosclerosis, pelvic inflammatory diseases (PID),
CC	psoriasis, eczema, scleroderma and other inflammatory diseases. Zcytorl3
CC	sequences and/or its antibodies are useful for treatment of disorders
CC	associated with vasoconstriction, heart arrhythmia, congestive heart
CC	disease, muscle spasms and fatigue. They are used for detecting human
CC	chromosomal abnormalities. Zcytorl3 cDNAs are used in gene therapy.
CC	Zcytorl3-cytokine fusion proteins or antibody-cytokine fusion proteins
CC	are useful for enhancing in vivo killing of target tissue. The present
CC	sequence is a polyA PCR primer, ZC7764B which is used to isolate full
CC	length zcytorl3 cDNA by screening human placental cDNA library
XX	
SQ	Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
	Query Match 1.2%; Score 21.4; DB 1; Length 26;
	Best Local Similarity 95.7%; Fred. No. 1.3e+02;
	Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	1733 TACAAAAAATAAAAAAAAAAAAAA 1755
Dd	26 TAAAAAATAAAAAAAAAAAAAA 4
RESULT 12	
AAS20596/c	
ID	AAS20596 standard; DNA; 26 BP.
XX	
AC	AAS20596;
XX	
DT	23-APR-2002 (first entry)
XX	
DE	Human zsig63 cDNA sequencing primer ZC7764a.
XX	
Kw	Human; zsig63; chromosome 4q12-q413; salivary protein; antimicrobial; ss;
Kw	microbial infection; tooth decay; periodontal disease; thrush; emphysema;
Kw	gastrointestinal disease; urinary tract infection; vaginal infection;
Kw	skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
Kw	acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
Kw	chronic bronchitis; gene therapy; protein therapy; primer; ZC7764a.
XX	
OS	Homo sapiens.

```

XX PN US6331413-B1.
XX PD 18-DEC-2001.
XX PF 17-MAR-2000; 2000US-00527345.
XX PR 17-MAR-1999; 99US-0124820P.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Adler DA, Sheppard PO;
XX WPI; 2002-096707/13.
XX
XX Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
PT
XX Example 1; Col 53; 29pp; English.
PS
XX The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbial activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, urinary tract infections,
CC vaginal infections, skin infections, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
XX
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA...AAAAAAAAA 1755
Db 26 TAAAAA...AAAAAAAAA 4

RESULT 13
ABSS2638/c
ID ABSS2638 standard; DNA; 26 BP.
AC
AC ABSS2638;
DT
DT 15-NOV-2002 (first entry)
XX
XX Human secreted salivary protein zsig63 PCR primer ZC7764a.
XX
XX Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
XX antibody-cytokine; in vivo killing; pathological microbe; bacteria;
XX fungal; viral; infection; salivary gland; anti-microbial; dental caries;
XX tooth decay; periodontal disease; thrush; gastrointestinal disease;
XX urinary tract infection; vaginal infection; skin infection; microflora;
XX epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
XX chronic tissue damage; vascular system; diabetes; anti-inflammatory;
XX incompetent immune system; AIDS; acquired immunodeficiency syndrome;
XX chemotherapy; radiation treatment; lung infection; cystic fibrosis;
XX digestion; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX US2002081701-A1.
FN
XX
XX 27-JUN-2002.
PD
XX
XX 03-AUG-2001; 2001US-00922480.
PF
XX
XX 17-MAR-1999; 99US-0124820P.
PR

```

```

PR 17-MAR-2000; 2000US-00527345.
XX
XX (ADLE/) ADLER D A.
XX PA (SHEP/) SHEPPARD P O.
XX
XX Adler DA, Sheppard PO;
XX PI
XX WPI; 2002-635468/68.
XX
XX Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
PT
XX Example 1; Page 29; 33pp; English.
PS
XX
XX The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC protein are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
CC inflammatory activity include the treatment of chronic tissue damage,
CC particularly in areas having a limited or damaged vascular system e.g.,
CC damage in extremities associated with diabetes. Antagonists to zsig63
CC polypeptides may be useful as anti-inflammatory agents. The invention is
CC useful for the treatment of patients having incompetent immune system,
CC such as AIDS (acquired immunodeficiency syndrome) patients or individuals
CC that have undergone chemotherapy, radiation treatment. The invention is
CC also useful for the treatment of lung infections associated with cystic
CC fibrosis and its agonists or antagonists are useful for aiding digestion.
CC The present nucleic acid sequence represents a PCR primer that was used
CC in the methods of the invention for identification of zsig63
XX
XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA...AAAAAAAAA 1755
Db 26 TAAAAA...AAAAAAAAA 4

RESULT 14
AAD45055/c
ID AAD45055 standard; DNA; 26 BP.
XX
XX AAD45055;
AC
XX
XX 27-DEC-2002 (first entry)
DT
XX
XX ZC7764a primer used in the identification of human zsig63 DNA.
XX
XX Human; secreted salivary protein; zsig63 protein; host defense protein;
XX immune modulating factor; antipathogenic; cell-cell signalling molecule;
XX growth factor; cytokine; growth factor hormone activity; dental caries;
XX infection; tooth decay; periodontal disease; gastrointestinal disease;
XX thrush; urinary tract infection; vaginal infection; diabetes; obesity;
XX anti-inflammatory; chronic tissue damage; lung dysfunction; restenosis;
XX gene therapy; salivary gland dysfunction; prostate gland dysfunction;
XX forensic DNA profiling; chondrosarcoma; atherosclerosis; primer; ss.
XX

```

```
XX OS Homo sapiens.
XX OS US2002090677-A1.
XX OS 11-JUL-2002.
XX OS 03-AUG-2001; 2001US-00923236.
XX OS 17-MAR-1999; 99US-0124820P.
XX OS 17-MAR-2000; 2000US-00527345.
XX OS (ADLER) ADLER D A.
XX OS (SHEP) SHEPPARD P O.
XX OS Adler DA, Sheppard PO;
XX OS WPI; 2002-642378/69.
XX OS Novel secreted salivary polypeptide, zsig63, useful as antimicrobial
XX OS agent for treating microbial infection, dental carries, periodontal
XX OS disease, thrush gastrointestinal disease, and for aiding digestion.
XX OS
XX OS Example 1; Page 30; 33pp; English.
XX OS
XX OS The invention relates to human secreted salivary polypeptide designated
XX OS as zsig63 and nucleic acid molecules encoding such polypeptides. zsig63
XX OS can be used in detecting agonists and antagonists of its activity, and is
XX OS also useful as a host defense polypeptide, immune modulating factor,
XX OS antipathogenic polypeptide, cell-cell signalling molecule, growth factor,
XX OS cytokine, or as secreted extracellular matrix associated proteins with
XX OS growth factor hormone activity. It is useful for treating conditions
XX OS associated with pathological microbes, including bacterial, fungal and
XX OS viral infections, for treating dental carries (tooth decay), periodontal
XX OS disease, thrush and gastrointestinal disease, for treating urinary tract
XX OS infection, vaginal infection and for preventing infection in skin and
XX OS other epithelial wounds. zsig63 is useful for establishing normal
XX OS microflora and protect against pathogenic colonisation and invasion, for
XX OS treating chronic tissue damage e.g. damage in extremities associated with
XX OS diabetes and useful as anti-inflammatory agents. It is useful as a marker
XX OS of lung dysfunction, salivary gland dysfunction, or dysfunction of
XX OS prostate gland. It is also therapeutically useful for aiding digestion.
XX OS Polynucleotides of the invention are used in gene therapy for increasing
XX OS or inhibiting zsig63 activity, for detecting abnormalities on human
XX OS chromosome 4 associated with disease or other human traits and as
XX OS diagnostics in forensic DNA profiling. Sequences of the invention are
XX OS useful for stimulating proliferation or differentiation of cardiac
XX OS myocytes, for proliferation or differentiation of adipocytes and for
XX OS inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
XX OS present sequence is a primer used in the identification of human zsig63
XX OS DNA
XX OS
XX OS Query Match 1.2%; Score 21.4; DB 1; Length 26;
XX OS Best Local Similarity 95.7%; Pred. No. 1.3e+02;
XX OS Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX OS
XX OS QY 1733 TACAAAAA..... 1755
XX OS |||.....
XX OS Db 26 TAAAAA..... 4
XX OS
XX OS RESULT 15
XX OS AAS20671/c
XX OS ID AAS20671 standard; DNA; 26 BP.
XX OS
XX OS AC AAS20671;
XX OS
XX OS DT 09-APR-2002 (first entry)
XX OS
XX OS DE Human zalphall Ligand sequencing primer ZC7764a.
XX OS
XX OS
XX OS Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;
XX OS natural killer cell proliferation; T-cell proliferation;
XX OS B-cell proliferation; anti-tumour response; immune system;
XX OS immunostimulant; cytostatic; human; sequencing primer; ss.
XX OS
XX OS Homo sapiens.
XX OS US6307024-B1.
XX OS 23-OCT-2001.
XX OS 09-MAR-2000; 2000US-00522217.
XX OS 09-MAR-1999; 99US-0123547P.
XX OS 11-MAR-1999; 99US-0123904P.
XX OS 01-JUL-1999; 99US-0142013P.
XX OS (ZYMO ) ZYMOGENETICS INC.
XX OS Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;
XX OS Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX OS WPI; 2002-040208/05.
XX OS
XX OS New zalphall ligand polypeptides and polynucleotides, useful for
XX OS stimulating proliferation, activation, differentiation and/or induction
XX OS of inhibition of specialized cell function, or for stimulating an
XX OS antigenic response.
XX OS
XX OS Example 7; Col 139; 105pp; English.
XX OS
XX OS The present invention relates to the isolation of a novel cytokine,
XX OS zalphall ligand and the polynucleotide encoding it. The invention also
XX OS gives the sequence for the zalphall receptor and the polynucleotide
XX OS encoding it. The zalphall ligand polypeptide stimulates proliferation of
XX OS natural killer (NK) cells or NK cell progenitors, the activation of NK
XX OS cells, proliferation of T-cells, proliferation of B-cells stimulated with
XX OS anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
XX OS reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
XX OS zalphall ligand polypeptide is also useful in preparing antibodies that
XX OS bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can
XX OS be used as probes or primers to clone regions of a zalphall ligand gene,
XX OS and in gene therapy. Zalphall ligand may also be used to identify
XX OS inhibitors of its activity, to enhance the generation of anti-tumour
XX OS responses with or without the infusion of donor lymphocytes, and to
XX OS activate or stimulate the immune system. The present sequence represents
XX OS a sequencing primer used to sequence cDNA clones in the isolation of
XX OS human zalphall ligand
XX OS
XX OS Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
XX OS
XX OS Query Match 1.2%; Score 21.4; DB 1; Length 26;
XX OS Best Local Similarity 95.7%; Pred. No. 1.3e+02;
XX OS Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX OS
XX OS QY 1733 TACAAAAA..... 1755
XX OS |||.....
XX OS Db 26 TAAAAA..... 4
XX OS
XX OS RESULT 16
XX OS ABX93599/c
XX OS ID ABX93599 standard; DNA; 26 BP.
XX OS
XX OS AC ABX93599;
XX OS
XX OS DT 28-MAY-2003 (first entry)
XX OS
XX OS DE Human zsig63 PCR/sequencing primer ZC7764a.
XX OS
XX OS ss; PCR; zsig63; adhesin; salivary gland; dental carries;
XX OS periodontal disease; thrush; gastrointestinal disease; epithelial wound;
XX OS urinary tract infection; vaginal infection; skin infection; primer;
```

KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
KW lung infection; cystic fibrosis; lung dysfunction; digestive;
KW salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
KW cell culture media; gene therapy; human chromosome 4q12-4q13;
KW dentinogenesis imperfecta; dentin dysplasia type II.

XX Synthetic.

OS US2002173027-A1.

PN 21-NOV-2002.

XX 03-AUG-2001; 2001US-00922469.

PF 17-MAR-1999; 99US-0124820P.

PR 17-MAR-2000; 2000US-00527345.

XX (ADLE/) ADLER D A.

PA (SHEP/) SHEPPARD P O.

PI Adler DA, Sheppard PO;

XX WPI; 2003-328428/31.

DR Novel isolated zsig63 polypeptide, member of the adhesin family, useful
XX for treating dental caries, periodontal disease, thrush,
PT gastrointestinal disease, urinary tract infections, vaginal infections,
PT skin infections.

XX Example 1; Page 29; 32pp; English.

PS The invention relates to an isolated zsig63 polypeptide comprising at
XX least 90% identity to an amino acid sequence which comprises domain 1 of
CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig3. Also
CC included are the polynucleotide encoding zsig63, a zsig63 expression
CC vector, a cultured cell comprising the vector and expressing the protein,
CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
CC zsig63 reporter gene construct to identify zsig63 agonists, and producing
CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is
CC useful for detecting in a test sample, the presence of antagonist of
CC zsig63 protein activity. Zsig63 has antimicrobial activity and since
CC exhibits high expression in salivary gland, can be used for treating
CC dental caries, periodontal disease, thrush, and gastrointestinal
CC disease, urinary tract infections, vaginal infections, skin infections
CC and other epithelial wounds. The polypeptides can be used to establish
CC normal microflora and protect against pathogenic colonization and
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC for treating chronic, tissue damage particularly in areas having limited
CC or damaged vascular system, e.g. in diabetes, and for treating
CC immunocompromised AIDS patients or in individuals that have undergone
CC chemotherapy, radiation treatment, for treating lung infections e.g. in
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC levels in the trachea may indicate that such polypeptides may serve as a
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC conditions associated with salivary gland or lung dysfunction including
CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC chronic bronchitis, prostate dysfunctions such as prostate
CC adenocarcinoma, aiding digestion, and as components of defined cell
CC culture media and may be used to replace serum that is commonly used in
CC culture. The DNA is useful in gene therapy applications to human or
CC inhibit zsig63 activity, and for detecting abnormalities on increase
CC chromosome 4 (e.g. 4q12-4q13, associated with dentinogenesis imperfecta,
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC present sequence is a primer used to isolate and sequence nucleic acids
CC encoding human zsig63

XX Sequence 26 BP; 1 A; 0 C; 0 G; 25 T; 0 U; 0 Other;

Query Match 1.2%; Score 21.4; DB 1; Length 26;
Best Local Similarity 95.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1733 TACAAAAA 1755
DB 26 TAAAAA 4

RESULT 17

ABX79828/c

ID ABX79828 standard; cDNA; 27 BP.

XX AC ABX79828;

XX DT 17-APR-2003 (first entry)

XX DE EST polymorphic DNA repeat polynucleotide #153.

KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

XX OS Homo sapiens.

XX PN US6472154-B1.

XX PD 29-OCT-2002.

XX PF 31-DEC-1999; 99US-00475947.

XX PR 31-DEC-1999; 99US-00475947.

XX PA (TEXA) UNIV TEXAS SYSTEM.

XX PI Garner HR, Wren JD, Minna JD, Fondon JW;

XX DR WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.

XX Example; Col 717; 588pp; English.

CC The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs

XX Sequence 27 BP; 1 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.2%; Score 21.4; DB 1; Length 27;
Best Local Similarity 95.7%; Pred. No. 1.3e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1733 TACAAAAA 1755

DB 24 TAAAAA 2

PT Alzheimer's disease.
 PS Example 1; Page 76; 90pp; Japanese.
 CC This sequence represents a PCR primer used to isolate DNA encoding the
 CC human Nck associated protein 1 (Nap1) of the invention. Nap1 inhibits
 CC apoptosis. The protein can be used in the investigation, diagnosis and
 CC treatment (e.g. by gene therapy) of Alzheimer's disease
 XX
 SQ Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
 Db 25 CAAAAAAAAAAAAAAAAAAAAA 5
 RESULT 21
 AAD34264
 ID AAD34264 standard; DNA; 25 BP.
 XX
 AC AAD34264;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE Human CYP2D6 gene polymorphic site 385 detecting sense 5' oligo.
 XX
 KW Human; cytochrome P450 2D6; CYP2D6; enzyme; detection; xenobiotic;
 KW ligase-based sequenced determination; drug metabolism; chromosome 22; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200218638-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 27-AUG-2001; 2001WO-IB001544.
 XX
 PR 30-AUG-2000; 2000GB-00021286.
 XX
 PA (GEMI-) GEMINI GENOMICS PLC.
 XX
 PI Risinger C, Andersson MK, Lewander T, Oliasson E;
 XX WPI; 2002-329785/36.
 XX
 PT New sequence determination oligonucleotides, useful for detecting
 PT polymorphic sites in a 5' flanking region of a CYP2D6 gene, as
 PT hybridization probes, as components of diagnostic assays, or in ligase-
 PT based sequence determination.
 XX
 PS Claim 2; Page 23; 63pp; English.
 XX
 CC The invention relates to sequence determination oligonucleotides for
 CC detecting polymorphic sites in a 5' flanking region of cytochrome P450
 CC 2D6 (CYP2D6) gene. CYP2D6 enzymes are involved in the metabolism of many
 CC different xenobiotics. Human CYP2D6 gene is located on chromosome 22. The
 CC oligonucleotides may be used as in situ hybridisation probes, in ligase-
 CC based sequenced determination, as components of diagnostic assays, as
 CC probes in sequence determination methods based on mismatches, as
 CC hybridisation-based diagnostic assays, and as components of diagnostic
 CC microarray. CYP2D6 is useful to predict variations in an individual's
 CC ability to metabolise certain drugs. The present sequence is a sense
 CC oligonucleotide used for detecting of human CYP2D6 gene 5' flanking
 CC region single nucleotide polymorphism (SNP)
 XX
 SQ Sequence 25 BP; 22 A; 2 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
 Db 2 CAAAAAAAAAAAAAAAAAAAAA 22
 RESULT 22
 AAD26900
 ID AAD26900 standard; DNA; 25 BP.
 XX
 AC AAD26900;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Bacterial PNP DNA fragment with an in-frame polyA tract.
 XX
 KW Hypermutable organism; dominant negative allele; mismatch repair gene;
 KW spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
 KW bacteria; ss.
 XX
 OS Bacteria.
 OS Unidentified.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..5
 FT /*tag= a
 FT /note= "Bacterial PNP gene"
 FT misc_feature 6..25
 FT /*tag= a
 FT /note= "In-frame polyA tract"
 XX
 PN WO200188192-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 14-MAY-2001; 2001WO-US015376.
 XX
 PR 17-MAY-2000; 2000US-0204769P.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 PA (MORP-) MORPHOTEK INC.
 PA (NICO-) NICOLAIDES N C.
 PA (SASS/) SASS P M.
 PA (GRAS/) GRASSO L.
 PA (VOGE/) VOGELSTEIN B.
 PA (KINZ/) KINZLER K W.
 XX
 PI Nicolaides NC, SASS PM, Grasso L, Vogelstein B, Kinzler KW;
 XX WPI; 2002-083004/11.
 XX
 PT Generating mutation in gene using cells which contain defective mismatch
 PT repair gene, useful to generate genetically altered mutations with new
 PT output traits.
 XX
 PS Example 5; Fig 7; 59pp; English.
 XX
 CC The patent discloses a method for generating hypermutable organisms.
 CC Dominant negative alleles of human mismatch repair genes can be used to
 CC generate hypermutable cells and organisms. They increase the rate of
 CC spontaneous mutations by reducing the effectiveness of DNA repair and
 CC thereby render the cells or animals hypermutable. The method is used to
 CC produce genetically altered organisms to produce new output traits. The
 CC present sequence is a bacterial poly purine nucleotide phosphorylase
 CC (polyPNP) DNA fragment containing an in-frame polyA tract. This sequence
 CC is used in the exemplification of the invention
 XX.
 SQ Sequence 25 BP; 21 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 25;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;

Seq. Local Similarity 100.00, Rec. No. 14302,
 Matches 21; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

OS Synthetic.


```

OS Homo sapiens.
XX WO9931274-A2.
XX 24-JUN-1999.
XX 11-DEC-1998; 98WO-US026441.
XX 15-DEC-1997; 97US-00990568.
XX (ABBO ) ABBOTT LAB.
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;
XX Russell JC, Stroupe SD;
XX WPI; 1999-405041/34.
XX PA153 cDNA transcribed from pancreatic tissue.
XX Example 2; Page 121; 123pp; English.
XX This invention describes novel contiguous and partially overlapping cDNA
XX sequences and their encoded polypeptides, designated PA153, transcribed
XX from human pancreatic tissue and which have cytostatic activity. The
XX PA153 polynucleotides, proteins and antibodies are all useful in methods
XX of detection. Detection of PA153 polynucleotide, antigens or anti-PA153
XX antibodies in a sample is indicative of pancreatic disease. PA153
XX antibodies (antagonists) can also be used in vivo for therapeutic use,
XX e.g. treatment of pancreatic disease, tumours or metastases. Antisense
XX PA153 polynucleotides can be used in gene therapy of pancreatic diseases.
XX AAX78712-X78725 represent primers used in the method of the invention
XX
SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 26 CAAAAAAAAAAAAAAAAAAAAA 6
RESULT 26
AAD26899
ID AAD26899 standard; DNA; 26 BP.
XX AC AAD26899;
XX 09-APR-2002 (first entry)
XX Bacterial PNP DNA fragment with an out-of-frame polyA tract.
XX Hypermutable organism; dominant negative allele; mismatch repair gene;
XX spontaneous mutation; DNA repair; purine nucleotide phosphorylase; PNP;
XX bacteria; ss.
XX Bacteria.
XX Unidentified.
XX Chimeric.
XX Key Location/Qualifiers
XX misc_feature 1..5
XX /tag= a
XX /note= "Bacterial PNP gene"
XX misc_feature 6..26
XX /tag= a
XX /note= "Out-of-frame polyA tract"
XX WO200188192-A2.
XX 22-NOV-2001.

```

```

XX 14-MAY-2001; 2001WO-US015376.
XX 17-MAY-2000; 2000US-0204769P.
XX (UYJO ) UNIV JOHNS HOPKINS.
XX (MORP-) MORPHOTEK INC.
XX (NICO/) NICOLAIDES N C.
XX (SASS/) SASS P M.
XX (GRAS/) GRASSO L.
XX (VOGE/) VOGELSTEIN B.
XX (KINZ/) KINZLER K W.
XX Nicolaides NC, SASS PM, Grasso L, Vogelstein B, Kinzler KW;
XX WPI; 2002-083004/11.
XX Generating mutation in gene using cells which contain defective mismatch
XX repair gene, useful to generate genetically altered mutations with new
XX output traits.
XX Example 5; Fig 7; 59pp; English.
XX The patent discloses a method for generating hypermutable organisms.
XX Dominant negative alleles of human mismatch repair genes can be used to
XX generate hypermutable cells and organisms. They increase the rate of
XX spontaneous mutations by reducing the effectiveness of DNA repair and
XX thereby render the cells or animals hypermutable. The method is used to
XX produce genetically altered organisms to produce new output traits. The
XX present sequence is a bacterial poly purine nucleotide phosphorylase
XX (polyPNP) DNA fragment containing an out-of-frame polyA tract. This
XX sequence is used in the exemplification of the invention
XX
SQ Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 1.2%; Score 21; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
Db 5 CAAAAAAAAAAAAAAAAAAAAA 25
RESULT 27
AAD39650
ID AAD39650 standard; DNA; 26 BP.
XX AC AAD39650;
XX 22-OCT-2002 (first entry)
XX PolyPNP out-of-frame polyA tract DNA.
XX Dominant negative allele; mismatch repair gene; D-MMR; gene discovery;
XX ITR; inducible transcriptional regulatory element;
XX recombinant gene mutagenesis; recombinant protein production;
XX drug target discovery; ds.
XX Unidentified.
XX US2002055106-A1.
XX 09-MAY-2002.
XX 14-MAY-2001; 2001US-00853646.
XX 12-MAY-2000; 2000US-0203905P.
XX 17-MAY-2000; 2000US-0204769P.
XX (NICO/) NICOLAIDES N C.
XX (SASS/) SASS P M.
XX (GRAS/) GRASSO L.

```

PA (VOGE/) VOGELSTEIN B.
 PA (KINZ/) KINZLER K W.
 XX
 PI Nicolaides NC, Sass PM, Grasso L, Vogelstein B, Kinzler KW;
 XX
 DR WPI; 2002-499469/53.
 XX
 XX Generating a mutation in a gene using a dominant negative allele of a
 PT mismatch repair gene which results in mismatch repair deficiency in cells
 PT containing the allele is useful in gene and drug target discovery and
 PT recombinant technology.
 XX
 PS Example 5; Fig 7; 25pp; English.
 XX
 CC The invention relates to methods for generating a mutation in a gene of
 CC interesting using a dominant negative allele of a mismatch repair gene (D
 CC -MMR) under control of an inducible transcriptional regulatory element
 CC (ITRE). The invention is useful to provide new cell lines that can be
 CC used for gene discovery, drug target discovery, recombinant gene
 CC mutagenesis or recombinant protein production. The present sequence is a
 CC polyPNP (purine phosphorylase) out-of-frame polyA tract DNA
 XX
 SQ Sequence 26 BP; 22 A; 1 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAAAAAA 1755
 DB 5 CAAAAA AAAAAAAAAAAAAA 25
 RESULT 28
 AAV71936/c
 ID AAV71936 standard; DNA; 27 BP.
 XX
 AC AAV71936;
 XX
 DT 18-FEB-1999 (first entry)
 XX
 DE Anchored poly T RT-PCR primer.
 XX
 KW Normalised; cDNA library; mRNA cloning; reverse transcription;
 KW immobilise; screening; hybridisation; nucleic acid amplification;
 KW expression pattern; drug development; PCR primer; RT-PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9851789-A2.
 XX
 PD 19-NOV-1998.
 XX
 PF 13-MAY-1998; 98WO-DK000186.
 XX
 PR 13-MAY-1997; 97DK-00000547.
 PR 19-MAY-1997; 97US-00871030.
 PR 27-MAR-1998; 98DK-00000432.
 XX
 PA (DISP-) DISPLAY SYSTEMS BIOTECH APS.
 XX
 PI Warthoe PR;
 XX
 DR WPI; 1999-009772/01.
 XX
 XX Preparation of normalised, subdivided cDNA libraries from mRNA - by
 PT reverse transcription and amplification, used to screen for new genes and
 PT interacting proteins, potential drugs, and for diagnosis.
 XX
 PS Example 1; Page 29; 71pp; English.
 XX
 CC The invention relates to preparation of a normalised, subdivided library
 CC of amplified cDNA from the coding regions of mRNA in a sample. The method

CC involves reverse transcription, with at least one cDNA primer of formula
 CC 5'-Con1-dTn2-Vn3-Nn4 to form first strand cDNA where Con1 = any sequence
 CC of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3 and n4
 CC are both 0, or n3 is 1 and n4 is at least 1; followed by second strand
 CC cDNA synthesis using the first strand as template and a second cDNA
 CC primer of a similar formula, in the presence of DNA polymerase I (or its
 CC Klenow fragment) and amplification of double-stranded cDNA with a set of
 CC database (a computer-generated list of molecular weights of restricted
 CC DNA fragments of known sequence) is used to determine presence of an
 CC expressed protein in a cell, also to detect changes in such expression
 CC (particularly for diagnosis of disease). Surfaces (chip) having amplified
 CC cDNA stably immobilised on it, obtained by a similar method, are used to
 CC screen for genes of a particular family, by hybridisation with nucleic
 CC acid from the family (to identify new genes) and to detect differences in
 CC expression patterns between cells. The polypeptides expressed by the
 CC libraries can be used for drug development. Sequences AAV71935 to
 CC AAV71946 represent primers used to exemplify the method of the invention
 XX
 SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;
 Query Match 1.2%; Score 21; DB 1; Length 27;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAAAAAA 1755
 DB 26 CAAAAA AAAAAAAAAAAAAA 6
 RESULT 29
 AAS11744
 ID AAS11744 standard; DNA; 28 BP.
 XX
 AC AAS11744;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human haemoglobin alpha 2 transcript (extreme 3' end).
 XX
 KW Peptide-based cDNA characterisation; haemoglobin alpha 2; human; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200161051-A1.
 XX
 PD 23-AUG-2001.
 XX
 PF 16-FEB-2001; 2001WO-US005305.
 XX
 PR 16-FEB-2000; 2000US-0182983P.
 XX
 PA (SEQU-) SEQUEL GENETICS INC.
 XX
 PI Jarvik JW;
 XX
 DR WPI; 2001-514778/56.
 XX
 PT Transcript, genetic, and especially nucleic acid sequence analysis
 PT comprises analysis of hybrid peptide products.
 XX
 PS Example 11; Page 30; 48pp; English.
 XX
 CC The invention relates to a method of peptide-based transcript or genetic
 CC analysis comprising: (a) providing multiple polynucleotides (I) derived
 CC from mRNAs from a biological sample, where (I) has homology to a known
 CC reference sequence (II); (b) expressing (I); and (c) assessing a physical
 CC property of the expression products to determine the sequences of (I) by
 CC comparison with the predicted properties of polypeptides encoded by (II).
 CC The method is useful for transcript or genetic analysis, especially
 CC nucleic acid analysis where the method comprises expressing polypeptides
 CC from two or more reading frames and determining the masses to create a
 CC peptide mass signature characteristic of the nucleic acid molecule. The

CC peptide is considerably smaller than the DNA molecule that encodes it
CC (individual amino acids averages about 110 Daltons each whereas the
CC trinucleotides (triplets) that encode them average N Daltons each). Also,
CC the peptides are much more diverse in composition than nucleic acids, as
CC they are composed of combinations of 20 different amino acids instead of
CC combinations of 4 different nucleotides, e.g., two random DNA fragments
CC of identical composition (e.g., with 10 adenines, 10 thymines, 15
CC guanines, and 15 cytosines) are extremely unlikely to encode peptides of
CC identical composition. This means that whereas the two nucleic acids have
CC identical masses and cannot be distinguished on the basis of mass, the
CC peptides that they encode will, except in statistically very rare cases,
CC have different masses and can be readily distinguished in the basis of
CC mass. The present sequence represents the coding sequence of human
CC haemoglobin alpha 2 transcript (extreme 3' end) used in an example to
CC demonstrate the method of the invention
XX
SQ Sequence 28 BP; 23 A; 2 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 21; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1755
Dd 5 CAAAAA...AAAAA 25

RESULT 30
ABK48140/c
ID ABK48140 standard; DNA; 24 BP.
XX
AC ABK48140;
XX
DT 18-JUN-2002 (first entry)
XX
DE Aspergillus niger aminopeptidase RT-PCR primer poly-T.
XX
KW Aminopeptidase; primer; ss; food composition; dough; flavour enhancer;
KW baked product; cheese; poly-T; reverse transcriptase PCR.
XX
OS Synthetic.
XX
FN WO200216618-A1.
XX
PD 28-FEB-2002.
XX
PF 22-AUG-2001; 2001WO-EP009925.
XX
PR 23-AUG-2000; 2000EP-00202995.
XX
PA (STAM) DSM NV.
XX
PI Baeten D, Dekker PUT, Schuurhuizen PW, Schaap PJ, Visser J;
XX
DR WPI; 2002-257917/30.
XX
PT An isolated polypeptide with aminopeptidase activity, for preparing food
PT compositions, such as bread and cheese, with enhanced flavoring.
XX
PS Example 5; Page 40; 94pp; English.
XX
CC The invention relates to an isolated polypeptide with aminopeptidase
CC activity and the gene encoding it (including sequences complementary to
CC the gene and which hybridise to it at high stringency), from Aspergillus
CC niger. Also included are a nucleic acid construct comprising the above
CC polynucleotide operably linked to one or more control sequences that
CC direct the production of the polypeptide in a suitable expression host, a
CC recombinant expression vector comprising the above nucleic acid
CC construct, a recombinant host cell comprising the above construct or
CC vector, and producing the protein comprising cultivating an above strain/
CC recombinant host cell to produce a supernatant and/or cells comprising
CC the polypeptide and recovering the polypeptide. The aminopeptidase is
CC used to prepare a food composition such as dough to enhance the flavour

CC of a baked product from the dough and for preparing a cheese to enhance
CC the flavour. The invention provides a bacterial enzyme for protein
CC hydrolysis i.e. with aminopeptidase activity, to produce flavouring
CC agents, and the enzyme has been isolated and characterised, compared to a
CC previously observed weak aminopeptidase activity which was detected in an
CC Aspergillus niger culture filtrate but the source was never isolated or
CC identified. The use of enzymes to produce flavouring agents from
CC proteinaceous material is better than use of strong acids which can
CC severely degrade the amino acids obtained. The present sequence is a
CC reverse transcriptase (RT)-PCR primer used to investigate the intron-exon
CC structure of the aminopeptidase gene
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 23 T; 0 U; 1 Other;

Query Match 1.2%; Score 20.6; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.5e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA...AAAAA 1755
Dd 24 BAAAAA...AAAAA 2

RESULT 31
AAS20595/c
ID AAS20595 standard; DNA; 26 BP.
XX
AC AAS20595;
XX
DT 23-APR-2002 (first entry)
XX
DE Human zsig63 cDNA sequencing primer ZC7231.
XX
KW Human; zsig63; chromosome 4q12-4q13; salivary protein; antimicrobial; ss;
KW microbial infection; tooth decay; periodontal disease; thrush; emphysema;
KW gastrointestinal disease; urinary tract infection; vaginal infection;
KW skin infection; epithelial wound; chronic tissue damage; cystic fibrosis;
KW acquired immunodeficiency syndrome; AIDS; lung infection; sarcoidosis;
KW chronic bronchitis; gene therapy; protein therapy; primer; ZC7231.
XX
OS Homo sapiens.
XX
FN US6331413-B1.
XX
PD 18-DEC-2001.
XX
PF 17-MAR-2000; 2000US-00527345.
XX
PR 17-MAR-1999; 99US-0124820P.
XX
PA (ZYMO) ZYMOGENETICS INC.
XX
PI Adler DA, Sheppard PO;
XX
DR WPI; 2002-096707/13.
XX
PT Polynucleotides encoding salivary proteins useful as anti-microbial
PT agents.
XX
PS Example 1; Col 53; 29pp; English.
XX
CC The invention relates to a polynucleotide derived from the 4q12-4q13
CC region of human chromosome 4 and encoding a zsig63 polypeptide, a
CC secreted salivary protein with anti-microbial activity. Due to their
CC microbial activity, the sequences can be used in the study of microbial
CC infections, e.g. for recombinant production of anti-microbial proteins.
CC The sequences can be used in the treatment of tooth decay, periodontal
CC disease, thrush, gastrointestinal disease, epithelial wounds, chronic tissue
CC damage, acquired immunodeficiency syndrome (AIDS), cystic fibrosis, lung
CC infections, sarcoidosis, emphysema and chronic bronchitis. This sequence
CC represents a sequencing primer for cDNA encoding human zsig63
XX

```
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 0 T; 25 T; 0 U; 1 Other;
Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 1.6e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 32
ABSS26377/C
ID ABS52637 standard; DNA; 26 BP.
XX
AC ABS52637;
XX
DT 15-NOV-2002 (first entry)
XX
DE Human secreted salivary protein zsig63 PCR primer ZC7321.
XX
KW Human; secreted salivary protein; zsig63; immunogen; zsig63-cytokine;
KW antibody-cytokine; in vivo killing; pathological microbe; bacteria;
KW fungal; viral; infection; salivary gland; anti-microbial; dental caries;
KW tooth decay; periodontal disease; thrush; gastrointestinal disease;
KW urinary tract infection; vaginal infection; skin infection; microflora;
KW epithelial wound; pathogenic colonisation; invasion; pro-inflammatory;
KW chronic tissue damage; vascular system; diabetes; anti-inflammatory;
KW incompetent immune system; AIDS; acquired immunodeficiency syndrome;
KW chemotherapy; radiation treatment; lung infection; cystic fibrosis;
KW digestion; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN US2002081701-A1.
XX
PD 27-JUN-2002.
XX
PF 03-AUG-2001; 2001US-00922480.
XX
PR 17-MAR-1999; 99US-0124820P.
XX
PR 17-MAR-2000; 2000US-00527345.
XX
PA (ADLER/) ADLER D A.
XX
PA (SHEP/) SHEPPARD P O.
XX
PI Adler DA, Sheppard PO;
XX
XX WPI; 2002-635468/68.
XX
PT Novel secreted salivary protein, zsig63 and polynucleotide encoding it
PT useful for treating microbial infections, inflammatory conditions, dental
PT caries and lung infections associated with cystic fibrosis.
XX
PS Example 1; Page 29; 33pp; English.
XX
CC The present invention relates to a new secreted salivary protein, zsig63.
CC The invention is useful for detecting in a test sample, the presence of
CC an antagonist or agonist of zsig63 protein activity. The invention is
CC also useful as an immunogen for producing an antibody to zsig63
CC polypeptide. zsig63-cytokine fusion proteins or antibody-cytokine fusion
CC protein are useful for enhancing in vivo killing of target tissues.
CC Pharmaceutical composition comprising purified zsig63 polypeptide are
CC useful in the treatment of conditions associated with pathological
CC microbes, including bacterial, fungal and viral infections. High
CC expression of zsig63 in salivary gland suggests that anti-microbial
CC polypeptides are useful for treatment of dental caries (tooth decay),
CC periodontal disease, thrush and gastrointestinal disease. Other
CC applications can be used in urinary tract infections, vaginal infections,
CC prevention of infection in skin and other epithelial wounds. The
CC polypeptides can be used to establish normal microflora and protect
CC against pathogenic colonisation and invasion. The invention is useful
CC when pro-inflammatory activity is desired. Applications for such pro-
```

CC associated with pathological microbes, including bacterial, fungal and
 CC viral infections, for treating dental carries (tooth decay), periodontal
 CC disease, thrush and gastrointestinal disease, for treating urinary tract
 CC infection, vaginal infection and for preventing infection in skin and
 CC other epithelial wounds. zsig63 is useful for establishing normal
 CC microflora and protect against pathogenic colonisation and invasion, for
 CC treating chronic tissue damage e.g. damage in extremities associated with
 CC diabetes and useful as anti-inflammatory agents. It is useful as a marker
 CC of lung dysfunction, salivary gland dysfunction, or dysfunction of
 CC prostate gland. It is also therapeutically useful for aiding digestion.
 CC Polynucleotides of the invention are used in gene therapy for increasing
 CC or inhibiting zsig63 activity, for detecting abnormalities on human
 CC chromosome 4 associated with disease or other human traits and as
 CC diagnostics in forensic DNA profiling. Sequences of the invention are
 CC useful for stimulating proliferation or differentiation of cardiac
 CC myocytes, for proliferation or differentiation of adipocytes and for
 CC inhibiting chondrosarcomas, atherosclerosis, restenosis and obesity. The
 CC present sequence is a primer used in the identification of human zsig63
 CC DNA
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
 Query Match 1.2%; Score 20.6; DB 1; Length 26;
 Best Local Similarity 91.3%; Pred. No. 1.6e+02;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1733 TACAAAAA AAAAAAAAAAAAAA 1755
 : |||||
 Db 26 BAAAAA AAAAAAAAAAAAAA 4
 RESULT 34
 AAD55692/c
 ID AAD55692 standard; DNA; 26 BP.
 XX
 AC AAD55692;
 XX
 DT 27-OCT-2003 (revised)
 DT 07-AUG-2003 (first entry)
 XX
 DE Bovine viral diarrhea virus gene 5' end amplifying PCR primer.
 XX
 KW Bovine Viral Diarrhea Virus; BVDV; infection; vaccine; prophylaxis;
 KW Gene therapy; PCR; primer; ss.
 XX
 OS Pestivirus type 1.
 XX
 PN WO2003023041-A2.
 XX
 PD 20-MAR-2003.
 XX
 PF 05-SEP-2002; 2002WO-EP009925.
 XX
 PR 06-SEP-2001; 2001DE-01043813.
 XX
 PA (BOEH) BOEHRINGER INGELHEIM VETMEDICA GMBH.
 XX
 PI Elbers K, Meyer C, Von Freyburg M, Meyers G;
 XX
 DR WPI; 2003-333043/31.
 XX
 PT New DNA molecule useful for manufacturing a vaccine for the prophylaxis
 PT and treatment of Bovine Viral Diarrhea Virus (BVDV) infections, comprises
 PT a sequence complementary to a BVDV RNA.
 XX
 PS Example 1; Page 20; 73pp; English.
 XX
 CC The invention relates to a DNA molecule containing a sequence
 CC complementary to a Bovine Viral Diarrhea Virus (BVDV) RNA. The RNA when
 CC introduced into susceptible host cells, induces the generation of
 CC infectious BVDV particles. The attenuated BVDV clone or strain is useful
 CC in the manufacture of a vaccine for the prophylaxis and treatment of BVDV
 CC infections. The invention is useful in gene therapy. The present sequence

CC is a PCR primer used to amplify BVDV gene. (Updated on 27-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;
 Query Match 1.2%; Score 20.6; DB 1; Length 26;
 Best Local Similarity 91.3%; Pred. No. 1.6e+02;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1733 TACAAAAA AAAAAAAAAAAAAA 1755
 : |||||
 Db 26 BAAAAA AAAAAAAAAAAAAA 4
 RESULT 35
 ABX93598/c
 ID ABX93598 standard; DNA; 26 BP.
 XX
 AC ABX93598;
 XX
 DT 28-MAY-2003 (first entry)
 XX
 DE Human zsig63 PCR/sequencing primer ZC7231.
 XX
 KW ss; PCR; zsig63; adhesin; salivary gland; dental carries;
 KW periodontal disease; thrush; gastrointestinal disease; epithelial wound;
 KW urinary tract infection; vaginal infection; skin infection; primer;
 KW pro-inflammatory; chronic tissue damage; vascular system; diabetes; AIDS;
 KW lung infection; cystic fibrosis; lung dysfunction; digestive;
 KW salivary gland carcinoma; Pneumocystis carinii infection; emphysema;
 KW chronic bronchitis; prostate dysfunction; prostate adenocarcinoma;
 KW cell culture media; gene therapy; human chromosome 4q12-4q13;
 KW dentinogenesis imperfecta; dentin dysplasia type II.
 XX
 OS Synthetic.
 XX
 PN US2002173027-A1.
 XX
 PD 21-NOV-2002.
 XX
 PF 03-AUG-2001; 2001US-00922469.
 XX
 PR 17-MAR-1999; 99US-0124820P.
 PR 17-MAR-2000; 2000US-00527345.
 XX
 PA (ADLE/) ADLER D A.
 PA (SHEP/) SHEPPARD P O.
 XX
 PI Adler DA, Sheppard PO;
 XX
 DR WPI; 2003-328428/31.
 XX
 PT Novel isolated zsig63 polypeptide, member of the adhesin family, useful
 PT for treating dental carries, periodontal disease, thrush,
 PT gastrointestinal disease, urinary tract infections, vaginal infections,
 PT skin infections.
 XX
 PS Example 1; Page 29; 32pp; English.
 XX
 CC The invention relates to an isolated zsig63 polypeptide comprising at
 CC least 90% identity to an amino acid sequence which comprises domain 1 of
 CC zsig63, domain 2, domain 3, mature zsig63 and full length zsig63. Also
 CC included are the polynucleotide encoding zsig63, a zsig63 expression
 CC vector, a cultured cell comprising the vector and expressing the protein,
 CC a DNA encoding a fusion protein (comprising amino acids 1-15, 16-37, 38-
 CC 126, 127-219 or 16-219 of zsig63 and an additional protein), using a
 CC zsig63 reporter gene construct to identify zsig63 agonists, and producing
 CC an anti-zsig63 antibody using zsig63 immunogenic peptides, zsig63 is
 CC useful for detecting in a test sample, the presence of antagonist of
 CC zsig63 protein activity. zsig63 has antimicrobial activity and since
 CC exhibits high expression in salivary gland, can be used for treating
 CC dental carries, periodontal disease, thrush, and gastrointestinal
 CC disease, urinary tract infections, vaginal infections, skin infections

CC and other epithelial wounds. The polypeptides can be used to establish
CC normal microflora and protect against pathogenic colonization and
CC invasion. Zsig63 can also be used for providing pro-inflammatory activity
CC for treating chronic, tissue damage particularly in areas having limited
CC or damaged vascular system, e.g. in diabetes, and for treating
CC immunocompromised AIDS patients or in individuals that have undergone
CC chemotherapy, radiation treatment, for treating lung infections e.g. in
CC cystic fibrosis. Detection of zsig63 polypeptide at relatively high
CC levels in the trachea may indicate that such polypeptides may serve as a
CC marker of lung dysfunction. Zsig63 is also useful in diagnosing
CC conditions associated with salivary gland or lung dysfunction including
CC salivary gland carcinoma, Pneumocystis carinii infection, emphysema,
CC chronic bronchitis, prostate dysfunctions such as prostate
CC adenocarcinoma, aiding digestion, and as components of defined cell
CC culture media and may be used to replace serum that is commonly used in
CC culture. The DNA is useful in gene therapy applications to increase or
CC inhibit zsig63 activity, and for detecting abnormalities on human
CC chromosome 4 (e.g. 4q12-q13, associated with dentinogenesis imperfecta,
CC and dentin dysplasia type II). Zsig63 is an adhesin family member. The
CC present sequence is a primer used to isolate and sequence nucleic acids
CC encoding human zsig63
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 1.6e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
DB 26 BAAAAA 4

RESULT 36
ACF36382/C
ID ACF36382 standard; DNA; 26 BP.
XX
AC ACF36382;
XX
AC ACF36382;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a second back primer.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW electrophoresis; PCR; primer; ss.
XX
OS Synthetic.
XX
PN WO2003064691-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000843.
XX
PR 29-JAN-2002; 2002US-0352215P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfor P, Bauren G, Metsis A, Pihlak A;
PI Montellius A;
XX
XX WPI; 2003-618365/58.
XX

PT Producing a population of double-stranded product DNA molecules, useful
PT for mRNA profiling, comprises amplification by nested polymerase chain
PT reaction.
XX
XX Claim 6; Page 85; 105pp; English.
XX
XX The invention relates to producing a population of double-stranded
CC product DNA molecules comprising amplification by a nested PCR method.
CC The method is useful in profiling mRNA transcribed in a system under
CC investigation. The oligonucleotides are used as size standards in

CC electrophoresis, and as internal controls allowing for calculation of
CC relative amounts of material present. The present sequence represents a
CC specific example of a PCR primer used in the method of the invention
XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 1 Other;

Query Match 1.2%; Score 20.6; DB 1; Length 26;
Best Local Similarity 91.3%; Pred. No. 1.6e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1755
DB 26 BAAAAA 4

RESULT 37
ABQ76254/C
ID ABQ76254 standard; DNA; 27 BP.
XX
AC ABQ76254;
XX
DT 08-NOV-2002 (first entry)
XX
DE Murine SCCE 5'-RACE oligonucleotide SEQ ID 42.
XX
KW SCCE; murine; stratum corneum chymotryptic enzyme; kallikrein 7;
KW serine protease; transgenic mammal; skin; skin disease; skin cancer;
KW hyperkeratosis; acanthosis; epidermal inflammation; dermal inflammation;
KW pruritus; atopic dermatitis; eczema; acne; itch; KUK7; ss.
XX
OS Mus musculus.
XX
PN WO200262135-A2.
XX
PD 15-AUG-2002.
XX
PF 08-FEB-2002; 2002WO-IB001300.
XX
PR 09-FEB-2001; 2001CA-02332655.
PR 09-FEB-2001; 2001DK-00000218.
XX
PA (EGEL/) EGELRUD T.
PA (HANS/) HANSSON L.
XX
PI Egelrud T, Hansson L;
XX
XX WPI; 2002-643380/59.
XX

PT Transgenic mammal or its embryo useful as model for human disease, has
PT heterologous nucleotide sequence coding for stratum corneum chymotryptic
PT enzyme operably linked to promoter that drives its expression in skin.
XX
XX Example 6; Page 36; 74pp; English.
XX
XX This invention describes a novel non-human transgenic mammal or mammalian
CC embryo having integrated within its genome, a heterologous nucleotide
CC sequence comprising at least a significant part of a nucleotide sequence
CC coding for a stratum corneum chymotryptic enzyme (SCCE) or its variant.
CC operably linked to a promoter that drives expression of heterologous scce
CC or its variant in skin. The product of the invention is useful as a model
CC for the study of disease with the aim of improving treatment, to relieve
CC or ameliorate a pathogenic condition, for development or testing of a
CC cosmetic or a pharmaceutical formulation, and for the development of a
CC diagnostic method. It can also be used as a model for a skin disease or
CC skin cancer. The invention is also useful for screening or identifying a
CC compound or composition effective for the prevention or treatment of an
CC abnormal or unwanted phenotype, and for screening or identifying a
CC compound or composition effective for the prevention or treatment of
CC inflammatory skin diseases selected from diseases consisting of epidermal
CC hyperkeratosis, acanthosis, epidermal inflammation, dermal inflammation,
CC pruritus, atopic dermatitis, eczema, acne and inherited skin diseases
CC with epidermal hyperkeratosis. The mammal of the invention is also useful
CC as a model for further studies of itch mechanisms and the testing of

CC potential compounds and compositions for relieve of various skin diseases
CC where itch is a component. This sequence represents a 5' RACE cDNA
CC synthesis primer used in a method of detecting homologues to human
CC stratum corneum chymotryptic enzyme, SCCE, gene. SCCE is a serine
CC protease synonymous with human kallikrein 7 (KLK7) and is used in the
CC development of the transgenic mammals described in the invention
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.6; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 1.7e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 26 BAAAAA 4

RESULT 38
ABX12469/c
ID ABX12469 standard; DNA; 27 BP.
XX
AC ABX12469;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921, PCR primer dt26V.
XX
KW Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; Blindness;
KW renal failure; leg amputation; PCR; primer; ss.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
PD 27-DEC-2002.
XX
PF 19-JUN-2002; 2002WO-IB003278.
XX
PR 20-JUN-2001; 2001SE-00002198.
XX
PA (INNO-) INNOVENTUS PROJECT AB.
XX
PI Tuvemo HT, Frisk GE, Yin H;
XX
DR WPI; 2003-278229/27.
XX
PT Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX
PS Example 5; Page 44; 79pp; English.
XX
CC The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a primer used to determine the
CC genomic structure of diabetogenic coxsackie B virus 4 (CBV-4) strain
CC VD2921
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;

Query Match 1.2%; Score 20.6; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 1.7e+02;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1755
Db 27 BAAAAA 5

RESULT 39
AAQ64724
ID AAQ64724 standard; cDNA to mRNA; 22 BP.
XX
AC AAQ64724;
XX
DT 25-MAR-2003 (revised)
DT 04-JAN-1995 (first entry)
XX
DE 2',5'-linked tetraadenylate-anti(dt)18 oligonucleotide chimeric mol.
XX
KW antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
KW RNA cleavage; antiviral therapy; chimeric molecule; PKR;
KW protein synthesis regulation; phosphorylation; eIF-2alpha;
KW eukaryotic translation initiation factor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..4
FT FT /*tag= a
FT FT /label= 2',5'-linked tetraadenylate
FT FT /note= "nucleotides linked through phosphodiester bonds
FT FT at hydroxyl groups of 2' and 5' carbons"
FT FT 4..5
FT FT /*tag= b
FT FT /note= "the 2-5A moiety (*tag = a) and the antisense DNA
FT FT sequence (*tag = c) are linked by two 1,4-butanediol
FT FT molecules linked through phosphodiester bonds"
FT FT 5..22
FT FT /*tag= c
FT FT /note= "antisense region, complementary to oligo dt"
XX
PN WO9409129-A2.
XX
PD 28-APR-1994.
XX
PF 20-OCT-1993; 93WO-US010103.
XX
PR 21-OCT-1992; 92US-00965666.
PR 17-SEP-1993; 93US-00123449.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (CLEV-) CLEVELAND CLINIC RES INST.
XX
PI Torrence P, Silverman R, Maitra R, Lesiak K;
XX
DR WPI; 1994-151315/18.
XX
PT Specific cleavage of RNA, useful partic. for treating viral infection,
PT cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
PT of 2-5A dependent RNase.
XX
PS Example 9; Page 66; 86pp; English.
XX
CC This sequence was used to determine whether 2-5A-antisense chimeric
CC molecules are inhibitory to cell growth. The molecules AAQ64709, AAQ64711
CC and AAQ64724 all lacked cytotoxicity. In the novel 2-5A-antisense
CC oligonucleotide chimeric molecules, the antisense region targets the
CC chimeric molecule to a particular region of RNA to be specifically
CC cleaved and the 2',5'-linked tetraadenylate tail activates the 2-5A
CC RNase. Typical applications are treatment of viral infections (esp. for
CC cleavage of an RNA virus genome), cancer; leukaemia, cardiovascular
CC disorders (e.g. restenosis after angioplasty), genetic disorders,
CC osteoarthritis or rheumatoid arthritis. (Updated on 25-MAR-2003 to
CC correct FN field.)
XX

25-MAR-2003 (revised)	07-DEC-1992 (first entry)	Oligomer IL6803 for forming triplex with HUMIL6 target duplex.	Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV; malignancy; hepatitis; inflammation; ss.	Synthetic.	Key modified_base 1	Location/Qualifiers	1	/*tag= a	/mod_base= OTHER	/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"	11. .12	/*tag= d	/note= "o-xyloso dimer synthon linkage"	12. .23	/*tag= c	/label= inverted_polarity_region	/note= "see comments"	23	/*tag= b	/mod_base= OTHER	/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"	W09209705-A1.	11-JUN-1992.	25-NOV-1991; 91WO-US0008811.	23-NOV-1990; 90US-00617907.	18-JAN-1991; 91US-00643382.	08-APR-1991; 91US-00683420.	17-APR-1991; 91US-00686544.	17-APR-1991; 91US-00686546.	17-APR-1991; 91US-00686547.	27-SEP-1991; 91US-00766733.	(GILE-) GILEAD SCI INC.	Proehler B, Krawczyk S, Matteucci MD, Milligan J; WPI; 1992-217083/26.	New oligomers contg. modified bases - which form a triplex with G-C doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis, herpes malignancy and inflammation.	Claim 12; Page 71; 77pp; English.	The synthetic oligomer is capable of forming a triplex at physiological pH with a purine rich target sequence by coupling into the major groove of the duplex. The specific target sequence of this oligomer is the human interleukin 6 gene untranslated sequence contg. a purine rich sequence conder. on one strand of the duplex. The oligomer, and others like it are useful in diagnosis and therapy of diseases characterised by specific DNA duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant tumours and inflammation. The triple helices form under mild conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The oligomer contains an inverted polarity region formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso (nucleotides have the 3 positions of xylose sugars linked via the o-xyloso ring). Two nucleotides are coupled through a xyloso residue to form the dimer synthon. This additional modifications may render the oligomer stable to nuclease activity. The oligomer is able to inhibit gene expression, as verified by in vitro systems. See also AAQ25452-25501 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)	Sequence 23 BP; 2 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
-----------------------	---------------------------	--	---	------------	---------------------	---------------------	---	----------	------------------	---	---------	----------	---	---------	----------	----------------------------------	-----------------------	----	----------	------------------	---	---------------	--------------	------------------------------	-----------------------------	-----------------------------	-----------------------------	-----------------------------	-----------------------------	-----------------------------	-----------------------------	-------------------------	--	--	-----------------------------------	--	--


```

Query Match      1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1754
Db 23 TAAAAA 2

RESULT 42
ID AAQ30431/c
XX AAQ30431 standard; DNA; 23 BP.
AC AAQ30431;
XX
XX
XX 25-MAR-2003 (revised)
DT 07-DEC-1992 (first entry)
XX
XX Oligomer IL6804 for forming triplex with HUMIL6 target duplex.
XX
XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
KW malignancy; hepatitis; inflammation; ss.
XX
XX Synthetic.
XX
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= N4 N4 ethanocytosine"
FT misc_feature 11..12
FT /tag= d
FT /note= "o-xyloso dimer synthon linkage"
FT misc_feature 12..23
FT /tag= c
FT /label= inverted_polarity_region
FT /note= "see comments"
FT modified_base 23
FT /tag= b
FT /mod_base= OTHER
FT /note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine"
XX
XX
XX WO9209705-A1.
XX
XX 11-JUN-1992.
XX
XX 25-NOV-1991; 91WO-US008811.
XX
XX 23-NOV-1990; 90US-00617907.
XX 18-JAN-1991; 91US-00643382.
XX 08-APR-1991; 91US-00683420.
XX 17-APR-1991; 91US-00686544.
XX 17-APR-1991; 91US-00686546.
XX 17-APR-1991; 91US-00686547.
XX 27-SEP-1991; 91US-00766733.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX WPI; 1992-217083/26.
XX
XX New oligomers contg. modified bases - which form a triplex with G-C
XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
XX herpes malignancy and inflammation.
XX
XX Claim 12; Page 71; 77pp; English.
XX
XX The synthetic oligomer is capable of forming a triplex at physiological
XX pH with a purine rich target sequence by coupling into the major groove
XX of the duplex. The specific target sequence of this oligomer is the human
XX interleukin 6 gene untranslated sequence contg. a purine rich sequence
XX concd. on one strand of the duplex. The oligomer, and others like it are

```

```

CC useful in diagnosis and therapy of diseases characterised by specific DNA
CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
CC tumours and inflammation. The triple helices form under mild conditions
CC thus assays may be carried out without subjecting the test specimen to
CC harsh conditions. The oligomer contains an inverted polarity region
CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
CC (nucleotides have the 3' positions of xylose sugars linked via the o-
CC xyloso ring). Two nucleotides are coupled through a xyloso residue to
CC form the dimer synthon. This additional modification may render the
CC oligomer stable to nuclease activity. The oligomer is able to inhibit
CC gene expression, as verified by in vitro systems. See also AAQ25452-25501
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 23 BP; 1 A; 1 C; 0 G; 21 T; 0 U; 0 Other;
SQ
Query Match      1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1754
Db 23 TAAAAA 2

RESULT 43
AAC62450/c
XX AAC62450 standard; DNA; 23 BP.
XX
XX AAC62450;
XX
XX 07-FEB-2001 (first entry)
DT
DE
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #1.
KW Nucleic acid cleavage; solid support; DNA-RNA hybrid;
KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
KW nucleic acid purification; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT misc_RNA 23
FT /tag= a
XX
XX WO200058329-A1.
XX
XX 05-OCT-2000.
XX
XX 28-MAR-2000; 2000WO-GB001190.
XX
XX 29-MAR-1999; 99GB-00007245.
XX
XX (GOLD/) GOLDSBOROUGH A.
XX
XX WPI; 2000-664908/64.
XX
XX Detaching nucleic acid molecule comprising unconventional nucleotide
XX incorporated at predetermined site from a solid support involves cleaving
XX the nucleic acid molecule at the site of unconventional nucleotide.
XX
XX Disclosure; Page 16; 47pp; English.
XX
XX The present invention is concerned with the cleavage of nucleic acids
XX from solid supports. This is carried out by adding a non-conventional
XX nucleotide into the nucleic acid attached to the support, so that it is
XX recognised and cleaved by a specific DNA glycosylase and the sequence is
XX released. This is useful in many molecular biological procedures such as
XX sequencing, in vitro amplifications, cDNA and template preparation, DNA-
XX based assays, mutagenesis procedures, nucleic acid purification and
XX affinity chromatography. The present sequence is an oligonucleotide used
XX in assays to demonstrate the methods of the invention
XX
XX Sequence 23 BP; 0 A; 0 C; 0 G; 22 T; 1 U; 0 Other;
SQ

```

```
Query Match          1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA...AAAAAAAAA 1755
DB 23 AAAAAAAAA...AAAAAAAAA 2

RESULT 44
AAC62451/c
ID AAC62451 standard; RNA; 23 BP.
XX
AC AAC62451;
XX
DT 07-FEB-2001 (first entry)
XX
DE Cleavage of nucleic acids from solid supports assay oligonucleotide #2.
XX
KW Nucleic acid cleavage; solid support; affinity chromatography;
XX sequencing; mutagenesis; DNA preparation; nucleic acid purification; ss.
XX
OS Synthetic.
XX
PN WO200058329-A1.
XX
PD 05-OCT-2000.
XX
PF 28-MAR-2000; 2000WO-GB001190.
XX
PR 29-MAR-1999; 99GB-00007245.
XX
PA (GOLD/) GOLDSBOROUGH A.
XX
XX WPI; 2000-664908/64.
XX
PT Detaching nucleic acid molecule comprising unconventional nucleotide
PT incorporated at predetermined site from a solid support involves cleaving
PT the nucleic acid molecule at the site of unconventional nucleotide.
XX
PS Example 1; Page 32; 47pp; English.
XX
CC The present invention is concerned with the cleavage of nucleic acids
CC from solid supports. This is carried out by adding a non-conventional
CC nucleotide into the nucleic acid attached to the support, so that it is
CC recognised and cleaved by a specific DNA glycosylase and the sequence is
CC released. This is useful in many molecular biological procedures such as
CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
CC based assays, mutagenesis procedures, nucleic acid purification and
CC affinity chromatography. The present sequence is an oligonucleotide used
CC in assays to demonstrate the methods of the invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 0 T; 23 U; 0 Other;

Query Match          1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA...AAAAAAAAA 1755
DB 23 AAAAAAAAA...AAAAAAAAA 2

RESULT 45
ABL01773
ID ABL01773 standard; DNA; 23 BP.
XX
AC ABL01773;
XX
DT 18-MAR-2002 (first entry)
XX
DE Human MSH2 (hMSH2) intronic sequence SEQ ID NO:126.
```

```
XX Human; MLH1; MSH2; hMLH1; hMSH2; variant gene; diagnosis; HNPCC;
KW hereditary non-polypoidis colorectal cancer; ds.
XX Homo sapiens.
OS
XX US200104936-A1.
XX 22-NOV-2001.
PD
XX 22-OCT-1999; 99US-00426548.
XX
PR 22-OCT-1998; 98US-0105180P.
XX
PA (ROBB/) ROBBINS D.
PA (LING/) LIN-GOERKE J L.
PA (LING/) LING J C.
XX
PI Robbins D, Lin-Goerke JL, Ling JC;
XX WPI; 2002-105577/14.
XX
PT New variants of the human MLH1 and MSH2 genes for diagnosing or
PT determining a predisposition for hereditary non-polypoidis colorectal
PT cancer.
XX
PS Disclosure; Page 4; 38pp; English.
XX
CC The present invention describes a variant human MLH1 or MSH2 gene. Also
CC described are: (1) a method for diagnosing or predicting susceptibility
CC to hereditary non-polypoidis colorectal cancer (HNPCC), comprising
CC screening a DNA sample for the variant MLH1 or MSH2 gene where presence
CC of the variant indicates presence of, or susceptibility to HNPCC; (2) a
CC method of identifying mutants in splice donor or acceptor sites of a
CC human MLH1 gene, comprising sequencing splice donor or acceptor sites of
CC the gene with intronic primers for the human MLH1 gene and analysing the
CC sequence to identify any mutants; (3) a method of identifying mutants in
CC splice donor or acceptor sites of a human MSH2 gene, comprising
CC sequencing splice donor or acceptor sites of the gene with intronic
CC primers for the human MSH2 gene and analysing the sequence to identify
CC any mutants; and (4) a transgenic model system for colorectal cancer
CC comprising cells expressing the variant MLH1 or MSH2 gene. The hMLH1 and
CC hMSH2 variants are used to diagnose or determine a patient's
CC susceptibility to hereditary non-polypoidis colorectal cancer. ABL01648 to
CC ABL01745 and ABL01746 to ABL01831 represent hMLH1 and hMSH2 gene
CC fragments from the present invention. ABL01832 to ABL01839 represent
CC mutagenic primers used in the exemplification of the present invention
XX
SQ Sequence 23 BP; 21 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match          1.2%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA...AAAAAAAAA 1754
DB 2 TAAAAA...AAAAAAAAA 23

RESULT 46
AAT99286
ID AAT99286 standard; DNA; 24 BP.
XX
AC AAT99286;
XX
DT 15-APR-1998 (first entry)
XX
DE POLYA, a competitor oligonucleotide for binding human PUR-alpha.
XX
KW PUR element; human; c-myc; inhibitor; hyperproliferative disease; ss;
XX cancer; probe; hybridisation.
XX
OS Synthetic.
```

```

OS Homo sapiens.
XX
XX US5672479-A.
XX
XX 30-SEP-1997.
XX
XX 07-JUN-1995; 95US-00486421.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1997-488859/45.
XX
XX Assays for PUR protein ligands or modulators - using immobilised PUR
XX protein or fragments, to treat hyper-proliferative diseases, e.g. cancer.
XX
XX Example; Col 33; 64pp; English.
XX
XX The oligonucleotides AAT9279-T9286 were used as competitor
XX oligonucleotides for the binding of PUR protein to DNA. The PUR sequence
XX can be used to identify chemical or biological compounds that bind to PUR
XX or binding fragments of PUR. Inhibitors of PUR activity may be used to
XX treat hyperproliferative diseases such as cancer
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20.4; DB 1; Length 24;
XX Best Local Similarity 95.5%; Pred. No. 1.6e+02;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 47
AAV31743
ID AAV31743 standard; DNA; 24 BP.
XX
XX AAV31743;
XX
XX 24-SEP-1998 (first entry)
XX
XX Nucleotide sequence of the oligonucleotide POLYA.
XX
XX PUR-alpha gene; inhibition; viral infection; cancer; PUR element;
XX hyperproliferative disease; ss.
XX
XX Synthetic.
XX
XX US5756684-A.
XX
XX 26-MAY-1998.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1998-321632/28.
XX
XX PUR protein and its fragments - that inhibit PUR protein binding to PUR
XX element or other proteins.
XX

```

```

PS Example 7.1.1; Col 33; 63pp; English.
XX
XX This is the nucleotide sequence of an oligonucleotide used as a
XX competitor with the PUR element in the method of the invention, involving
XX the use of the PUR protein and its fragments, which inhibit PUR protein
XX binding to PUR element or other proteins. Inhibitors of PUR activity may
XX be useful for treating viral infections and hyperproliferative diseases
XX such as cancer
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20.4; DB 1; Length 24;
XX Best Local Similarity 95.5%; Pred. No. 1.6e+02;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 48
AAV04086
ID AAV04086 standard; DNA; 24 BP.
XX
XX AAV04086;
XX
XX 12-APR-1999 (first entry)
XX
XX Oligonucleotide POLYA used in PUR cloning and sequencing.
XX
XX PUR element; PUR-alpha; hyperproliferative disease; cancer; human;
XX monoclonal antibody; identification; characterisation; ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX US5869622-A.
XX
XX 09-FEB-1999.
XX
XX 07-JUN-1995; 95US-00486809.
XX
XX 28-AUG-1992; 92US-00938189.
XX
XX 02-FEB-1993; 93US-00014943.
XX
XX 06-JUN-1995; 95US-00470911.
XX
XX (MOUN ) MOUNT SINAI SCHOOL MEDICINE.
XX
XX Bergemann AD, Johnson EM;
XX
XX WPI; 1999-152881/13.
XX
XX Monoclonal antibody specific for PUR protein - useful for treating
XX cancer.
XX
XX Example; Col 33; 64pp; English.
XX
XX The present invention describes a monoclonal antibody that specifically
XX binds to an epitope of the PUR protein. Antibodies that bind to the PUR
XX protein and neutralise PUR activity may be used to treat
XX hyperproliferative diseases such as cancer. PUR antibodies may be used
XX diagnostically to detect aberrant expression of the PUR protein and/or
XX mutations in the PUR gene. The present sequence represents an
XX oligonucleotide used in the cloning and sequencing of the PUR protein and
XX its sequence element PUR repeat, in an example from the present invention
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.2%; Score 20.4; DB 1; Length 24;
XX Best Local Similarity 95.5%; Pred. No. 1.6e+02;
XX Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

```


PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieg AM, Schetter C, Vollmer J;
 XX WPI; 2001-273485/28.
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PT Claim 101; Page 57; 338pp; English.
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 ACACAAAAA 1755
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 3
 RESULT 52
 AAF99304/C
 ID AAF99304 standard; DNA; 24 BP.
 AC AAF99304;
 XX 12-JUN-2001 (first entry)
 DT Immunostimulatory nucleic acid #420.
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 XX immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX Synthetic.
 OS WO200122972-A2.
 PN 05-APR-2001.
 XX 25-SEP-2000; 2000WO-US026383.
 PD 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieg AM, Schetter C, Vollmer J;
 XX WPI; 2001-273485/28.
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PT Claim 101; Page 57; 338pp; English.
 XX The present invention relates to a method for stimulating an immune

DR WPI; 2001-273485/28.
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PT Claim 101; Page 46; 338pp; English.
 XX The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone
 XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
 SQ Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 ACACAAAAA 1755
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 3
 RESULT 53
 AAF99757
 ID AAF99757 standard; DNA; 24 BP.
 AC AAF99757;
 XX 12-JUN-2001 (first entry)
 DT Immunostimulatory nucleic acid #873.
 DE Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX Synthetic.
 OS WO200122972-A2.
 PN 05-APR-2001.
 XX 25-SEP-2000; 2000WO-US026383.
 PD 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX Krieg AM, Schetter C, Vollmer J;
 XX WPI; 2001-273485/28.
 DR Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PT Claim 101; Page 57; 338pp; English.
 XX The present invention relates to a method for stimulating an immune

XX	RESULT 57	
AB	ABS78478	
XX	ID ABS78478 standard; DNA; 24 BP.	
XX	AC	
XX	ABS78478;	
XX	13-DEC-2002 (first entry)	
XX	Angiogenesis inhibitory oligonucleotide #962.	
XX	Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;	
XX	Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;	
KW	tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;	
KW	diabetic retinopathy; retinopathy of prematurity; macular degeneration;	
KW	corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;	
KW	rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;	
KW	plaque neovascularisation; telangiectasia; haemophilic joint;	
KW	angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;	
KW	scleroderma; hypertrophic scar.	
XX	Synthetic.	
OS	WO200253141-A2.	
PN	11-JUL-2002.	
PD	14-DEC-2001; 2001WO-US048458.	
XX	14-DEC-2000; 2000US-0255534P.	
XX	(COLB-) COLBY PHARM GROUP INC.	
PA	Bratzler RL;	
PI	WPI; 2002-566690/60.	
XX	Inhibiting angiogenesis in a subject, involves administering at least one	
XX	antiangiogenic nucleic acid molecule to the subject.	
XX	Claim 2; Page 36; 276pp; English.	
XX	The invention relates to inhibiting angiogenesis in a subject, comprising	
CC	administering at least one antiangiogenic nucleic acid molecule. Also	
CC	included is a kit comprising a first container housing the antiangiogenic	
CC	nucleic acids, and instructions for administering them to a subject	
CC	having a condition characterised by unwanted angiogenesis. The method is	
CC	useful for inhibiting angiogenesis associated with solid tumour growth,	
CC	tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,	
CC	diabetic retinopathy, retinopathy of prematurity, macular degeneration,	
CC	corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,	
CC	rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque	
CC	neovascularisation, telangiectasia, haemophilic joints, angiofibroma,	
CC	wound granulation, intestinal adhesions, atherosclerosis, scleroderma and	
CC	hypertrophic scars. The present sequence is an antiangiogenic nucleic	
CC	acid of the invention	
XX	Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;	
SQ	Query Match 1.2%; Score 20.4; DB 1; Length 24;	
	Best Local Similarity 95.5%; Pred. No. 1.6e+02;	
	Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY	1734 AAAAAAAAAAAAAAAAAAAAAA 1755	
DB	1 AAAAAAAAAAAAAAAAAAAAAA 22	
XX	RESULT 58	
XX	ABL39405/c	
XX	ID ABL39405 standard; DNA; 24 BP.	
XX	ABL39405;	

```
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 841.
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..24
FT /*tag= a
FT /mod_base= OTHER
FT /notes= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
XX 27-DEC-2001.
PD
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
XX
XX Weiner G, Hartmann G;
PI
XX WPI; 2002-154611/20.
DR
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 309; 312pp; English.
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3
RESULT 59
ABA98840
ID ABA98840 standard; DNA; 24 BP.
XX
AC ABA98840;
XX
XX 01-JUL-2002 (first entry)
DT
XX A24 oligonucleotide for the creation of Pc-A24.
DE
XX
```

```
KW Component detection; clinical diagnosis; cell detection; drug detection;
KW metabolite detection; pesticide detection; ligand detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 24
FT /*tag= a
FT /label= OTHER
FT /note= "modified by P020CH2CH2CH2SSCH2CH2CH2OH"
XX
PN WO200184157-A2.
XX
XX 08-NOV-2001.
PD
XX
PF 03-MAY-2001; 2001WO-US014528.
XX
PR 04-MAY-2000; 2000US-00564230.
XX
PA (DADE-) DADE BEHRING INC.
XX
XX Pease JS, Cromer R, Ratel R, Kurn N, De Keczer S;
PI
XX WPI; 2002-164078/21.
DR
XX
XX Detection of multiple analytes, e.g. ligands, receptors, polynucleotides
PT and pollutants, involves adding a combination of sensitizer reagents and
PT reactive reagent Actuable by a product of the sensitizer reagents.
XX
XX Example; Page 58; 87pp; English.
XX
XX The invention relates to the detection of multiple components in a
CC medium, comprising combining the medium with at least two sensitizer
CC reagents, and at least one reactive reagent activated by a product
CC generated by the sensitizer reagents when activated; and differentially
CC activating the sensitizer reagents. The combination of sensitizer
CC reagents and reactive reagent(s) allows differential detection of the
CC components. Methods of the invention may be used for the detection of
CC ligands, receptors and polynucleotides, and also for the detection of
CC e.g. cells, various drugs, metabolites, pesticides (e.g. polyhalogenated
CC biphenyls, phosphate esters, thiophosphates, carbamates and
CC polynucleotides) and pollutants. Methods of the invention
CC allow the detection of multiple analytes in a single test medium. An
CC application of the methods of the present invention would be in the field
CC of clinical diagnostics. The current sequence represents A24
CC oligonucleotide for the creation of oligonucleotide coated phthalocyanine
CC sensitizer particles (Pc-A24)
XX
XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 60
AAI66361/c
ID AAI66361 standard; DNA; 24 BP.
XX
XX AAI66361;
AC
XX
XX 23-JAN-2002 (first entry)
DT
XX Human phosphatidylinositol-3 kinase 35 cDNA PCR primer #2.
XX
XX Human; phosphatidylinositol-3 kinase 35; PTDINS-3 kinase 35; cancer;
KW haemopathy; development disorder; HIV infection; immunological disease;
KW inflammation; gene therapy; PCR primer; ss.
XX
```



```

OS Homo sapiens.
FN WO200175014-A2.
PD 11-OCT-2001.
XX
PF 16-MAR-2001; 2001WO-CN000328.
XX
PR 17-MAR-2000; 2000CN-00114973.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
PI Mao Y, Xie Y;
XX
DR WPI; 2002-025836/03.
XX
PT New human phosphatidylinositol-3 (PTDING3) kinase 35 for diagnosing and
PT treating malignant tumor, hemopathy, human immunodeficiency virus
PT infection, immunological diseases and various inflammations.
XX
PS Example 2; Page 12; 34pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC phosphatidylinositol-3 (PTINS-3) kinase 35. The sequences can be used in
CC the treatment of cancer, haemopathy, HIV infection, development
CC disorders, immunological diseases and inflammation. The present sequence
CC is a PCR primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1732 TTACAAAAAATAAAAAAAAAA 1753
DB 22 TTAATAAAAAAAAAAAAAAAAAA 1
RESULT 61
AAS17869
ID AAS17869 standard; DNA; 24 BP.
XX
AC AAS17869;
XX
DT 08-MAY-2002 (first entry)
XX
DE A24 oligonucleotide used to create dopTAR chemiluminescer particles.
XX
KW Polymorphism detection; sequence detection; mutation detection; A24;
KW probe; non-dissociative termolecular complex; dopTAR sensitiser particle;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 24
FT /tags= a
FT /note= "A is covalently linked to a
FT PO2OCH2CH2CH2SCH2CH2CH2OH moiety"
XX
FN WO200190399-A2.
XX
PD 29-NOV-2001.
XX
PF 17-MAY-2001; 2001WO-US016089.
XX
PR 19-MAY-2000; 2000US-00574596.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Patel RD;
XX

```

```

DR WPI; 2002-097664/13.
XX
PT Detecting presence of polynucleotide, differences between polynucleotide
PT sequences, useful for detecting single nucleotide polymorphism and
PT alleles of polynucleotide sequence involves use of three competitive
PT probes.
XX
PS Example; Page 47; 75pp; English.
XX
CC This invention represents a method for detecting the presence of a
CC polynucleotide sequence, differences in polynucleotide sequences or
CC mutations in genomic DNA. The method involves contacting 3
CC oligonucleotide probes with a sample containing a polynucleotide. The
CC first probe hybridises to a region of the polynucleotide sequence and the
CC second and third probes can bind a second region of the polynucleotide
CC sequence. The second and third probes are identical except for the
CC presence or difference of one or more nucleotides. The reaction medium is
CC then subjected to conditions for forming substantially non-dissociative
CC termolecular complexes, which can be at least one of, the polynucleotide
CC sequence with the first and second probes or the polynucleotide sequence
CC with the first and third probes. The oligonucleotide probes have labels
CC non-covalently bound to allow for their detection upon binding. The
CC method of the invention is useful for detecting the presence of a single
CC nucleotide polymorphism (SNP) in a fragment of genomic DNA. The method
CC can be used for the direct detection of nucleic acid in very small
CC quantities without amplification. In addition, the method may be carried
CC out with amplification of the target and reference sequences. This
CC sequence represents an oligonucleotide probe A24 used to create dopTAR
CC chemiluminescer sensitiser particles in the method of the invention.
CC Binding the nucleic acid to a suspendable particle acts as a support and
CC provides a means of segregating the bound polynucleotide target from the
CC bulk solution
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAAATAAAAAAAAAA 1755
DB 1 AAAAAAAAAAAAAAAAAAAAAA 22
RESULT 62
ABK15639/c
ID ABK15639 standard; DNA; 24 BP.
XX
AC ABK15639;
XX
DT 08-MAY-2002 (first entry)
XX
DE RNA-PCR procedure primer poly(dT)24.
XX
KW RNA-PCR; primer; ss; poly(dT)24; cytostatic; antibacterial; gene therapy;
KW mRNA-cDNA hybrid; gene function inhibition; cancer; PTGS; antisense;
KW high throughput screening; D-RNAi; DNA-RNA interference; RdRp;
KW RNA dependent RNA polymerase; posttranscriptional gene silencing.
XX
OS Synthetic.
XX
FN WO200210374-A2.
XX
PD 07-FEB-2002.
XX
PF 02-AUG-2001; 2001WO-US024412.
XX
PR 02-AUG-2000; 2000US-0222479P.
XX
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Lin S, Chuong C, Widelitz RB;
XX

```

```
DR WPI; 2002-188740/24.
XX
XX Generating mRNA-cDNA hybrids for suppressing cancer-related genes, or
PT treating or preventing microbe related genes, comprises thermocycling
PT steps of promoter-linked double-stranded cDNA or RNA synthesis.
XX
XX Example 5; Page 26; 53pp; English.
XX
XX The invention relates to generating mRNA-cDNA hybrids, comprising (a)
CC providing a solution containing a nucleic acid template, one or more
CC primers complementary to the sense conformation of the nucleic acid
CC template, and one or more promoter-linked primers complementary to the
CC antisense conformation of the nucleic acid template, and with an RNA
CC promoter, (b) treating the nucleic acid template with the one of more
CC primers to synthesise a first cDNA strand, (c) treating the first cDNA
CC strand with one or more promoter-linked primers to synthesise a promoter-
CC linked double-stranded nucleic acid, (d) treating the promoter-linked
CC double-stranded nucleic acid to synthesise amplified mRNA fragments and
CC (e) treating the mRNA fragments with one or more primers to synthesise
CC mRNA-cDNA hybrids by reverse transcription of the amplified mRNA
CC fragments. The method is useful for preparing high amounts of pure and
CC specific mRNA-cDNA hybrids for transducing biological effects of interest
CC in vitro as well as in vivo, for inhibiting gene function in prokaryotes
CC and eukaryotes in vivo and in vitro, for suppressing cancer-related
CC genes, in treating or preventing microbe related genes, in studying
CC candidate molecular pathways with systematic knock out of involved
CC molecules, in high throughput screening of gene functions based on
CC microarray analysis, and as a tool in studying gene function in
CC physiological conditions. The mRNA-cDNA hybrids may be used to screen for
CC special gene functions, for manipulating gene expression in vitro, and
CC for designing therapy for genetic diseases in vivo. The cDNA part of a D-
CC RNAi (DNA-RNA interference) can be modified by nucleotide analogue
CC incorporation to increase the stability and effectiveness of transfected
CC probe activities. The RdRp (RNA dependent RNA polymerase) enzyme may
CC provide higher affinity of the mRNA template of a D-RNAi compared to de-
CC RNA due to lower binding interaction between DNA-RNA duplexes than RNA-
CC RNA duplexes. The cDNA part of a D-RNAi provides further antisense gene
CC knockout activity in addition to the posttranscriptional gene silencing
CC (PTGS) mechanisms of the sense-RNA template, resulting in multiple
CC specific gene interference effects with one probe. The present sequence
CC is a poly(dT) PCR primer used in conjunction with oligo(dC)10N primers to
CC reverse transcribe mRNA into first strand cDNA in the method of the
XX invention
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 24 AAAAAAAAAA 3
RESULT 63
ACA58802/c
ID ACA58802 standard; DNA; 24 BP.
XX
XX ACA58802;
XX
XX 10-JUN-2003 (first entry)
XX
XX Gastric ulcer treatment immunostimulatory nucleic acid #148.
DE
XX Gastric ulcer; ss; immunostimulant; equine gastric ulcer syndrome; EGUS;
KW Helicobacter pylori.
XX
XX Synthetic.
OS
XX US2002198165-A1.
PN
XX 26-DEC-2002.
PD
```

```
XX
XX 01-AUG-2001; 2001US-00920313.
XX
XX 01-AUG-2000; 2000US-0222248P.
XX
XX (BRAT/) BRATZLER R L.
XX (PETE/) PETERSEN D M.
XX
XX Bratzler RL, Petersen DM;
XX
XX WPI; 2003-370798/35.
XX
XX Prevention or treatment of gastric ulcer involves administering nucleic
XX acid.
XX
XX Disclosure; Page 14; 45pp; English.
XX
XX The invention relates to a method of prevention or treatment of gastric
XX ulcer comprising administering a nucleic acid to a subject in need for
XX treatment of gastric ulcer. A nucleic acid sample comprising
XX oligonucleotide 2006 was administered to a mouse model by an oral route
XX or a vehicle control. Colonisation of mice by Helicobacter pylori was
XX assessed at time points from 1 day to 1 month after treatment. The
XX ability of the nucleic acid to reduce H. pylori colonisation was
XX assessed. The method is useful for preventing or treating a gastric ulcer
XX on a subject e.g. human or non-human vertebrate animal including dog,
XX cat, horse (equine gastric ulcer syndrome, EGUS), cow, goat, sheep, pig,
XX rabbit, turkey, chicken, primate, rat and mouse. The method effectively
XX treats or prevents gastric ulcers. The present sequence represents an
XX immunostimulatory nucleic acid for the treatment of gastric ulcers
XX
XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 24 AAAAAAAAAA 3
RESULT 64
ABX79809/c
ID ABX79809 standard; cDNA; 24 BP.
XX
XX ABX79809;
XX
XX 17-APR-2003 (first entry)
XX
XX EST polymorphic DNA repeat polynucleotide #134.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW Polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
OS
XX
XX US6472154-B1.
PN
XX
XX 29-OCT-2002.
PD
XX
XX 31-DEC-1999; 99US-00475947.
XX
XX 31-DEC-1999; 99US-00475947.
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
PI
XX
```

DR WPI; 2003-208818/20.
 XX Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX Example; Col 579; 588pp; English.
 XX The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedreich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX
 SQ Sequence 24 BP; 0 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 Db 23 AAAAAAAAAAAAAAAAAAAAAA 2
 RESULT 65
 ABZ80181/c
 ID ABZ80181 standard; DNA; 24 BP.
 XX AC ABZ80181;
 XX 23-MAY-2003 (first entry)
 XX Immunostimulatory oligonucleotide SEQ ID NO:53.
 DE Immunostimulation; immune response; natural killer cell; interferon;
 KW type 1 interferon; IFN; cancer; infectious disease; allergic disorder;
 KW immune related disorder; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH modified_base 1..24
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "optionally phosphorothioate backbone"
 XX WO2003015711-A2.
 XX 27-FEB-2003.
 XX 19-AUG-2002; 2002WO-US026468.
 XX 17-AUG-2001; 2001US-0313273P.
 XX 03-JUL-2002; 2002US-0393952P.
 XX (COLE-) COLEY PHARM GROUP INC.
 PA (COLE-) COLEY PHARM GMBH.
 PA (IOWA) UNIV IOWA RES FOUND.
 XX Krieg AM, Vollmer J, Ullman E;
 XX

DR WPI; 2003-268241/26.
 XX New immunostimulatory nucleic acid, useful for preparing a composition
 PT for treating an allergic condition.
 XX Example 1; Page 44; 115pp; English.
 XX The present invention describes immunostimulatory nucleic acids of 14-100
 CC nucleotides in length comprising the formula 5' X1DCGHX2 3' (I), where X1
 CC or X2 = independently any sequence 0-10 nucleotides; D = nucleotide other
 CC than C; C = cytosine; G = guanine; H = nucleotide other than G. The
 CC immunostimulatory nucleic acid further comprises a sequence consisting of
 CC P and N positioned immediately 5' to X1 or 3' to X2 and N is a B cell
 CC neutralising sequence, where N begins with a CGG trinucleotide and is at
 CC least 10 nucleotides long and P is GC-rich palindromic containing sequence
 CC at least 10 nucleotides long. Also described: (1) a pharmaceutical
 CC composition comprising the immunostimulatory nucleic acid and a carrier;
 CC and (2) treating an allergic condition. (I) has anti-allergic activity and
 CC can be used in gene therapy. (I) can be used for preparing a composition
 CC for treating a variety of immune related disorders such as cancer,
 CC infectious diseases and allergic disorders. (I) also stimulates the
 CC activation of natural killer cells and the production of type 1
 CC interferon (IFN). The present sequence represents an immunostimulatory
 CC oligonucleotide, which is used in an example from the present invention
 XX
 SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 Db 24 AAAAAAAAAAAAAAAAAAAAAA 3
 RESULT 66
 ACA62284/c
 ID ACA62284 standard; DNA; 24 BP.
 XX AC ACA62284;
 XX 12-AUG-2003 (first entry)
 XX Oligo (dt)24 RT-PCR primer.
 DE ss: PCR; RT-PCR; primer; reverse transcriptase PCR; antisense therapy;
 KW mRNA expression profile; promoter containing primer.
 XX Synthetic.
 OS
 XX US2003022318-A1.
 XX 30-JAN-2003.
 XX 07-SEP-2001; 2001US-00949305.
 XX 25-JAN-2000; 2000US-00494212.
 XX (EPIC-) EPICLONE INC.
 XX Lin S, Ying S;
 XX WPI; 2003-479488/45.
 XX Improved polymerase thermocycling reaction for nucleic acid
 FT amplification, by thermal cycling of promoter-linked nucleic acid
 FT template synthesis and in vitro transcriptional amplification of nucleic
 FT acid sequences.
 XX Example 7; Page 14; 28pp; English.
 XX The invention relates to an improved polymerase thermocycling reaction
 CC

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 34; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 22

RESULT 69
ACH03284/C
ID ACH03284 standard; DNA; 24 BP.
XX
AC ACH03284;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #919.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; SR.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A. M.
PA (BERG/) BERG D. J.
PI Krieg AM, Berg DJ;
XX WPI; 2003-521815/49.
XX
XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 34; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory
CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid

XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAA 3

RESULT 70
ADA66379
ID ADA66379 standard; mRNA; 24 BP.
XX
AC ADA66379;
XX
DT 20-NOV-2003 (first entry)
XX
DE mRNA poly A.
XX
KW ss; nucleic acid amplification; multiple step elimination;
KW varying reaction condition elimination; poly A tract.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT primer_bind 1..24
FT /*tag= a
FT /note= "Binds to nucleotides 42-19 of the 1st strand cDNA
synthesis primer"
XX
XX US6582938-B1.
XX
PD 24-JUN-2003.
XX
PF 11-MAY-2001; 2001US-00854317.
XX
PR 11-MAY-2001; 2001US-00854317.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Su X, Dong H, Ryder TB;
XX WPI; 2003-656427/62.
XX
PT Amplification of nucleic acids, where the promoter is blocked from
PT extension at the 3' end, useful for eliminating multiple step reactions.
XX
PS Disclosure; Fig 2; 9pp; English.
XX
CC The invention relates to a method of amplification of nucleic acid which
CC comprises primer extension by reverse transcriptase and hybridising an
CC oligonucleotide to the single stranded DNA, where the oligonucleotide is
CC blocked from extension at the 3' end. The method is useful for
CC amplification of nucleic acids. In the method, a promoter is
CC protected from degradation throughout the method. The promoter is
CC constructed so that it does not serve as a primer for extension of a
CC sequence that is complementary to the target sequence, i.e. it is
CC blocked. The method can be combined with other processes to eliminate the
CC need for multiple steps and varying reaction conditions and their
CC associated problems. At least three otherwise separate enzymatic
CC reactions can occur consecutively in one phase (i.e., without organic
CC extraction and precipitation), more preferably in the same reaction
CC vessel. Preferably, cDNA synthesis according to the new method may occur
CC in a modified low salt buffer. The present sequence represents the poly A
CC tract of a mRNA used to illustrate the method of the invention.
XX
SQ Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;

```
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 71
ADB37258/c
ID ADB37258 standard; DNA; 24 BP.
XX
AC ADB37258;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #872.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 11; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 1.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 72
ADB36806/c
ID ADB36806 standard; DNA; 24 BP.
XX
AC ADB36806;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #420.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 73
ADB37259
ID ADB37259 standard; DNA; 24 BP.
XX
AC ADB37259;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #873.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
```

PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 18; 221pp; English.

CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.

XX Sequence 24 BP; 24 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
 Db 1 AAAAAAAAAA 22

RESULT 74

ADD31867/c

ID ADD31867 standard; DNA; 24 BP.

XX AC ADD31867;

XX 15-JAN-2004 (first entry)

DE Butterfly biliverdin binding protein BBP-BIX oligonucleotide SEQ ID:106.

XX recombination product; synthetic gene technology; butterfly;

XX biliverdin binding protein; ss.

XX synthetic.

XX WO2003064611-A2.

XX 07-AUG-2003.

XX 29-JAN-2003; 2003WO-US002612.

XX 30-JAN-2002; 2002US-00062188.

XX (EGEA-) EGEA BIOSCIENCES INC.

XX Evans GA;

XX WPI; 2003-663477/62.

XX Creating recombination products between two distinct nucleotide
 PT sequences, useful in the field of synthetic gene technology, and in
 PT assembling a library, or a population or a collection of polypeptide
 PT variants.

XX Example 3; SEQ ID NO 106; 132pp; English.

CC The present invention describes a method for creating a collection of
 CC recombination products between two nucleotide sequences. The method
 CC comprises combining an initial set of oligonucleotides corresponding to a
 CC first nucleotide sequence with a subsequent set of oligonucleotides
 CC corresponding to a distinct nucleotide sequence and further combining the
 CC initial and subsequent sets of combination oligonucleotides having a
 CC sequence region corresponding to the initial nucleotide sequence and a
 CC sequence region corresponding to the second oligonucleotide sequence.
 CC Also described is a method of creating a collection of recombination
 CC products between two genes. The methods and compositions of the present
 CC invention are useful in the field of synthetic gene technology, and more
 CC specifically, to generating a collection of recombination products
 CC between distinct nucleotide sequences. They can also be used in
 CC assembling a library, or a population or a collection of polypeptide

CC variants that correspond to single or multiple polynucleotide
 CC recombination products. The present sequence is used in the
 CC exemplification of the present invention.

XX Sequence 24 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
 Db 24 AAAAAAAAAA 3

RESULT 75

ADE25524/c

ID ADE25524 standard; DNA; 24 BP.

XX AC ADE25524;

XX 29-JAN-2004 (first entry)

DE Rolling circle amplification related probe control oigo POS1/2.

XX RCA; rolling circle amplification; genotyping;

XX single-nucleotide polymorphism; single base extension; SBE;

XX immuno-hybridisation; probe; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 24

FT /*tag= a

FT /mod_base= OTHER

FT /note= "optional biotin label"

XX WO2003066817-A2.

XX 14-AUG-2003.

XX 06-FEB-2003; 2003WO-US003533.

XX 06-FEB-2002; 2002US-0355374P.

XX (AMSH) AMERSHAM BIOSCIENCES AB.

XX Xia J;

XX WPI; 2003-697450/66.

XX Detecting nucleic acid targets, useful e.g. for diagnosing single
 PT nucleotide polymorphisms, by extension of capture probe complementary to
 PT open circle probe.

XX Example 1; Fig 5; 66pp; English.

XX The invention is directed to novel methods of amplifying and detecting
 CC DNA using rolling circle amplification (RCA). The invention relates to
 CC detecting a target sequence (I), which involves using a capture probe
 CC (CP) that is complementary to an open circle probe and includes a
 CC cleavage site. The method comprises: attaching a capture probe (CP) to a
 CC substrate, at both ends, where the CP includes one domain complementary
 CC to an OCP (open circle probe) and a second domain that contains a
 CC cleavage site (CS), to form a device; treating CP with (I) and OCP for
 CC form a hybridisation complex (HC); treating HC with a ligase so that OCP
 CC is circularised, forming a second complex (HC2); treating CP with a
 CC cleavage agent, to cut at CS, and adding an extension enzyme (EE) and
 CC nucleotide triphosphates (NTPs) to form an extended CP, which is
 CC detected. The method is used for detecting (I) that comprises two target
 CC domains (TD1, TD2) and (I) that comprises two adjacent target domains.
 CC The method is used for detection, genotyping and/or quantification of
 CC target sequences, for research, clinical use, quality control or field

CC testing, particularly detection of single-nucleotide polymorphisms. The
 CC method permits a high level of multiplexing, and since it provides
 CC localized product detection, with linear kinetics, is sensitive enough
 CC for direct detection and quantitation of unmodified targets. The present
 CC sequence is that of a single base extension (SBE) probe used in SNP
 CC genotyping with RCA signal amplification to demonstrate the method of the
 CC invention.

XX SQ Sequence 24 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 24;
 Best Local Similarity 95.5%; Pred. No. 1.6e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 76
 AAQ95960/c
 ID AAQ95960 standard; DNA; 25 BP.

XX AC AAQ95960;

XX DT 06-FEB-1996 (first entry)

XX DE Oligonucleotide biotin-T25 for novel nucleic acid immobilisation method.

XX KW Immobilisation; solid support; salt; cationic detergent; capture probe;
 KW hybridisation; primer; template-dependent extension; target organism;
 KW sequencing; genetic polymorphism; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a
 FT /note= "biotinylated"

XX PN W09515970-Al.

XX PD 15-JUN-1995.

XX PF 06-DEC-1994; 94WO-US014096.

XX PR 06-DEC-1993; 93US-00162397.

XX PR 16-NOV-1994; 94US-00341148.

XX PA (MOLE-) MOLECULAR TOOL INC.

XX PI Nikiforov T, Knapp MR;

XX DR WPI; 1995-224282/29.

XX PT Immobilising synthetic nucleic acid on solid support - by incubation in
 PT presence of salt or cationic detergent, for use in hybridisation assays,
 PT sequencing and analysis of polymorphism.

XX PS Example 1; Page 18; 61pp; English.

XX CC Oligonucleotides AAQ95959-82 are examples of oligonucleotides used in a
 CC novel method of immobilising oligonucleotides to a solid support by
 CC incubating in the presence of a salt or cationic detergent e.g. NaCl (50-
 CC 250 mM, pH 6.0-8.0) or 1-ethyl-3-(3'-dimethyl amino propyl)-1,3
 CC carbodiimide hydrochloride (EDC). The oligonucleotides can be capture
 CC probes for detection of specific nucleic acids by hybridisation or can be
 CC primers for template-dependent extension from the immobilised primers on
 CC nucleic acid from a target organism. The method can be used in
 CC hybridisation assays, sequencing and analysis of genetic polymorphism

XX SQ Sequence 25 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 25;
 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 DB 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 77
 AA84260/c
 ID AA84260 standard; DNA; 25 BP.

XX AC AA84260;

XX DT 08-SEP-1999 (first entry)

XX DE PCR primer for human Nck associated protein 1 coding sequence.

XX KW Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;
 KW therapy; PCR primer; ss.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN W09931239-Al.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-JP005646.

XX PR 15-DEC-1997; 97JP-00363183.

XX PA (KYOW) KYOWA HAKKO KOGYO KK.

XX PA (SAKA/) SAKAKI Y.

XX PI Sakaki Y;

XX DR WPI; 1999-395181/33.

XX PT Protein inhibiting apoptosis, useful in the diagnosis and treatment of
 PT Alzheimer's disease.

XX PS Disclosure; Page 77; 90pp; Japanese.

XX CC This sequence represents a PCR primer used to isolate DNA encoding the
 CC human Nck associated protein 1 (Napi) of the invention. Napi inhibits
 CC apoptosis. The protein can be used in the investigation, diagnosis and
 CC treatment (e.g. by gene therapy) of Alzheimer's disease

XX SQ Sequence 25 BP; 0 A; 1 C; 0 G; 24 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 25;
 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 DB 24 AAAAAAAAAAAAAAAAAAAAAA 3

RESULT 78
 AAA39306/c
 ID AAA39306 standard; RNA; 25 BP.

XX AC AAA39306;

XX DT 11-SEP-2000 (first entry)

XX DE Rapid capture probe designated Neu-probe SEQ ID NO:1.

XX KW Rapid detection; probe; target nucleic acid; enzymatic amplification;
 KW isolation; detection; ss.

PT absence or identity of single polynucleotide polymorphism in a nucleic
 PT acid sample.
 XX
 PS Claim 1; Page 56; 83pp; English.
 XX
 CC Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
 CC primer extension (SNPE) primers, and the sequences of regions flanking
 CC sites of single nucleotide polymorphisms SNPs. The present invention
 CC includes kits for determining the presence or absence of a SNP, using the
 CC oligonucleotides of the invention. The PCR primers are used to amplify a
 CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
 CC The oligonucleotides are useful for genotyping a nucleic acid sample by
 CC performing a single-nucleotide primer extension reaction. The
 CC oligonucleotides are useful for determining the presence, absence or
 CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
 CC assess by association analysis the genotype of an individual or group of
 CC individuals, having a pathological phenotypic trait suspected of being
 CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
 CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
 CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
 CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
 CC traits also include symptoms of or susceptibility to multifactorial
 CC disease of which a component is or may be genetic such as autoimmune
 CC diseases, including, rheumatoid arthritis, multiple sclerosis,
 CC inflammation, cancer, nervous system diseases and infection by pathogenic
 CC microorganism. The method is also useful in forensic investigations and
 CC paternity analysis. The present sequence represents a single nucleotide
 CC primer extension (SNPE) primer specific for a human SNP containing DNA
 CC sequence
 XX
 SQ Sequence 25 BP; 1 A; 1 C; 0 G; 23 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20.4; DB 1; Length 25;
 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 4
 RESULT 81
 ABK49986/c
 ID ABK49986 standard; DNA; 25 BP.
 AC ABK49986;
 XX
 XX 15-JUL-2002 (first entry)
 DT
 XX Example oligonucleotide #2 prepared on glass-synthetic resin membrane.
 DE
 XX Glass-synthetic resin membrane; pore glass-polytetrafluoroethylene resin;
 KW Chromatography membrane; PTPE; ss.
 XX
 OS Synthetic.
 XX US6261497-B1.
 PN
 XX 17-JUL-2001.
 PD
 XX 04-MAY-1999; 99US-00305219.
 PF
 XX 21-FEB-1996; 96US-00604440.
 PR
 XX (CPGC-) CPG INC.
 PA
 XX Wong YN, Chen R;
 PI WPI; 2001-534961/59.
 DR
 XX Preparation of controlled pore glass-polytetrafluoroethylene resin
 PT chromatography membrane by heating, calendering and sintering mixture of
 PT controlled pore glass and aqueous dispersion of polytetrafluoroethylene.

XX Example 12; Col 8; 6pp; English.
 PS
 XX The invention relates to a method of preparing a controlled pore glass-
 CC polytetrafluoroethylene (PTFE) resin chromatography membrane, comprising
 CC combining controlled pore glass and an aqueous dispersion of PTFE to form
 CC a paste-like mass, heating the paste-like mass at 50-70 plus OC,
 CC calendering to form a foldable sheet, and sintering the sheet to produce
 CC a rigid, porous sheet. The method prepares a controlled pore glass-PTFE
 CC resin chromatography membrane for use in various biotechnical procedures.
 CC The membrane is useful in place of controlled pore glass as a support for
 CC the synthesis, isolation, and purification of nucleic acids and for the
 CC isolation and purification of proteins. The method produces a membrane
 CC that may be used in lieu of controlled pore glass. The present sequence
 CC represents an oligonucleotide prepared on the membrane in an example
 CC which demonstrates the method of the invention
 XX
 SQ Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20.4; DB 1; Length 25;
 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 4
 RESULT 82
 ADC54009/c
 ID ADC54009 standard; DNA; 25 BP.
 AC ADC54009;
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX Oligonucleotide of the invention SEQ ID NO:4.
 DE
 XX ss; probe carrier; discharge.
 KW
 XX Synthetic.
 OS
 XX JP2003035711-A.
 PN
 PD 07-FEB-2003.
 XX
 PF 28-MAR-2002; 2002JP-00093023.
 PR
 XX 28-MAR-2001; 2001JP-00094400.
 PA (CANO) CANON KK.
 XX
 XX WPI; 2003-535999/51.
 DR
 XX Probe carrier manufacturing method for inkjet system, involves scanning
 PT liquid discharge head in direction orthogonal to scanning direction, at
 PT angle satisfying predetermined relation.
 XX
 PS Example 2; SEQ ID NO 4; 17pp; Japanese.
 XX
 CC The invention relates to a novel probe carrier and the method for
 CC manufacturing the carrier. The invention enables stable discharge of
 CC solution, and removes liquid droplets adhering to discharge nozzle. The
 CC present sequence is used in the exemplification of the invention.
 CC
 XX Sequence 25 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 0 Other;
 Query Match 1.2%; Score 20.4; DB 1; Length 25;
 Best Local Similarity 95.5%; Pred. No. 1.7e+02;
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
 Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

Db 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 83

ADC54008
ID ADC54008 standard; DNA; 25 BP.

AC ADC54008;
DT 18-DEC-2003 (first entry)
DE Oligonucleotide of the invention SEQ ID NO.3.
KW ss; probe carrier; discharge.

OS Synthetic.

PN JP2003035711-A.

PD 07-FEB-2003.

PF 28-MAR-2002; 2002JP-00093023.

PR 28-MAR-2001; 2001JP-00094400.

PA (CANO) CANON KK.

XX WPI; 2003-535999/51.

PT Probe carrier manufacturing method for inkjet system, involves scanning liquid discharge head in direction orthogonal to scanning direction, at angle satisfying predetermined relation.

PS Example 2; SEQ ID NO 3; 17pp; Japanese.

XX The invention relates to a novel probe carrier and the method for manufacturing the carrier. The invention enables stable discharge of solution, and removes liquid droplets adhering to discharge nozzle. The present sequence is used in the exemplification of the invention.

SQ Sequence 25 BP; 25 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 25;

Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 84

AAN70276/C
ID AAN70276 standard; DNA; 26 BP.

AC AAN70276;

DT 03-OCT-2002 (revised)
DT 26-MAY-1991 (first entry)

XX Sequence of scissile link probe MRC060 (HL).

DE Hybridisation; probe; ss.

KW Synthetic.

OS EP227976-A.

PN 08-JUL-1987.

XX 04-DEC-1986; 86EP-00116906.

PR 05-DEC-1985; 85US-00805279.

XX (MEIO-) MEIOGENICS INC.

PI Duck P, Bender R, Crosby W, Robertson JG;

XX WPI; 1987-186567/27.

DR Synthetic nucleic acid probes - comprising two nucleic acid sequences linked by a scissile linkage.

XX Example; p29; 46pp; English.

XX The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile linkage; n= 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid Support). The differential liability of DNA and RNA may be exploited in a heterogeneous system when the scissile linkage is an RNA molecule. In the examples, counter probe molecules 9 through 16 were used to determine suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing OS field.)

XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 26;

Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 85

AAN70275/C
ID AAN70275 standard; DNA; 26 BP.

XX AAN70275;

DT 03-OCT-2002 (revised)
DT 26-MAY-1991 (first entry)

XX Sequence of scissile link probe MRC059 (HL).

DE Hybridisation; probe; ss.

KW Synthetic.

OS EP227976-A.

PN 08-JUL-1987.

XX 04-DEC-1986; 86EP-00116906.

PR 05-DEC-1985; 85US-00805279.

XX (MEIO-) MEIOGENICS INC.

PI Duck P, Bender R, Crosby W, Robertson JG;

XX WPI; 1987-186567/27.

DR Synthetic nucleic acid probes - comprising two nucleic acid sequences linked by a scissile linkage.

XX Example; p29; 46pp; English.

XX The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile linkage; n= 1 or 1,000, which is used for the detection of specific DNA or RNA sequences in a test soln. The scissile link probes may be PL (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid

CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)

XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;
SQ Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1734 ACACAAAAA 1755
Db 26 AAAAAAAAAA 5

RESULT 86
AAN92241/c
ID AAN92241 standard; DNA; 26 BP.
XX
AC AAN92241;
XX
AC 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRC059.
XX
KW Probe MRC059; solid support; ribonuclease.
OS Synthetic.

XX Key Location/Qualifiers
FH misc_feature 1..10
FT /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 11..14
FT /tag= b
FT /note= "ribonucleotides."
FT misc_feature 15..26
FT /tag= c
FT /note= "deoxyribonucleotides."
XX

PN WO8910415-A.
XX
XX 02-NOV-1989.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX 29-APR-1988; 88US-00187814.
XX
XX (MEIO-) MEIOGENICS INC.

XX Duck P, Bender R;
XX WPI; 1989-339977/46.
XX

XX Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.

XX Disclosure; Page 24; 34pp; English.

XX Probe MRC059 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

SQ Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1734 ACACAAAAA 1755
Db 26 AAAAAAAAAA 5

RESULT 87
AAN92242/c
ID AAN92242 standard; DNA; 26 BP.

XX
AC AAN92242;
XX
XX 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX

DE SS probe MRC060.

XX Probe MRC060; solid support; ribonuclease.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_feature 1..12
FT /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 13..16
FT /tag= b
FT /note= "ribonucleotides."
FT misc_feature 17..26
FT /tag= c
FT /note= "deoxyribonucleotides."
XX

PN WO8910415-A.

XX 02-NOV-1989.

XX 29-APR-1988; 88US-00187814.

XX 29-APR-1988; 88US-00187814.

XX (MEIO-) MEIOGENICS INC.

XX Duck P, Bender R;

XX WPI; 1989-339977/46.

XX Detecting target nucleic acid molecules - using excess complementary
XX nucleic acid probes and nicking to complete a cycling sequence.

XX Disclosure; Page 24; 34pp; English.

XX Probe MRC060 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)

XX (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 26 BP; 0 A; 0 C; 0 G; 22 T; 4 U; 0 Other;

```

Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 88
AAF77536/c
ID AAF77536 standard; DNA; 26 BP.
XX AC AAF77536;
XX XX
XX DT 23-MAY-2001 (first entry)
XX XX
XX DE CDNA library production method related oligonucleotide SEQ ID NO: 5.
XX XX
XX KW CDNA library production; SCLA; gene chip technology;
XX KW differential screening; pathological diagnosis; genetic identification;
XX KW single-cell cDNA library amplification; ds.
XX XX
XX OS Synthetic.
XX XX
XX PN US6197554-B1.
XX PN
XX PD 06-MAR-2001.
XX XX
XX PF 20-NOV-1998; 98US-00197951.
XX XX
XX PR 20-NOV-1998; 98US-00197951.
XX XX
XX PA (LINS/) LIN S.
XX PA (CHUO/) CHUONG C.
XX PA (YING/) YING S.
XX XX
XX PI Lin S, Chuong C, Ying S;
XX XX
XX WPI; 2001-243448/25.
XX XX
XX PT Generating a complete full-length cDNA library from single cells for use
XX PT in gene chip technology, involves reverse transcribing intracellular
XX PT mRNAs, adding polynucleotide tail and amplifying formed cDNAs.
XX XX
XX PS Disclosure; Col 11-12; 11pp; English.
XX XX
XX CC The present invention describes a method of producing full-length cDNA
XX CC libraries from single cells, designated single-cell cDNA library...
XX CC amplification (SCLA). The method is useful in gene chip technology.
XX CC differential screening, pathological diagnosis, physiological prognosis
XX CC and genetic identification. No further information about this sequence is
XX CC given in the specification
XX XX
XX SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match          1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 89
AAF23526/c
ID AAF23526 standard; DNA; 26 BP.
XX AC AAF23526;
XX XX
XX DT 22-MAR-2001 (first entry)
XX XX

```

```
PI Ju J, Li Z, Tong A, Russo JJ;
XX WPI; 2002-575158/61.
XX Composition of matter useful for multi-component analyses, comprises
PT multiple fluorophores bound to molecular scaffold at preset positions to
PT permit fluorescence energy transfer between two fluorophores.
XX Disclosure; Page 43; 113pp; English.
XX This sequence represents a molecular scaffold which may be used in a
CC composition of matter comprising multiple fluorophores. The fluorophores
CC are bound to the molecular scaffold at separate predetermined positions,
CC to permit fluorescence energy transfer between two fluorophores. The
CC fluorophores are characterized by maximum emission wavelength of one
CC being greater than the minimum excitation wavelength of the other. The
CC composition is useful for determining whether a preselected nucleotide
CC residue is present at a predetermined position within a nucleic acid. It
CC is also useful in multicomponent analysis including multiplex biological
CC analysis, and identifying multiple single nucleotide polymorphisms. The
CC presence of a number of given nucleotide residues is determined
CC simultaneously by the composition of the invention
XX Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
DB 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 91
ID AAS20672 standard; DNA; 26 BP.
XX AAS20672;
XX 09-APR-2002 (first entry)
XX Human zalphall Ligand sequencing primer ZC7764b.
XX Cytokine; zalphall Ligand; zalphall receptor; NK cell progenitor;
XX natural killer cell proliferation; T-cell proliferation;
XX B-cell proliferation; anti-tumour response; immune system;
XX immunostimulant; cytostatic; human; sequencing primer; ss.
XX - Homo sapiens.
XX OS
XX US6307024-B1.
XX 23-OCT-2001.
XX 09-MAR-2000; 2000US-00522217.
XX 09-MAR-1999; 99US-0123547P.
XX 11-MAR-1999; 99US-0123304P.
XX 01-JUL-1999; 99US-0142013P.
XX (ZYMO ) ZYMOGENETICS INC.
XX Novak JE, Preenell SR, Sprecher CA, Foster DC, Holly RD;
PI Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;
XX WPI; 2002-040208/05.
XX New zalphall ligand polypeptides and polynucleotides, useful for
PT stimulating proliferation, activation, differentiation and/or induction
PT of inhibition of specialized cell function, or for stimulating an
XX antigenic response.
XX

PS Example 7; Col 139; 105pp; English.
XX The present invention relates to the isolation of a novel cytokine,
CC zalphall ligand and the polynucleotide encoding it. The invention also
CC gives the sequence for the zalphall receptor and the polynucleotide
CC encoding it. The zalphall ligand polypeptide stimulates proliferation of
CC natural killer (NK) cells or NK cell progenitors, the activation of NK
CC cells, proliferation of T-cells, proliferation of B-cells stimulated with
CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and
CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The
CC zalphall ligand polypeptide is also useful in preparing antibodies that
CC bind to zalphall Ligand epitopes. The zalphall Ligand polynucleotides can
CC be used as probes or primers to clone regions of a zalphall Ligand gene,
CC and in gene therapy. Zalphall Ligand may also be used to identify
CC inhibitors of its activity, to enhance the generation of anti-tumour
CC responses with or without the infusion of donor lymphocytes, and to
CC activate or stimulate the immune system. The present sequence represents
CC a sequencing primer used to sequence cDNA clones in the isolation of
CC human zalphall Ligand
XX Sequence 26 BP; 0 A; 1 C; 0 G; 25 T; 0 U; 0 Other;
SQ Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
DB 25 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 92
ID AAD43853/c
XX AAD43853 standard; DNA; 26 BP.
XX AAD43853;
XX 14-NOV-2002 (first entry)
XX Primer #2 used to illustrate the method of the invention.
XX Single stranded polynucleotide tag; cleavage agent; gene expression;
XX primer; ss.
XX Unidentified.
XX OS
XX WO200259357-A2.
XX 01-AUG-2002.
XX 24-JAN-2002; 2002WO-DK000052.
XX 24-JAN-2001; 2001DK-00000126.
XX 12-FEB-2001; 2001US-0267704P.
XX (GENO-) GENOMIC EXPRESSION APS.
XX Pedersen ML;
XX WPI; 2002-636542/68.
XX Obtaining single stranded polynucleotide tags from a biological sample,
PT for analyzing gene expression or diagnosing clinical conditions,
PT comprises employing nicking endonucleases that cleave complementary
PT strands.
XX Example; Page 294; 302pp; English.
XX The invention relates to a method for obtaining a single stranded
CC polynucleotide tag from a biological sample by cleaving one of the
CC complementary strands of a double stranded polynucleotide with a cleavage
CC agent capable of recognising a double stranded polynucleotide comprising
CC complementary strands and cleaving only one of the strands of the
```


CC carrier. M1 is also useful for predicting the efficacy of a proposed drug
CC targeted against an aberrant protein, by determining aberrant protein
CC production of cell in a diseased state by the above method, amplifying
CC the aberrant protein by M1 and using recombinant techniques to determine
CC the effect of proposed drug on the aberrant protein. M1 is also useful
CC for differential screening of tissue-specific gene expression at a
CC cellular level, for preparing labeled RNA/DNA probes for a gene chip
CC technology, and for determining the efficacy of a drug regimen against a
CC gene or its cDNAs. The present sequence is an Oligo (dT) primer used to
CC produce second strand cDNA in the method of the invention

XX
SQ Sequence 26 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 1.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0

QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | |
Db 26 AAAAAAAAAAAAAAAAAAAAAA 5

RESULT 96
AAN70281/c
ID AAN70281 standard; DNA; 27 BP.
XX AC AAN70281;
XX
DT 03-OCT-2002 (revised)
DT 26-MAY-1991 (first entry)
XX
DE Sequence of scissile link probe MRC071 (HL).
XX
KW Hybridisation; probe; ss.
XX
OS Synthetic.
XX
XX EP227976-A.
XX
PD 08-JUL-1987.
XX
PF 04-DEC-1986; 86EP-00116906.
XX
PR 05-DEC-1985; 85US-00805279.
XX
PA (MEIO-) MEIOGENICS INC.
XX
PI Duck P, Bender R, Crosby W, Robertson JG;
XX
DR WPI; 1987-186567/27.
XX
XX
PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT linked by a scissile linkage.
XX
XX Example; p29; 46pp; English.
XX
XX The patent claims a new molecule of formula (NA1-----S-----NA2)n. NA1 and
XX NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
XX linkage; n= 1 or 1,000, which is used for the detection of specific DNA
XX or RNA sequences in a test soln. The scissile link probes may be PL
XX (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
XX Support). The differential lability of DNA and RNA may be exploited in a
XX heterogeneous system where the scissile linkage is an RNA molecule. In the
XX examples, counter probe molecules 9 through 16 were used to determine
XX suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
XX OS field.)


```

Qy 1734 ACACAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 97
AAN70274/c
ID AAN70274 standard; DNA; 27 BP.
XX
AC AAN70274;
XX
DT 03-OCT-2002 (revised)
DT 26-MAY-1991 (first entry)
XX
DE Sequence of scissile link probe MRC046 (PL).
XX
KW Hybridisation; probe; ss.
XX
OS Synthetic.
XX
FN EP227976-A.
XX
PD 08-JUL-1987.
XX
PF 04-DEC-1986; 86EP-00116906.
XX
PR 05-DEC-1985; 85US-00805279.
XX
PA (MEIO-) MEOGENICS INC.
XX
PI Duck P, Bender R, Crosby W, Robertson JG;
XX
DR WPI; 1987-186567/27.
XX
PT Synthetic nucleic acid probes - comprising two nucleic acid sequences
PT linked by a scissile linkage.
XX
PS Example; p29; 46pp; English.
XX
CC The patent claims a new molecule of formula (NA1----S----NA2)n. NA1 and
CC NA2 are noncomplementary nucleic acid sequences; ---S--- = a scissile
CC linkage; n = 1 or 1,000, which is used for the detection of specific DNA
CC or RNA sequences in a test soln. The scissile link probes may be PL
CC (Permanent Linkage to Solid Support) or HL (Hydrolysable Linkage to Solid
CC Support). The differential liability of DNA and RNA may be exploited in a
CC heterogeneous system when the scissile linkage is an RNA molecule. In the
CC examples, counter probe molecules 9 through 16 were used to determine
CC suitable hybridisation conditions. (Updated on 03-OCT-2002 to add missing
CC OS field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACACAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 98
AAN92240/c
ID AAN92240 standard; DNA; 27 BP.
XX
AC AAN92240;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRC046.
XX

```

```

KW Probe MRC046; solid support; ribonuclease.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT misc_feature 1..10
FT /tag= a
FT /note= "deoxyribonucleotides."
FT misc_feature 11..16
FT /tag= b
FT /note= "ribonucleotides."
FT misc_feature 17..27
FT /tag= c
FT /note= "deoxyribonucleotides."
XX
PN WO8910415-A.
XX
PD 02-NOV-1989.
XX
PF 29-APR-1988; 88US-00187814.
XX
PR 29-APR-1988; 88US-00187814.
XX
PA (MEIO-) MEOGENICS INC.
XX
PI Duck P, Bender R;
XX
DR WPI; 1989-339977/46.
XX
PT Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
PS Disclosure; Page 24; 34pp; English.
XX
CC Probe MRC046 is bound by a permanent linkage to a solid support at its 3'
CC end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obtd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 21 T; 6 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACACAAAAAAAAAAAAAAAAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAAAA 6

RESULT 99
AAN92247/c
ID AAN92247 standard; DNA; 27 BP.
XX
AC AAN92247;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 25-APR-1990 (first entry)
XX
DE SS probe MRC071.
XX
KW Probe MRC071; solid support; ribonuclease.
XX
OS Synthetic.
XX

```

```

FH Key                               Location/Qualifiers
FT misc_feature 1..15
FT                                     /tag= a
FT                                     /note= "deoxyribonucleotides."
FT misc_feature 16..17
FT                                     /tag= b
FT                                     /note= "ribonucleotides."
FT misc_feature 18..27
FT                                     /tag= c
FT                                     /note= "deoxyribonucleotides."
XX
XX
PN W08910415-A.
XX
XX
PD 02-NOV-1989.
XX
XX
PF 29-APR-1988; 88US-00187814.
XX
XX
PR 29-APR-1988; 88US-00187814.
XX
XX
PA (MEIO-) MEIOGENICS INC.
XX
XX
PI Duck P, Bender R;
XX
XX
DR WPI; 1989-339977/46.
XX
XX
PT Detecting target nucleic acid molecules - using excess complementary
PT nucleic acid probes and nicking to complete a cycling sequence.
XX
XX
PS Disclosure; Page 24; 34pp; English.
XX
XX
CC Probe MRCO71 is bound by a hydrolysable linkage to a solid support at its
CC 3' end. It is used by reacting excess probe with a target nucleic acid;
CC nicking hybridised probe at least once within a predetermined sequence to
CC form 2 or more probe fragments hybridised to the target sequence, which
CC results in the probe fragments becoming hybridised to another probe; and
CC identifying probe fragments, so detecting the target sequence. The probe
CC can react with target sequence to complete a cycling sequence. Using this
CC system, sensitivity of 10 exp. -19 to 10 exp. -20 molecules of target can
CC be obt'd. The probe is cleavable at the ribonucleotides by a ds RNase, eg
CC RNase H or ExoIII. (Updated on 31-OCT-2002 to add missing OS field.)
XX
XX
CC (Updated on 25-MAR-2003 to correct PR field.)
XX
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 2 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 100
AAQ40854
ID AAQ40854 standard; DNA; 27 BP.
XX
XX
AC AAQ40854;
XX
XX
DT 23-SEP-1993 (first entry)
DE
DE DNA sequence used in DNA replication method.
XX
XX
KW ss.
XX
XX
OS Synthetic.
XX
XX
PN JP05103673-A.
XX
XX
PD 27-APR-1993.
XX
XX
PF 26-AUG-1991; 91JP-00240525.
XX

PR 26-AUG-1991; 91JP-00240525.
XX
XX
PA (UYAR-) UNIV ARIZONA.
XX
XX
DR WPI; 1993-171830/21.
XX
XX
PT Replication of DNA - useful in genetic engineering and medical
PT applications.
XX
XX
PS Disclosure; Page 20; 20pp; Japanese.
XX
XX
CC The sequence is given in the disclosure to illustrate the invention
XX
XX
SQ Sequence 27 BP; 27 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 22

RESULT 101
AAZ43904/c
ID AAZ43904 standard; DNA; 27 BP.
XX
XX
AC AAZ43904;
XX
XX
DT 10-MAR-2000 (first entry)
DE
DE M. tuberculosis rpo-beta primer 17.
XX
XX
KW RNA polymerase; rpo-beta; detection; diagnostic; trap probe; primer; ss.
XX
XX
OS Mycobacterium tuberculosis.
XX
XX
PN EP962536-A1.
XX
XX
PD 08-DEC-1999.
XX
XX
PF 29-MAY-1999; 99EP-00110458.
XX
XX
PR 04-JUN-1998; 98DE-01024900.
XX
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
XX
PI Weindel K, Brand J;
XX
XX
DR WPI; 2000-055287/05.
XX
XX
PT Selective detection of nucleic acids by amplification with labeled
PT primers and detection with a trap probe.
XX
XX
PS Example 1c; Page 19; 27pp; German.
XX
XX
CC This invention describes a novel method for the selective detection of
CC nucleic acids which comprises amplification of the nucleic acid with the
CC help of labeled primers and detection with a trap probe. The methods and
CC reagents are used for the detection of a marker primer and at least 2
CC immobilized (or immobilizable) trap probes with the corresponding nucleic
CC acid sequence of interest for mutation analysis. The method can be used
CC to detect a specific sequence in a sample of one or more nucleic acids by
CC using several sets of primers and trap probes (i.e. in an array). The
CC methods are useful in molecular biology and diagnostic applications,
CC especially for simultaneous detection of multi-pathogens, typing of
CC organisms, analyzing genetic diversity and sequencing of genes or
CC genomes. This sequence represents a primer used in the method of the
XX
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 26 T; 0 U; 1 Other;
```

RESULT:103
ABS78427/c

ID ABS78427 standard; DNA; 27 BP.

XX AC

XX ABS78427;

XX AC

XX DT 13-DEC-2002 (first entry)

XX DE

XX XX Angiogenesis inhibitory oligonucleotide #911.

XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;

XX KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;

XX KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;

XX KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;

XX KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;

XX KW plaque neovascularisation; telangiectasia; haemophilic joint;

XX KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

XX KW scleroderma; hypertrophic scar.

XX OS Synthetic.

XX PN WO200253141-A2.

XX PD 11-JUL-2002.

XX PF 14-DEC-2001; 2001WO-US048458.

XX PR 14-DEC-2000; 2000US-0255534P.

XX PA (COLE-) COLEY PHARM GROUP INC.

XX PI Bratzler RL;

XX DR WPI; 2002-566690/60.

XX PT Inhibiting angiogenesis in a subject, involves administering at least one antiangiogenic nucleic acid molecule to the subject.

XX PS Claim 2; Page 35; 276pp; English.

XX CC The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma and hypertrophic scars. The present sequence is an antiangiogenic nucleic acid of the invention

XX SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;

Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred.No.1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | |
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

RESULT 104
ABL39406/c

ID ABL39406 standard; DNA; 27 BP.

XX AC

XX ABL39406;

```
DT 16-APR-2002 (first entry)
XX Immunostimulatory nucleic acid SEQ ID NO: 842.
DE
XX
XX Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT modified_base 1..27 /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate backbone"
XX
XX WO200197843-A2.
PN
XX
XX 27-DEC-2001.
PD
XX
XX 22-JUN-2001; 2001WO-US020154.
PF
XX
XX 22-JUN-2000; 2000US-0213346P.
PR
XX
XX (IOWA ) UNIV IOWA RES FOUND.
PA
XX
XX Weiner G, Hartmann G;
PI
XX
XX WPI; 2002-154611/20.
DR
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
XX Disclosure; Page 310; 312pp; English.
PS
XX
XX The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, esophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
XX Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
SQ
Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
DB 27 AAAAAAAAAAAAAAAAAAAAAA 6
RESULT 105
ABS53863/c
ID ABS53863 standard; DNA; 27 BP.
XX
XX
XX ABS53863;
AC
XX
XX 25-NOV-2002 (first entry)
DT
XX
XX Human androgen receptor complex-associated protein 5'RACE PCR primer #1.
DE
XX
XX Human; androgen receptor complex-associated protein; ARCAP; primer; ss;
```

```
KW androgen receptor; AR; cancer; liver tumour; cytostatic; PCR; 5'RACE.
XX
XX Homo sapiens.
OS
XX
XX EP1227150-A2.
PN
XX
XX 31-JUL-2002.
PD
XX
XX 16-JAN-2002; 2002EP-00250305.
PF
XX
XX 17-JAN-2001; 2001US-0262312P.
PR
XX
XX 12-FEB-2001; 2001US-00781693.
XX
XX (VETE-) VETERANS GEN HOSPITAL.
PA
XX
XX Tai-Jay C;
PI
XX
XX WPI; 2002-676576/73.
DR
XX
XX Novel substantially pure androgen receptor (AR) complex-associated
PT protein which binds to AR and increases ability of AR to transactivate
PT androgen-responsive gene, useful as drug target for treating liver
PT cancer.
XX
XX Example; Page 11; 26pp; English.
PS
XX
XX The invention relates to an androgen receptor complex-associated protein
CC (ARCAP) sequence and the cDNA encoding it. The protein is useful for
CC screening a compound that decreases AR-mediated (androgen receptor
CC mediated) transactivation which involves contacting the ARCAP protein
CC with a protein complex comprising an AR in the presence of a candidate
CC compound, measuring the extent of binding between the polypeptide, and
CC determining if the extent of binding is less than the extent of binding
CC between the polypeptide and the protein complex in the absence of the
CC candidate compound. The ARCAP DNA is useful for determining if a sample
CC contains cancerous cells which involves providing a sample from a human
CC patient and detecting ARCAP expression in the sample. The sequences are
CC useful for determining whether a sample contains liver tumour cells. This
CC sequence represents a 5'RACE PCR primer used to amplify human ARCAP DNA
XX
XX Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;
SQ
Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
DB 25 AAAAAAAAAAAAAAAAAAAAAA 4
RESULT 106
ABS54324/c
ID ABS54324 standard; DNA; 27 BP.
XX
XX
XX ABS54324;
AC
XX
XX 10-DEC-2002 (first entry)
DT
XX
XX Human ARCAP associated 5'RACE PCR primer.
DE
XX
XX Human; androgen receptor complex-coupled protein; ARCAP; PCR; primer; ss.
XX
XX Homo sapiens.
OS
XX
XX JP2002262871-A.
PN
XX
XX 17-SEP-2002.
PD
XX
XX 28-FEB-2001; 2001JP-00055192.
PF
XX
XX 12-FEB-2001; 2001US-00781693.
PR
XX
```

PA (VETE-) VETERANS GEN HOSPITAL.
PI Tai-Jay C;
XX WPI; 2002-676576/73.
XX Novel substantially pure androgen receptor (AR) complex-associated
PT protein which binds to AR and increases ability of AR to transactivate
PT androgen-responsive gene, useful as drug target for treating liver
PT cancer.
XX Example; Page 15; 18pp; Japanese.
PS
XX The present invention relates to the isolation of human androgen receptor
CC complex-coupled protein (ARCAP), and the polynucleotide sequence encoding
CC it. The ARCAP polypeptide complexes with an androgen receptor to increase
CC the activity of the androgen receptor, transactivating the androgen
CC responding gene. The invention also describes a vector containing the
CC ARCAP polynucleotide sequence, and a host cell containing the ARCAP
CC polynucleotide sequence. The ARCAP polypeptide can be used as a treating
CC agent. The present sequence represents a PCR primer used in the example
CC of the present invention
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 25 T; 0 U; 2 Other;
Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 25 AAAAAAAAAAAAAAAAAAAAAA 4
RESULT 107
ACH03245/C
ID ACH03245 standard; DNA; 27 BP.
XX
AC ACH03245;
XX
DT 25-SEP-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #890.
XX
KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW antiulcer; Gene therapy; vaccine; non-allergic inflammatory disease;
KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS Synthetic.
XX
PN US2003050268-A1.
XX
PD 13-MAR-2003.
XX
PF 29-MAR-2002; 2002US-00112653.
XX
PR 29-MAR-2001; 2001US-0279642P.
XX
PA (KRIE/) KRIEG A M.
PA (BERG/) BERG D J.
XX
PI Krieg AM, Berg DJ;
XX
DR WPI; 2003-521815/49.
XX
PT Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT disease by administering an immunostimulatory nucleic acid.
XX
PS Disclosure; Page 32; 229pp; English.
XX
CC The invention describes a method of treating non-allergic inflammatory

CC disease comprising administering to a subject having or at risk of
CC developing a non-allergic inflammatory disease an immunostimulatory
CC nucleic acid for prevention or treatment of the disease. The method is
CC useful for treating non-allergic inflammatory diseases, such as
CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC This sequence represents an immunostimulatory nucleic acid
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6
RESULT 108
ADB37208/C
ID ADB37208 standard; DNA; 27 BP.
XX
AC ADB37208;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #822.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
PN US2003087848-A1.
XX
PD 08-MAY-2003.
XX
PF 02-FEB-2001; 2001US-00776479.
XX
PR 03-FEB-2000; 2000US-0179991P.
XX
PA (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
DR WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 17; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 27 BP; 0 A; 0 C; 0 G; 27 T; 0 U; 0 Other;
Query Match 1.2%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 1.8e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACACAAAAA 1755
Db 27 AAAAAAAAAAAAAAAAAAAAAA 6

```
RESULT 109
AAL50570/c
ID AAL50570 standard; DNA; 22 BP.
XX
AC AAL50570;
XX
DT 12-DEC-2002 (first entry)
XX
DE Molecular array production method-related PCR primer.
XX
KW Molecular array; ss; target molecule identification; genetic analysis;
KW Gene expression; SNP detection; haplotyping; sequencing; PCR; primer.
XX
OS Unidentified.
XX
PN WO200274988-A2.
XX
PD 26-SEP-2002.
XX
PF 18-MAR-2002; 2002WO-GB001245.
XX
PR 16-MAR-2001; 2001GB-00006635.
PR 02-AUG-2001; 2001GB-00018879.
XX
PA (UYCH-) UNIV CHANCELLOR MASTER & SCHOLARS OXP.
XX
PI Mir K;
XX
WPI; 2002-732872/79.
XX
PT Producing a molecular array with a plurality of molecules immobilized to
PT a solid substrate, useful in genetic analysis, gene expression studies or
PT the detection or typing of single nucleotide polymorphisms in a sample of
PT nucleic acids.
XX
PS Example 15; Page 122; 166pp; English.
XX
CC The invention comprises a method for producing a molecular array, the
CC method involves immobilising molecules to a solid phase at a density
CC which allows individual immobilised molecules to be individually
CC resolved. The molecular array produced by the method of the invention is
CC useful for identifying one or more target molecules in a sample. The
CC molecular array is also useful in genetic analysis, gene expression
CC studies, identifying molecules which interact with a target molecule,
CC detection/typing of single nucleotide polymorphisms, haplotyping and
CC sequencing. The present DNA sequence represents a PCR primer that was
CC used in an example of the invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA..... 1755
Db 21 BAAAAA..... 1

RESULT 110
ABX74887/c
ID ABX74887 standard; DNA; 22 BP.
XX
AC ABX74887;
XX
DT 21-MAR-2003 (first entry)
XX
DE Oligo-dT primer used in human CC-RCC invention.
XX
KW Microarray; solid surface; immobilised probe; CC-RCC;
KW differential expression profile; aggressive CC-RCC tumour type;
KW non-aggressive CC-RCC tumour type; clear cell renal carcinoma;
KW gene expression profiling; tumour tissue; oligo-dT; primer; ss.
```

```
XX Synthetic.
OS WO200279411-A2.
XX
PN 10-OCT-2002.
XX
PD 29-MAR-2002; 2002WO-US009576.
XX
PF 29-MAR-2001; 2001US-0279411P.
XX
PR (VAND-) VAN ANDEL INST.
XX
PI Haab B, Rhodes D, Teh BT, Takashi M;
XX WPI; 2003-040679/03.
XX
DR New microarray, comprising a matrix of cDNA probe from a set of probes
PT immobilized to a solid surface in predetermined order, useful in the
PT prognosis of patients with clear cell renal carcinoma.
XX
PS Example 2; Page 30; 179pp; English.
XX
CC The present invention relates to a microarray comprising a matrix of at
CC least one cDNA probe from a set of probes immobilised to a solid surface
CC in a predetermined order, where a row of pixels corresponds to replicates
CC of one distinct probe from the set. The probes are complementary to
CC nucleic acid sequences that are expressed differentially in aggressive as
CC compared to non-aggressive types of clear cell renal carcinoma (CC-RCC)
CC and that hybridise to the probes under high stringency conditions. The
CC microarray is useful for the prognosis of patients with CC-RCC, wherein
CC aggressive and non-aggressive CC-RCC tumour types are characterised by
CC differential expression profiles of genes that hybridise with one or more
CC probes immobilised on the microarray. The arrays are useful for gene
CC expression profiling of tumour and normal tissues. The present sequence
CC represents an oligo-dT primer used in the examples of the present
XX invention
XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;
Best Local Similarity 95.2%; Pred. No. 1.6e+02;
Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA..... 1755
Db 21 BAAAAA..... 1

RESULT 111
ACC48484/c
ID ACC48484 standard; DNA; 22 BP.
XX
AC ACC48484;
XX
DT 11-AUG-2003 (first entry)
XX
DE Locked nucleic acid anchored oligo(I) primer ON14.
XX
KW Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT modified_base 1..21
FT /tag= m
FT /mod_base= um
FT /note= "2'-O-methyluridine"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "OTHER= locked nucleic acid"
FT modified_base 3
```

FT /tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 5
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 7
 FT /tag= d
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 9
 FT /tag= e
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 11
 FT /tag= f
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 13
 FT /tag= g
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 15
 FT /tag= h
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 17
 FT /tag= i
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 19
 FT /tag= j
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 21
 FT /tag= k
 FT /mod_base= OTHER
 FT /note= "OTHER= locked nucleic acid"
 FT modified_base 22
 FT /tag= l
 FT /mod_base= OTHER
 FT /note= "OTHER= Compound 17d"

WO2003020739-A2.

13-MAR-2003.

04-SEP-2002; 2002WO-IB003911.

04-SEP-2001; 2001US-0317034P.

22-SEP-2001; 2001US-0323967P.

(EXIQ-) EXIQON AS.

Wengel J, Kauppinen S;

WPI; 2003-363021/34.

Novel nucleic acid comprising a locked nucleic acid unit having a modified base that comprises an optionally substituted carbocyclic aryl moiety, or modified nucleobase or nucleosidic base other than oxazole/imidazole.

Example 24a; Page 90; 119pp; English.

The present sequence is that of pyrene-anchored locked nucleic acid (LNA) oligo (dT) primer ON14, which was used in first-strand cDNA synthesis from eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based on an LNA-type 2'-O,4'-C-methylene-beta-D-ribofuranosyl moiety. It is one of a set of such primers (see also ACC48482-85) that were used in an example from the invention to demonstrate improved reverse transcription of mRNA using pyrene-LNA anchored oligo(T) primers. The following results

CC were observed: efficient priming on mRNAs with short poly(A) tails; efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T units resulting in an improved T20-VN anchor primer and thus avoiding reverse transcription of long poly(A) tracts; and improved reverse transcription of eukaryotic poly(A)-RNA directly from total RNA extracts due to increased specificity. The invention relates to modified LNA units that comprise unique base groups. Desirable nucleobase and nucleosidic base substitutions can mediate universal hybridisation when incorporated into nucleic acid strands. The novel LNA compounds can be used e.g. as PCR primers, in sequencing, the synthesis of antisense oligonucleotides, and in diagnostics

SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;

Best Local Similarity 95.2%; Pred. No. 1.6e+02;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1755

Db 21 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 112

ACC48485/C

ID ACC48485 standard; DNA; 22 BP.

XX ACC48485;

XX 11-AUG-2003 (first entry)

DE Locked nucleic acid anchored oligo(1) primer ON15.

XX Locked nucleic acid; LNA; gene therapy; primer; ss.

OS Synthetic.

Key Location/Qualifiers

modified_base 21

/tag= a

/mod_base= OTHER

/note= "OTHER= locked nucleic acid"

modified_base 22

/tag= b

/mod_base= OTHER

/note= "OTHER= Compound 17d"

WO2003020739-A2.

13-MAR-2003.

04-SEP-2002; 2002WO-IB003911.

04-SEP-2001; 2001US-0317034P.

22-SEP-2001; 2001US-0323967P.

(EXIQ-) EXIQON AS.

Wengel J, Kauppinen S;

WPI; 2003-363021/34.

Novel nucleic acid comprising a locked nucleic acid unit having a modified base that comprises an optionally substituted carbocyclic aryl moiety, or modified nucleobase or nucleosidic base other than oxazole/imidazole.

Example 24a; Page 90; 119pp; English.

The present sequence is that of pyrene-anchored locked nucleic acid (LNA) oligo(dT) primer ON15, which was used in first-strand cDNA synthesis from eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based on an LNA-type 2'-O,4'-C-methylene-beta-D-ribofuranosyl moiety. It is

one of a set of such primers (see also ACC48482-84) that were used in an example from the invention to demonstrate improved reverse transcription of mRNA using pyrene-LNA anchored oligo(T) primers. The following results were observed: efficient priming on mRNAs with short poly(A) tails; efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T units resulting in an improved T20-VN anchor primer and thus avoiding reverse transcription of long poly(A) tracts; and improved reverse transcription of eukaryotic poly(A)+RNA directly from total RNA extracts due to increased specificity. The invention relates to modified LNA units that comprise unique base groups. Desirable nucleobase and nucleosidic base substitutions can mediate universal hybridisation when incorporated into nucleic acid strands. The novel LNA compounds can be used e.g. as PCR primers, in sequencing, the synthesis of antisense oligonucleotides, and in diagnostics

Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.6e+02;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAAAAAA 1755
 Db 21 BAAAAA...AAAAAAAAA 1

RESULT 113

ACC48483/C
 ID ACC48483 standard; DNA; 22 BP.

XX ACC48483;

XX 11-AUG-2003 (first entry)

XX Locked nucleic acid anchored oligo(I) primer ON13.

DE Locked nucleic acid; LNA; gene therapy; primer; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 2 /*tag= a
 /mod_base= OTHER

FT modified_base 5 /note= "OTHER= locked nucleic acid"

FT modified_base 8 /*tag= b
 /mod_base= OTHER

FT modified_base 11 /*tag= c
 /mod_base= OTHER

FT modified_base 14 /*tag= d
 /mod_base= OTHER

FT modified_base 17 /*tag= e
 /mod_base= OTHER

FT modified_base 21 /*tag= f
 /mod_base= OTHER

FT modified_base 24 /*tag= g
 /mod_base= OTHER

FT modified_base 27 /*tag= h
 /mod_base= OTHER

FT modified_base 30 /*tag= i
 /mod_base= OTHER

FT modified_base 33 /*tag= j
 /mod_base= OTHER

FT modified_base 36 /*tag= k
 /mod_base= OTHER

XX WO2003020739-A2.
 PN 13-MAR-2003.
 PD 04-SEP-2002; 2003WO-IB003911.
 PF 04-SEP-2001; 2001US-0317034P.
 PR 22-SEP-2001; 2001US-0323967P.
 XX (EXIQ-) EXIQON AS.
 PA Wengel J, Kauppinen S;
 PI WPI; 2003-363021/34.
 DR Novel nucleic acid comprising a locked nucleic acid unit having a
 XX modified base that comprises an optionally substituted carbocyclic aryl
 PT moiety, or modified nucleobase or nucleosidic base other than
 PT oxazole/imidazole.
 XX Example 24a; Page 90; 119pp; English.

XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
 CC oligo(dT) primer ON13, which was used in first-strand cDNA synthesis from
 CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
 CC on an LNA-type 2'-O,4'-C-methylene-beta-D-ribofuranosyl moiety. It is
 CC one of a set of such primers (see also ACC48482-85) that were used in an
 CC example from the invention to demonstrate improved reverse transcription
 CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
 CC were observed: efficient priming on mRNAs with short poly(A) tails;
 CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
 CC units resulting in an improved T20-VN anchor primer and thus avoiding
 CC reverse transcription of long poly(A) tracts; and improved reverse
 CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
 CC due to increased specificity. The invention relates to modified LNA units
 CC that comprise unique base groups. Desirable nucleobase and nucleosidic
 CC base substitutions can mediate universal hybridisation when incorporated
 CC into nucleic acid strands. The novel LNA compounds can be used e.g. as
 CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
 CC and in diagnostics

XX Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;

Query Match 1.2%; Score 20.2; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.6e+02;

Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAAAAAA 1755
 Db 21 BAAAAA...AAAAAAAAA 1

RESULT 114

AAD51324/C

XX AAD51324 standard; DNA; 22 BP.

XX AAD51324;

XX 16-APR-2003 (first entry)

XX Anchored oligo dT primer used to illustrate the method of the invention.

XX Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
 KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
 KW musculoskeletal damage; ss.

XX Unidentified.

XX WO200290579-A1.

XX 14-NOV-2002.

PF 03-MAY-2002; 2002WO-AU000553.
 XX
 PR 04-MAY-2001; 2001AU-00004809.
 XX 29-JUN-2001; 2001US-00896941.
 XX
 PA (GENO-) GENOMICS RES PARTNERS PTY LTD.
 XX
 PI Brandon RB;
 XX
 DR WPI; 2003-120558/11.
 XX
 XX Assessing condition e.g. athletic ability, stage of disease, presence of
 PT drugs, response to exercise, response to vaccines, therapies, nutritional
 PT status, of performance animal involves analyzing nucleic acid expression.
 XX
 PS Disclosure; Page 46; 87pp; English.
 XX
 CC The invention relates to a method for assessing a condition of a
 CC performance animal. The method involves determining in sample abundance
 CC of expressed target nucleic acid; transmitting digital sample signal to
 CC remote diagnostic server; processing digital sample signal at remotely
 CC located database to correlate digital signal with digital information and
 CC returning report of particular condition of animal. The method is useful
 CC for assessing a condition of a performance animal preferably human, dog
 CC or camel. The condition can be an athletic ability and a condition that
 CC enhances, hinders, impedes or does not change an expected ability of the
 CC performance animal; and also normal, pre-clinical, overt progress and/or
 CC stage of disease, undiagnosed or unclassified conditions, presence of
 CC drugs, response to exercise, response to vaccines, therapies, nutritional
 CC status and response to environmental conditions. Diseases assessed by the
 CC invention include laminitis, lameness, viral or bacterial disease,
 CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
 CC musculoskeletal damage or disorders and joint diseases. The present
 CC sequence is a primer used to illustrate the method of the invention
 XX
 SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
 Query Match 1.2%; Score 20.2; DB 1; Length 22;
 Best Local Similarity 95.2%; Pred. No. 1.6e+02;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
 Db :|||||
 21 BAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 115
 ABK13916/C
 ID ABK13916 standard; DNA; 23 BP.
 XX
 AC ABK13916;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE 3'-PCR primer used in method of identifying transcribed genes.
 XX
 KW Identification of transcribed gene; mRNA profile; gene expression;
 KW cellular process; fingerprinting; susceptibility to external factor;
 KW development; disease; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200208461-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 23-JUL-2001; 2001WO-IB001539.
 XX
 PR 21-JUL-2000; 2000GB-00018016.
 XX
 PR 21-JUL-2000; 2000US-0219925P.
 XX
 PA (GLOB-) GLOBAL GENOMICS AB.
 XX

PI Linnarsson S, Ernfors P, Bauren G;
 XX
 DR WPI; 2002-217065/27.
 XX
 PT Providing mRNA profile, by generating two independent patterns
 PT characteristic of sample mRNA population, analyzing patterns, comparing
 PT gene expression by cell types under varied conditions, and identifying
 PT genes.
 XX
 PS Example 2; Page 45; 67pp; English.
 XX
 CC The present invention relates to a method for providing a profile of mRNA
 CC molecules present in a sample. The method comprises generating two
 CC independent patterns characteristic of the population of mRNA molecules
 CC expressed in the sample and analyzing the patterns using a combinatorial
 CC algorithm, comparing gene expression by different or same cell types
 CC under different conditions, and identifying genes having a role in
 CC various cellular processes. The method is useful for the analysis and
 CC identification of transcribed genes, and fingerprinting. The method can
 CC be used to identify genes which play a role in determining various
 CC cellular processes, including susceptibility to external factors,
 CC development, and disease. The present sequence for a PCR primer is used
 CC in the methods of the present invention
 XX
 SQ Sequence 23 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 3 Other;
 Query Match 1.2%; Score 20.2; DB 1; Length 23;
 Best Local Similarity 95.2%; Pred. No. 1.7e+02;
 Matches 20; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1755
 Db :|||||
 21 BAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 116
 ABX94936/C
 ID ABX94936 standard; DNA; 26 BP.
 XX
 AC ABX94936;
 XX
 DT 25-AUG-2003 (first entry)
 XX
 DE Renilla luciferase associated PCR primer N-Termrev.
 XX
 KW Luciferase; ubiquitin promoter; glucocorticoid receptor; PCR; primer;
 KW transrepression protein-protein reciprocal effect; immunosuppressive;
 KW transactivation deficient inflammation; ss.
 XX
 OS Renilla reniformis.
 XX
 PN DE10222714-A1.
 XX
 PD 02-JAN-2003.
 XX
 PF 23-MAY-2002; 2002DE-01022714.
 XX
 PR 28-MAY-2001; 2001DE-01024575.
 XX
 PA (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
 XX
 XX Goettlicher M, Heilbock C, Herrlich P, Litfin M, Schneider S;
 XX WPI; 2003-291460/29.
 XX
 XX A genetically modified glucocorticoid receptor which is transactivation
 PT deficient is used to identify cofactors which will be useful to provide
 PT inflammation-inhibiting and immunosuppressive treatment.
 XX
 PS Disclosure; Col 12; 12pp; German.
 XX
 CC This invention describes a novel genetically modified glucocorticoid
 CC receptor, which has transrepression protein-protein reciprocal effects

and is transactivation deficient. The invention also describes (1) a gene construct comprising at least a nucleic acid encoding the glucocorticoid receptor, operably linked with regulatory sequences of a reporter gene, preferably a DNA-binding domain for a reporter gene; (2) identifying a gene encoding a cofactor involved in glucocorticoid receptor modulation of at least another transcription factor comprising: (a) using the above construct with an expression bank of a eukaryotic cell expressed in a yeast two hybrid system; (b) detecting a specific protein-protein complex or the receptor and a cofactor through growth in a selective medium for the reporter and (c) isolating and characterising the nucleic acid encoding the cofactor in the cDNA clone; (3) a cofactor with transcription repression specific for the glucocorticoid receptor which in a protein-protein interaction achieves a reciprocal effect, whereby within a downstream segment the N-terminal AF-1 and the DNA-binding domain of the receptors are bound; (4) identifying an agent which affects the reciprocal effect of the glucocorticoid receptor with other transcription factors and/or cofactors, whereby the receptor or construct is contacted with a potential agent and modulation of the interaction of the protein partner is measured by expression of the reporter gene or detecting protein-protein complex binding; (5) an agent for modulating interaction of the glucocorticoid receptor with a cofactor which binds either at the binding site of a physiological hormone or at a separate binding place and (6) a compound with an inflammation-inhibiting or immunosuppressive effect comprising the above agent. The genetically modified glucocorticoid receptor is useful to identify coreceptors which are used to produce an inflammation-inhibiting or immunosuppressive treatment. This sequence represents a PCR primer NTermrev used to amplify a Renilla reniformis luciferase gene which is then cloned into a reporter construct behind a ubiquitin promoter

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1-2%; Score 20.2; DB 1; Length 26;
Best Local Similarity 88.0%; Pred. No. 1.8e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 976 GGGAGTACTTTGGCCAGTGTGGTG 1000
|||||
Db 26 GGGAGTACTTTGGCCAGTCTCGAG 2

RESULT 117
AAQ25565/c
ID AAQ25565 standard; DNA; 20 BP.

XX AAQ25565;

XX 25-MAR-2003 (revised)

DT 02-DEC-1992 (first entry)

DE Dye-coupled 3'-amino modified oligonucleotide.

KW DNA synthesis; RNA; antisense strands; detection; ss.

OS Synthetic.

FT Key Location/Qualifiers

FT modified_base 20

FT /*tag= a

FT /note= "3-amino modified"

XX EP490281-A1.

XX 17-JUN-1992.

XX 06-DEC-1991; 91EP-00120935.

XX 11-DEC-1990; 90DE-04039488.

XX (FARH) HOECHST AG.

XX Engels J, Herrlein M, Konrad R, Mag M;

DR WPI; 1992-201578/25.
XX New dye-coupled modified nucleosides, nucleotides and oligonucleotides -
PT useful for synthesis of antisense DNA and RNA strands in presence of
PT template, also for in-vivo and in-vitro detection of genetic material.

PS Example; Page 9; 17pp; German.

XX The sequence is an example of a dye coupled 3'-amino modified oligo-
CC nucleotide, it can be used in the synthesis of DNA and RNA nucleosides,
CC nucleotides and oligonucleotides and for the synthesis of opposite
CC strands in the presence of a template strand and in fluorescence
CC microscopic and macroscopic detection in vivo and in vitro of genetic
CC material. It is labelled with a fluorescent dye. See also AAQ25566 and
CC AAQ25567. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 118

AAQ33554/c

ID AAQ33554 standard; DNA; 20 BP.

XX AAQ33554;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Microsatellite sequence from clone AGLA247.

KW PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KW genetic mapping; traits; amplification; ss.

OS Bos taurus.

XX WO9213102-A1.

XX 06-AUG-1992.

XX 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

XX (GENM-) GENMARK.

XX Georges M, Massey JM;

XX WPI; 1992-284684/34.

XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.

PS Table 7; Page 150; 517pp; English.

XX The sequence is that of a bovine microsatellite sequence obt'd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)₁₅ and a (TC)₁₅ oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)_n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic
 CC mapping of economic trait loci, or genes involved the determinism of
 CC economically important traits esp. in cattle, to allow selective
 CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 119
 AAQ58578
 ID AAQ58578 standard; RNA; 20 BP.
 XX
 AC AAQ58578;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-AUG-1994 (first entry)
 XX
 XX Sequence of synthetic RNA oligo which is a target nucleotide for a novel
 DE receptor.
 DE
 XX Novel receptor; nucleic acid; transport; oligo; ss.
 KW
 XX Synthetic.
 OS
 XX WO9404194-A1.
 PN
 XX 03-MAR-1994.
 PD
 XX 13-AUG-1993; 93WO-US007603.
 PF
 XX 14-AUG-1992; 92US-00930087.
 PR
 XX (MASI) MASSACHUSETTS INST TECHNOLOGY.
 PA
 XX Usman N, Rebek J, De Mendoza J;
 PI
 XX WPI; 1994-082846/10.
 DR
 XX Transport of nucleic acid deriva. across membranes - using new receptors
 PT which use salt bridging, aromatic stacking, hydrogen bonding and
 PT chelation.
 XX
 XX Example; Table 1, page 38; 103pp; English.
 PS
 XX The inventors claim a method of transporting a nucleic acid deriv. across
 CC a membrane which comprises using a receptor that uses salt bridging,
 CC aromatic stacking, H bonding and chelation to recognise the nucleic acid
 CC deriv. AAQ58577-86 are nucleic acid derivs used in the
 CC examples. (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 120
 AAQ94205/C
 ID AAQ94205 standard; DNA; 20 BP.

XX AAQ94205;
 AC 25-MAR-2003 (revised)
 DT 24-AUG-1995 (first entry)
 XX
 XX Alpha-anomeric oligonucleotide ligand 1803 for oestradiol hapten.
 DE
 XX Oligonucleotide ligand; steroid hormone; hapten; immobilisation;
 KW immunodetection; estradiol; alpha-anomer; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..21
 FT /tag= b
 FT /note= "the glycosidic bonds between nucleotides are all
 FT in the alpha-anomer form"
 FT modified_base 20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "carries a group derived ffrom aminopropanediol"
 PN
 XX WO9429723-A1.
 XX
 PD 22-DEC-1994.
 XX
 XX 10-JUN-1994; 94WO-FR000689.
 PF
 XX 11-JUN-1993; 93FR-00007093.
 PR
 XX (CROS/) CROS P.
 PA (KURF/) KURFURST R.
 PA (BATT/) BATTAIL N.
 PA (PIGA/) PIGA N.
 XX
 XX Cros P, Kurfurst R, Battail N, Piga N;
 FI
 XX WPI; 1995-036665/05.
 DR
 XX Assay device for hapten or its specific antibodies - comprises support
 PT having competitive reagent immobilised via nucleic acid ligand to improve
 PT orientation and accessibility.
 PT
 XX Example 1; Page 10; 39pp; French.
 PS
 XX Oligonucleotides (AAQ94201-Q94205) were synthesised for use as ligands.
 CC The ligands are covalently linked to a hapten (esp. a steroid hormone) to
 CC form a conjugate which is then immobilised on a solid support for
 CC interaction with antibodies against the haptens. Nucleic acid ligands are
 CC less likely to be recognised by the antibodies than are peptide ligands
 CC and nucleic acids are also less likely to undergo intramolecular
 CC organisation which interferes with accessibility of the hapten to the
 CC antibodies. For immunodiagnosis of oestradiol, the active hapten
 CC oestradiol-6-carboxymethoxime-N- hydroxysuccinimide ester was used.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 121
 AAQ75568/C
 ID AAQ75568 standard; DNA; 20 BP.
 XX
 AC AAQ75568;

```

XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX KW Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ9547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1752
DB 20 TACAAAAA 1

RESULT 122
AAQ90405/c
ID AAQ90405 standard; DNA; 20 BP.
XX AC AAQ90405;
XX DT 08-JAN-1996 (first entry)
XX DE T2 (synthetic DNA probe with 5' amino terminal #4).
XX KW T2; HLA; dQa; self-addressable electronic device; SAED; hybridisation;
XX KW ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT misc_feature 1 /*tag= a
XX FT /note= "3' aminolink2 Thymine; allows binding to any
XX FT amine"
XX PN WO9512808-A1.
XX PD 11-MAY-1995.
XX PF 26-OCT-1994; 94WO-US012270.

```

```

XX PR 01-NOV-1993; 93US-00146504.
XX PA (NANO-) NANOGEN INC.
XX PI Heller MJ, Tu E;
XX DR WPI; 1995-185870/24.
XX PT New self-addressable electronic devices - used for multi-step and
XX PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
XX PT and bio:polymer synthesis.
XX PS Example 1; Page 41; 86pp; English.
XX CC The sequences represented by, AAQ90402-15 are synthetic DNA probes
XX CC containing 5' amino termini. The sequences shown in AAQ90390-401 are
XX CC synthetic DNA probes with 3' ribonucleoside termini. These sequences were
XX CC specific for the polymorphisms of HLA gene dQa. The sequences were used
XX CC in the device of the invention. This is a self-addressable electronic
XX CC device (SAED) that can be used to carry out multi-step and multiplex
XX CC reactions, such as nucleic acid hybridisations. The advantages of this
XX CC method are that these reactions can be carried out with complete and
XX CC precise electronic control, and that the rate, specificity and
XX CC sensitivity of these reactions are greatly improved at micro-locations
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA 1755
DB 20 AAAAAA 1

RESULT 123
AAT63649/c
ID AAT63649 standard; DNA; 20 BP.
XX AC AAT63649;
XX DT 06-JUN-1997 (first entry)
XX DE Anti-HTLV antisense reference oligonucleotide HT.
XX KW antisense; complementary; tax gene; inhibit; HTLV-1;
XX KW human T-cell lymphotropic virus type 1; viral antigen expression; ss.
XX OS Synthetic.
XX PN JP09052898-A.
XX PD 25-FEB-1997.
XX PF 09-AUG-1995; 95JP-00224606.
XX PR 09-AUG-1995; 95JP-00224606.
XX PA (SOYA-) SOYAKU GIJUTSU KENKYUSHO KK.
XX DR WPI; 1997-197252/18.
XX PT Anti-HTLV-1 anti-sense oligo:nucleotide - is complementary to region of
XX PT tax gene from human T-cell lymphotropic virus type 1 and inhibits viral
XX PT antigen expression.
XX PS Example 1; Page 8; 10pp; Japanese.
XX CC Oligonucleotides having a partial sequence consisting of at least 15
XX CC bases of AAT63641 (an antisense oligo complementary to a region of the
XX CC tax gene which can inhibit human T-cell lymphotropic virus type 1 (HTLV-

```

CC 1) viral antigen expression) are claimed. In an example, six antisense
CC oligos were designed, TI-T6 (AAT63650-55) and were compared to six oligos
CC derived from other regions of HTLV-1, i.e. SJ1 (splice junction), P1
CC (p21), R1 (rex), RRI (rex response element), E1 (env) and G1 (gag), four
CC reference oligonucleotides TIS (tax-sense), HC (dc20), HT (dt20)
CC (AAT63647-49) and a random 20mer (RAN) in a HTLV-1 virus antigen
CC expression inhibiting test. Oligonucleotide T1 gave the best results
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | | |
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 124
AAV34591
ID AAV34591 standard; DNA; 20 BP.
XX
AC AAV34591;
XX
DT 25-AUG-1998 (first entry)
XX
DE M. vaccae antigenic sequence hybridising oligo AD12.
XX
KW Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
KW M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
KW mycobacteria infection; vaccine; cancer; ss.
XX
OS Synthetic.
OS Mycobacterium vaccae.
XX
PN WO9808542-A2.
XX
PD 05-MAR-1998.
XX
PF 28-AUG-1997; 97WO-NZ000105.
XX
PR 29-AUG-1996; 96US-00705347.
PR 12-JUN-1997; 97US-00873970.
XX
PA (GENE-) GENESIS RES & DEV CORP.
XX
PI Tan P, Hiyana J, Visser E, Skinner MA, Scott LM, Prestidge RL;
XX WPI; 1998-216926/19.
XX
DR Mycobacterium vaccae polypeptides - used to develop products for use in
XX detection, therapy and prevention of mycobacteria infections or as immune
XX response enhancers.
XX
PS Example 8; Page 99; 153pp; English.

CC This oligonucleotide is used in the DNA cloning strategies of the
CC Mycobacterium vaccae antigens. The invention provides M. vaccae
CC polypeptides that comprise an immunogenic portion of a soluble M. vaccae
CC antigen, or a variant, where the antigen induces an immune response in
CC patients previously exposed to a mycobacterium. Such M. vaccae
CC polypeptides can be used in methods for enhancing non-specific immune
CC response. The methods and products can be used for the detection,
CC treatment and prevention of infectious diseases caused by mycobacteria
CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
CC the ability to induce cell proliferation and cytokine production (e.g.
CC interferon-gamma and interleukin-12 production) in T cells, NK cells, B
CC cells, or macrophages. They can be used for enhancing immune responses
CC for use in vaccines or immunotherapy of infectious diseases and cancers
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
| | | | | | | | | | | | | | | | | | | | | |
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 125
AAT86606/c
ID AAT86606 standard; DNA; 20 BP.
XX
AC AAT86606;
XX
DT 04-JUN-1998 (first entry)
XX
DE Oligonucleotide separated by capillary affinity gel electrophoresis.
XX
KW Capillary affinity gel electrophoresis; separation; polymer-gel;
KW polyacrylamide; ss.
XX
OS Synthetic.
XX WO9745721-A1.
XX
PD 04-DEC-1997.
XX
PF 23-MAY-1997; 97WO-EP002647.
XX
PR 24-MAY-1996; 96CH-00001320.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Muscate A, Paulus A, Natt F;
XX WPI; 1998-041763/04.
XX
DR Separation of electrically charged target molecules - by capillary
XX affinity gel electrophoresis using polymer-gel to which receptors for
XX target molecules are bound.
XX
PS Example D3; Page 25; 41pp; English.

CC A mixture of oligonucleotides (AAT86604-7) were separated by a new
CC process using capillary affinity gel electrophoresis. The invention
CC relates to selective separation of electrically charged target molecules
CC in an analytical mixture. It comprises capillary affinity gel
CC electrophoresis using a capillary tube which is at least partly filled
CC with a polymer gel. Receptors for target molecules are covalently bound
CC to the polymer. An electric field of at least 50 volts/cm is applied. The
CC capillary tube is charged with the analytical mixture. In a first
CC separation stage, the target molecules in the mixture are bound to the
CC receptors and the remaining components are eluted. Optionally whilst
CC splitting open. In a second stage, the elution conditions are changed,
CC optionally in stages, so that the affinity of the target molecules for
CC the receptor is eliminated and the target molecules are eluted and
CC detected, optionally whilst splitting open. The process is useful for
CC selective separation and/or determination of charged organic compounds,
CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
CC for isolation of specific proteins and DNA molecules, purification of
CC antibodies, analysis of antisense compounds or screening for enzyme
CC inhibitors. The process achieves higher resolution and selectivity than
CC prior art processes, especially in the case of complex biological
CC analytical mixtures. It has high sensitivity, even with small amounts of
CC samples. The derivatised polymers may be synthesised specifically using
CC standard methods
XX.
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 126
AA27533/C
ID AAX27533 standard; RNA; 20 BP.
AC AAX27533;
XX
DT 27-MAY-1999 (first entry)
XX
DE Synthetic RNA sequence produced by the method of the invention.
XX
KW Silyloxymethyl; phosphonate; silyloxymethyl halide; diagnosis; ss;
KW cyanoethyl phosphoramidate coupling; isomerisation; steric hindrance.
XX
OS Synthetic.
XX
PN WO9909044-A1.
XX
PD 25-FEB-1999.
XX
PF 17-AUG-1998; 98WO-EP005215.
XX
PR 18-AUG-1997; 97CH-00001931.
XX
PA (PITS/) PITSCH S.
PA (WEIS/) WEISS P A.
PA (JENN/) JENNY L.
XX
PI Pitsch S, Weiss PA, Jenny L;
XX
DR WPI; 1999-180963/15.
XX
PT 2-Silyloxymethyl ribonucleosides and their phosphonate derivatives - have
PT high purity, use in machine synthesis of ribonucleic acids, enable longer
PT oligonucleotide chain construction, and larger amounts.
XX
PS Example 6; Page 25; 38pp; English.
XX
CC The invention relates to silyloxymethyl protected D- or L-ribonucleosides
CC and their phosphonates (I), and silyloxymethyl halides (II). (I) are
CC intermediates for synthesis of RNA-oligonucleotides with predetermined
CC nucleotide sequence, particularly by machine synthesis. The groups
CC specified above, apart from those on silyl, are those particularly for
CC the cyanoethyl phosphoramidate coupling. Uses of the oligoribonucleotide
CC products in diagnosis, therapy, and as research tools, are well known,
CC and are not dealt with in detail. (II) is an intermediate for (I). The
CC silyloxymethyl halide reagent is easy to prepare, and yields are high.
CC Introduction of the silyloxymethyl group into the ribonucleoside is
CC simple and rapid, and the acetal bond formed does not migrate,
CC eliminating particularly the prior art problem of 2' to 3' isomerisation.
CC The methylenedioxy group spacer between the silyl group and nucleoside
CC ring results in less steric hindrance than bulky direct silyloxy
CC linkages, enabling first, a range of choices for the silyl substituents,
CC to provide, e.g., acid or base stability; and second, higher yields in
CC coupling. Purer products are therefore obtained than in prior art,
CC enabling larger quantities and longer chains of oligoribonucleotides to
CC be synthesised successfully, and in shorter times
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 20 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 127
AA211326
ID AAZ11326 standard; DNA; 20 BP.
XX
AC AAZ11326;
XX
DT 25-OCT-1999 (first entry)
XX
DE Mycobacterial 16S rRNA specific oligo AD12.
XX
KW Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KW dendritic cell maturation; infectious disease; immune disorder; cancer;
KW respiratory system; mycobacterial infection; allergy; tuberculosis;
KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KW squamous cell carcinoma; melanoma; PCR primer; ss.
XX
OS Synthetic.
OS Mycobacterium vaccae.
XX
PN WO9932634-A2.
XX
PD 01-JUL-1999.
XX
PF 23-DEC-1998; 98WO-NZ000189.
XX
PR 23-DEC-1997; 97US-00996624.
PR 23-DEC-1997; 97US-00997080.
PR 23-DEC-1997; 97US-00997362.
PR 11-JUN-1998; 98US-00098855.
PR 17-SEP-1998; 98US-00156181.
PR 04-DEC-1998; 98US-00205426.
XX
PA (GENE-) GENESIS RES & DEV CORP LTD.
XX
PI Tan P, Watson J, Visser ES, Skinner MA, Prestidge RL;
XX
DR WPI; 1999-430163/36.
XX
PT Enhancing immune response to an antigen.
XX
PS Example 15; Page 177; 243pp; English.
XX
CC The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC M. vaccae proteins. The M. vaccae proteins may be employed to activate T
CC cells and natural killer cells, to stimulate the production of cytokines,
CC to enhance the expression of co-stimulatory molecules on dendritic cells
CC and monocytes, and to enhance dendritic cell maturation and function. The
CC proteins can be expressed by standard recombinant methodology.
CC Pharmaceutical compositions comprising the proteins or nucleic acid
CC sequences encoding the proteins can be used for the treatment
CC prevention, and detection of disorders including infectious diseases,
CC immune disorders and cancer. In particular, the compounds and methods are
CC used for treatment of diseases of the respiratory system, such as
CC mycobacterial infections, asthma, allergies, tuberculosis, leprosy,
CC sarcoidosis and lung cancers, and disorders of the skin such as
CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC carcinoma and melanoma
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

```

RESULT 128

```

AAA40449
ID AAA40449 standard; DNA; 20 BP.
XX AC AAA40449;
XX DT 13-NOV-2000 (first entry)
XX DE Electrochemical detection method sample DNA target.
XX KW Electrochemical detection; glucose; cholesterol; urea nitrogen;
XX KW bilirubin; uric acid; haemoglobin; lactic acid; body fluid; blood;
XX KW plasma; serum; urine; lymph diagnosis; ss.
XX OS Synthetic.
XX PN EP1018646-A2.
XX PD 12-JUL-2000.
XX PF 07-JAN-2000; 2000EP-00100126.
XX PR 06-JAN-1999; 99JP-00001111.
XX PR 24-MAY-1999; 99JP-00143599.
XX PA (FUJF ) FUJI PHOTO FILM CO LTD.
XX PI Ogawa M, Takenaka S, Takagi M;
XX DR WPI; 2000-444372/39.
XX PT Quantitative analysis of a biochemical compound such as glucose, in body
XX PT a body fluid such as blood, comprising detecting enhanced electron
XX PT transfer between an oxidase and a DNA-immobilized electrode, useful for
XX PT diagnosis of disease.
XX PS Example 1; Page 8; 14pp; English.
XX CC This invention describes a novel method for quantitatively analysing a
XX CC biochemical compound (I) which comprises contacting (I) with double
XX CC stranded DNA fixed to the surface of an electrode at their terminals in
XX CC which electrochemically active threading intercalators are intercalated,
XX CC in an aqueous medium under application of electric potential to the
XX CC electrode in the presence of an oxidase which oxidizes the biochemical
XX CC compound and becomes reduced, and detecting electric current flowing
XX CC between the electrode and a second electrode in the aqueous medium. The
XX CC method is useful for detection of biochemical compounds such as glucose,
XX CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
XX CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
XX CC for diagnosis of various diseases. The method allows detection of
XX CC biochemical compounds quickly and easily with a high sensitivity using a
XX CC sample apparatus. This sequence represents DNA fragment used as a target
XX CC sample in the method of the invention
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 129
AAA40448/C
ID AAA40448 standard; DNA; 20 BP.
XX AC AAA40448;
XX DT 13-NOV-2000 (first entry)
XX DE Electrochemical detection method fixed probe DNA.

```

```

XX OS Synthetic.
XX PN EP1018646-A2.
XX PD 12-JUL-2000.
XX PF 07-JAN-2000; 2000EP-00100126.
XX PR 06-JAN-1999; 99JP-00001111.
XX PR 24-MAY-1999; 99JP-00143599.
XX PA (FUJF ) FUJI PHOTO FILM CO LTD.
XX PI Ogawa M, Takenaka S, Takagi M;
XX DR WPI; 2000-444372/39.
XX PT Quantitative analysis of a biochemical compound such as glucose, in body
XX PT a body fluid such as blood, comprising detecting enhanced electron
XX PT transfer between an oxidase and a DNA-immobilized electrode, useful for
XX PT diagnosis of disease.
XX PS Example 1; Page 7; 14pp; English.
XX CC This invention describes a novel method for quantitatively analysing a
XX CC biochemical compound (I) which comprises contacting (I) with double
XX CC stranded DNA fixed to the surface of an electrode at their terminals in
XX CC which electrochemically active threading intercalators are intercalated,
XX CC in an aqueous medium under application of electric potential to the
XX CC electrode in the presence of an oxidase which oxidizes the biochemical
XX CC compound and becomes reduced, and detecting electric current flowing
XX CC between the electrode and a second electrode in the aqueous medium. The
XX CC method is useful for detection of biochemical compounds such as glucose,
XX CC cholesterol, urea nitrogen, bilirubin, uric acid, haemoglobin and lactic
XX CC acid in body fluids such as whole blood, plasma, serum, urine, and lymph
XX CC for diagnosis of various diseases. The method allows detection of
XX CC biochemical compounds quickly and easily with a high sensitivity using a
XX CC sample apparatus. This sequence represents DNA fragment used as fixed
XX CC probe DNA in the method of the invention
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 130
AAZ91117/C
ID AAZ91117 standard; DNA; 20 BP.
XX AC AAZ91117;
XX DT 06-JUN-2000 (first entry)
XX DE Oligonucleotide #5 for conjugation to abietane derivative.
XX KW Abietane derivative; labelling; diagnostic test; biotin substitute; ss.
XX OS Synthetic.
XX PN FR2781802-A1.
XX PD 04-FEB-2000.

```

```
XX PF 31-JUL-1998; 98FR-00010084.
XX PR 31-JUL-1998; 98FR-00010084.
XX PA (INMR ) BIO MERIEUX.
XX PI Charles MH, Piga N, Battail PN, Veron L, Delair T, Mandrand B;
XX DR WPI; 2000-239603/21.
XX PT Saturated and unsaturated derivatives of abietic acid and their
PT conjugated derivatives with natural and synthetic polymers, having use in
PT diagnostics, chemical reactions and analysis.
XX PS Example 5; Page 20; 39pp; French.
XX CC The invention relates to novel saturated and unsaturated abietane
CC derivatives. The new compounds may be used directly or indirectly in the
CC development of new diagnostic tests, to follow infections, especially
CC viral infections, to follow and/or measure chemical products, especially
CC potential pollutants. In diagnostic tests they may be used as markers, or
CC to form a universal solid phase after immobilization on a solid support,
CC to produce monoclonal antibodies or polyclonal antibodies having
CC diagnostic uses. The oligonucleotides AA29113-29117 represent examples
CC of sequences that can be labeled with the new abietane derivatives. The
CC new derivatives may be used to substitute for biotin in diagnostic tests,
CC but because they are not found naturally in humans the risk of potential
CC interactions with biological molecules is eliminated
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 131
AAA50193/c
XX ID AAA50193 standard; DNA; 20 BP.
XX AC AAA50193;
XX DT 07-NOV-2000 (first entry)
XX DE 2'-Methoxyethoxy-modified oligonucleotide.
XX KW Phosphodiester oligonucleotide; H-phosphonate chemistry; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX modified_base 1..19
XX FT /*tag= a
XX FT /note= "2'-methoxyethoxy modified thymidine"
XX PN WO200047593-A1.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003543.
XX PR 12-FEB-1999; 99US-00250075.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Manoharan M, Maier MA;
XX DR WPI; 2000-558188/51.
```

```
XX PT Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT linkages to phosphodiester internucleoside linkages.
XX PS Example 12; Page 34; 49pp; English.
XX CC The present sequence is that of a phosphodiester oligonucleotide
CC containing 20 T nucleobases, 19 having a 2'-methoxyethoxy group on its 5'
CC ribosyl sugar moiety. It is an example of an oligomeric compound produced
CC according to the methods of the invention. The invention provides
CC compounds and methods for the preparation of mixed backbone oligomeric,
CC or chimeric, compounds having phosphodiester internucleoside linkages in
CC addition to phosphorothioate and/or phosphoramidate internucleoside
CC linkages. The methods also include incorporation of boranophosphate
CC internucleoside linkages. The methods utilise H-phosphonate intermediates
CC that are coupled together forming contiguous regions of 1 or more H-
CC phosphonate internucleoside linkages. Each contiguous region is
CC subsequently oxidized to phosphodiester, phosphorothioate,
CC phosphoramidate or boranophosphate internucleoside linkages prior to
CC further elongation. Mixed backbone oligomeric compounds are prepared in
CC this manner by oxidizing adjacent regions with different reagents.
CC Oligomeric compounds of the invention are prepared using novel oxidation
CC steps that oxidize a region of 1 or more H-phosphonate internucleoside
CC linkages without degrading existing linkages that have been previously
CC oxidized. The oligonucleotides obtained are useful as primers in PCR,
CC probes, linkers, gene fragments and for other diagnostic tests on e.g.
CC biological tissue, fluid, cells etc., as research reagents, and as
XX antiviral agents
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 132
AAC87238/c
XX ID AAC87238 standard; DNA; 20 BP.
XX AC AAC87238;
XX DT 09-MAR-2001 (first entry)
XX DE Phosphorothioate poly T oligonucleotide, SEQ ID NO:17.
XX KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
KW hnRNP A1; lupus Ia protein; functional modifier identification; agonist;
KW antagonist; mimic; inhibitor; drug screening;
KW cellular target identification; oligonucleotide optimisation;
KW immunotherapy; ss.
XX OS Synthetic.
XX PN WO200067023-A1.
XX PD 09-NOV-2000.
XX PF 28-APR-2000; 2000WO-US011697.
XX PR 29-APR-1999; 99US-0131830P.
XX PR 03-MAR-2000; 2000US-0186845P.
XX PA (CPGI-) CPi IMMUNOPHARMACEUTICALS GMBH.
XX PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Noll BO, Schetter C, Krieg AM;
```



```

XX DR WPI; 2001-016002/02.
XX PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
XX PT functional modifiers, immunostimulatory DNA binding competitors and to
XX PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX PS Example 1; Page 45; 95pp; English.
XX CC The invention relates to the use of an immunostimulatory single-stranded
XX CC DNA-binding protein in screening assays to identify compounds which bind
XX CC to it and thereby act as functional modifiers of immunostimulatory
XX CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
XX CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
XX CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
XX CC Immunostimulatory DNA-binding proteins can also be used in screening
XX CC methods to identify immunostimulatory DNA binding competitors, and to
XX CC optimize an immunostimulatory ODN for immune stimulation. Isolated
XX CC complexes of an immunostimulatory DNA-binding protein bound to an
XX CC immunostimulatory ODN can additionally be used to screen a panel of
XX CC candidate target molecules to identify the cellular target molecules of
XX CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
XX CC used in the methods of the invention are the RNA-binding proteins
XX CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
XX CC methods are useful for identifying a compound that inhibits interaction
XX CC between immunostimulatory DNA and an immunostimulatory DNA-binding
XX CC protein and for identifying agonists useful in immunotherapy. The complex
XX CC is useful in screening for immunostimulatory ODN competitors allow the
XX CC molecules. The candidate immunostimulatory ODN competitors allow the
XX CC investigation of structure/activity relationships of immunostimulatory
XX CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
XX CC represents an oligonucleotide used in an exemplification of the invention
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 133
AAC87230/c
ID AAC87230 standard; DNA; 20 BP.
XX AC AAC87230;
XX DT 09-MAR-2001 (first entry)
XX DE Digoxigenin-labelled poly T oligonucleotide, SEQ ID NO:9.
XX KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
XX KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
XX KW hnRNP A1; lupus La protein; functional modifier identification; agonist;
XX KW antagonist; mimic; inhibitor; drug screening;
XX KW cellular target identification; oligonucleotide optimisation;
XX KW immunotherapy; ss.
XX OS Synthetic.
XX PN WO200067023-A1.
XX PD 09-NOV-2000.
XX PP 28-APR-2000; 2000WO-US011697.
XX PR 29-APR-1999; 99US-0131830P.
XX PR 03-MAR-2000; 2000US-0186845P.
XX PA (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.

```

```

PA (IOWA ) UNIV IOWA RES FOUND.
XX PI Noll BO, Schetter C, Krieg AM;
XX DR WPI; 2001-016002/02.
XX PT Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
XX PT functional modifiers, immunostimulatory DNA binding competitors and to
XX PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX PS Example 1; Page 45; 95pp; English.
XX CC The invention relates to the use of an immunostimulatory single-stranded
XX CC DNA-binding protein in screening assays to identify compounds which bind
XX CC to it and thereby act as functional modifiers of immunostimulatory
XX CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
XX CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
XX CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
XX CC Immunostimulatory DNA-binding proteins can also be used in screening
XX CC methods to identify immunostimulatory DNA binding competitors, and to
XX CC optimize an immunostimulatory ODN for immune stimulation. Isolated
XX CC complexes of an immunostimulatory DNA-binding protein bound to an
XX CC immunostimulatory ODN can additionally be used to screen a panel of
XX CC candidate target molecules to identify the cellular target molecules of
XX CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
XX CC used in the methods of the invention are the RNA-binding proteins
XX CC nucleolin, hnRNP D, AUF1, hnRNP A1 and lupus La protein. The screening
XX CC methods are useful for identifying a compound that inhibits interaction
XX CC between immunostimulatory DNA and an immunostimulatory DNA-binding
XX CC protein and for identifying agonists useful in immunotherapy. The complex
XX CC is useful in screening for immunostimulatory ODN competitors allow the
XX CC molecules. The candidate immunostimulatory ODN competitors allow the
XX CC investigation of structure/activity relationships of immunostimulatory
XX CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
XX CC represents an oligonucleotide used in an exemplification of the invention
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 134
AAC87241/c
ID AAC87241 standard; DNA; 20 BP.
XX AC AAC87241;
XX DT 09-MAR-2001 (first entry)
XX DE Poly T oligonucleotide, SEQ ID NO:20.
XX KW Immunostimulatory oligodeoxynucleotide; immunostimulatory ODN;
XX KW immunostimulatory DNA-binding protein; nucleolin; hnRNP D; AUF1;
XX KW hnRNP A1; lupus La protein; functional modifier identification; agonist;
XX KW antagonist; mimic; inhibitor; drug screening;
XX KW cellular target identification; oligonucleotide optimisation;
XX KW immunotherapy; ss.
XX OS Synthetic.
XX PN WO200067023-A1.
XX PD 09-NOV-2000.
XX PP 28-APR-2000; 2000WO-US011697.
XX PR 29-APR-1999; 99US-0131830P.

```

```
PR 03-MAR-2000; 2000US-0186845P.
XX (CPGI-) CPG IMMUNOPHARMACEUTICALS GMBH.
PA (IOWA ) UNIV IOWA RES FOUND.
XX
XX Noll BO, Schetter C, Krieg AM;
XX
XX WPI; 2001-016002/02.
XX
XX Immunostimulatory DNA binding proteins to identify immunostimulatory DNA
PT functional modifiers, immunostimulatory DNA binding competitors and to
PT optimize immunostimulatory oligodeoxynucleotides for stimulation.
XX
XX Example 1; Page 45; 95pp; English.
XX
XX The invention relates to the use of an immunostimulatory single-stranded
CC DNA-binding protein in screening assays to identify compounds which bind
CC to it and thereby act as functional modifiers of immunostimulatory
CC oligodeoxynucleotide (ODN) activity. Such modifiers of ODN activity
CC consist of immunostimulatory DNA binding inhibitors, immunostimulatory
CC DNA mimics, and immunostimulatory DNA agonists and antagonists.
CC Immunostimulatory DNA-binding proteins can also be used in screening
CC methods to identify immunostimulatory DNA binding competitors, and to
CC optimize an immunostimulatory ODN for immune stimulation. Isolated
CC complexes of an immunostimulatory DNA-binding protein bound to an
CC immunostimulatory ODN can additionally be used to screen a panel of
CC candidate target molecules to identify the cellular target molecules of
CC the immunostimulatory ODN. The immunostimulatory DNA-binding proteins
CC used in the methods of the invention are the RNA-binding proteins
CC nucleolin, hnRNP D, AUFI, hnRNP A1 and lupus La protein. The screening
CC methods are useful for identifying a compound that inhibits interaction
CC between immunostimulatory DNA and an immunostimulatory DNA-binding
CC protein and for identifying agonists useful in immunotherapy. The complex
CC is useful in screening for immunostimulatory DNA cellular target
CC molecules. The candidate immunostimulatory ODN competitors allow the
CC investigation of structure/activity relationships of immunostimulatory
CC DNA-binding proteins and immunostimulatory ODNs. The present sequence
CC represents an oligonucleotide used in an exemplification of the invention
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAA 1
RESULT 135
AAS10402/C
ID AAS10402 standard; DNA; 20 BP.
XX
XX AAS10402;
XX
XX 24-OCT-2001 (first entry)
XX
XX DNA template for 3' end labeling of an RNA molecule, #14.
DE
XX 3' RNA end labeling; DNA template; Okazaki fragment; 5' overhang; ss.
XX
XX Synthetic.
XX
XX US6238865-B1.
XX
XX 29-MAY-2001.
XX
XX 16-OCT-1998; 98US-00173936.
XX
XX 17-OCT-1997; 97US-0063757P.
XX
XX (CHEN/) CHEN G.
PA
```

```
PA (HUAN/) HUANG Z.
PA (SZOS/) SZOSTAK J W.
XX
XX Huang Z, Szostak JW;
XX
XX WPI; 2001-366470/38.
XX
XX Modifying a 3' terminus of a pre-selected DNA sequence, useful for
PT labeling and modifying 3'-termini of other nucleic acids, comprises using
PT a synthetic nucleotide template with a defined overhang nucleotide.
XX
XX Example 5; Col 13; 22pp; English.
XX
XX The sequence represents a synthetic DNA template molecule used to
CC demonstrate the method of the invention. The invention relates to a
CC method of modifying (e.g. 3' end labelling with 32P dATP) the 3' terminus
CC of an RNA molecule by providing a DNA oligonucleotide, complementary to
CC the 3' end of the RNA molecule, with an overhang at the 5' end which
CC allows incorporation of the labeling nucleotide into the RNA molecule.
CC The method, based on the synthesis of Okazaki fragments, is useful for
CC labeling and modifying the 3'-termini of other nucleic acids such as DNA
CC fragments. The method is a simple and efficient way of labeling or
CC modifying RNA 3'-termini using DNA polymerase and a synthetic template
CC with defined overhang nucleotides
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAA 1
RESULT 136
AAD16997/C
ID AAD16997 standard; DNA; 20 BP.
XX
XX AAD16997;
XX
XX 29-NOV-2001 (first entry)
XX
XX Capture probe CP5'.
XX
XX Scaffold protein; antibody mimic; fibronectin type III domain;
XX randomised loop; randomised beta-sheet; diagnostic purpose;
XX protein designing; probe; tenth module of human Fn3; 10Fn3;
XX fibronectin module of type III; Fn3; ss.
XX
XX Unidentified.
XX
XX WO200164942-A1.
XX
XX 07-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006414.
XX
XX 29-FEB-2000; 2000US-00515260.
XX
XX (PHYL-) PHYLLOS INC.
XX
XX Lipovsek D, Wagner RW, Kuimelis RG;
XX
XX WPI; 2001-557782/62.
XX
XX Fibronectin scaffold protein array for obtaining a protein/compound which
PT binds to a compound/protein, comprises a fibronectin type III domain
PT having a randomized loop, a randomized beta-sheet or their combination.
XX
XX Disclosure; Page 41; 67pp; English.
XX
```

CC The present invention relates to an array of proteins (antibody mimics)
 CC comprising a fibronectin type III domain having a randomised loop, a
 CC randomised beta-sheet, or their combination, and has the capacity to bind
 CC to a compound that is not bound by a corresponding naturally- occurring
 CC fibronectin, immobilised onto a solid support. The antibody mimics is
 CC useful for detecting a compound preferably a protein, in a biological
 CC sample. It is also useful to detect one or more different analytes
 CC simultaneously in a sample. Hence is useful for diagnostic purposes. It
 CC is also useful for the purpose of designing proteins capable of binding
 CC to virtually any compound of interest. The present sequence is a capture
 CC probe used to self-assemble and anchor the tenth module of human
 CC fibronectin module of type III (Fn3) (10Fn3) which is used in an
 CC exemplification of the invention

XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 |||||
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 137

AAF60896
 ID AAF60896 standard; DNA; 20 BP.

AC AAF60896;

DT 15-MAY-2001 (first entry)

XX Conjugate forming oligonucleotide ON5 SEQ ID 5.

XX Transport; membrane; cytostatic; virucide; vasotropic; dermatological;
 KW antiporiatic; antiasthmatic; gene therapy; tumor cell; antisense;
 KW tumor therapy; drug; phosphodiester linkage; ss.

XX Unidentified.

XX DE19935302-A1.

XX 08-FEB-2001.

XX 28-JUL-1999; 99DE-01035302.

XX 28-JUL-1999; 99DE-01035302.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Uhlmann E, Greiner B, Unger E, Gothe G, Schwerdel M;

XX WPI; 2001-203679/21.

XX New substituted aryl conjugates of parent molecules, especially
 PT oligonucleotides, having improved transmembrane and intracellular
 PT transport properties, useful as medicaments or diagnostic agents.

XX Disclosure; Page 9; 28pp; German.

XX This invention describes a novel conjugate (I) which consists of (A) a
 CC molecule to be transported and (B) at least one aryl residue of formula -
 CC Ar-(X-C(V)-R₁)_n (II). Ar = group containing at least one aromatic ring;
 CC X = O or N (sic); Y = O, S or NH-R₂ (sic); R₁ = optionally substituted
 CC 1-23C alkyl (optionally containing double and/or triple bonds); R₂ =
 CC optionally substituted 1-18C alkyl (optionally containing double and/or
 CC triple bonds); n = integer of 1 or more. (A) is bonded to (B) directly or
 CC via a chemical group, provided that the chemical group is other than CH₂
 CC -S if the bond is via a phosphodiester linkage of (A). The invention also
 CC describes (i) the preparation of a conjugate (I') of (A') a molecule to
 CC be transported and (B') at least one aryl residue (not restricted to
 CC (II)), by preparing (A') containing a reactive function at the position

CC at which (B') is to be bonded, preparing (B') and reacting (A') and (B');
 CC and (ii) the use of aryl groups (II) (optionally bonded via a chemical
 CC group) for transporting (A) across biological membranes. The products of
 CC the invention have cytostatic, virucide, vasotropic, dermatological,
 CC antiporiatic and antiasthmatic activity and can be used for gene
 CC therapy. Conjugation of (A) with (B) is useful for transporting (A)
 CC across biological membranes or into eukaryotic or prokaryotic cells
 CC (specifically bacterial, yeast or mammalian cells, including human cells,
 CC particularly tumor cells). Medicaments, diagnostic agents and test kits
 CC containing (I) are also claimed. Typically (I) are antisense
 CC oligonucleotide derivatives for tumor therapy; oligonucleotide drugs for
 CC treating viral infections or diseases associated with integrins or cell-
 CC cell interactions (e.g. restenosis, vitiligo, psoriasis or asthma); or
 CC labeled oligonucleotides for in vivo diagnostic use, e.g. by in situ
 CC hybridization. Conjugation with (B) markedly improves the cellular uptake
 CC of (A), e.g. in tumor cells. (B) include fluorescein derivative residues,
 CC in which case the conjugates (I) are fluorescently labeled, allowing
 CC microscopic monitoring of cellular uptake etc. The cellular uptake of (I)
 CC is superior to that obtained using other conjugated groups related to
 CC (II); e.g. oligonucleotides conjugated with fluorescein diacetate (within
 CC the scope of (B)) have superior uptake to corresponding fluorescein
 CC conjugates

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 138

AAS63428
 ID AAS63428 standard; DNA; 20 BP.

XX AAS63428;

XX 29-JAN-2002 (first entry)

XX Oligonucleotide-nanoparticle probe #52.

XX Oligonucleotide-nanoparticle probe; diagnostic; forensic analysis;
 KW nucleic acid detection; nanostructure; biochip; biofilter; drug delivery;
 KW ss.

XX Synthetic.

XX WO200173123-A2.

XX 04-OCT-2001.

XX 28-MAR-2001; 2001WO-US010071.

XX 28-MAR-2000; 2000US-0192699P.

XX 26-APR-2000; 2000US-0200161P.

XX 26-JUN-2000; 2000US-00603830.

XX 26-JUN-2000; 2000US-0213906P.

XX 08-DEC-2000; 2000US-0254392P.

XX 11-DEC-2000; 2000US-0255235P.

XX 12-JAN-2001; 2001US-00760500.

XX 28-MAR-2001; 2001US-00820279.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 PT Taton TA, Park S, Li Z;
 XX WPI; 2001-656926/75.

XX Detecting and separating nucleic acid, useful e.g. for diagnosis,

comprises reaction with nanoparticles that carry oligonucleotides complementary to parts of the target.

Example 18; Page 158; 404pp; English.

The invention relates to a method for detection of nucleic acid (I) having at least 2 portions, comprising treatment with nanoparticles that carry oligonucleotides complementary to at least 2 parts of (I), where detectable change caused by hybridisation of the oligonucleotide to (I) is observed. The method is used to detect (or to separate) specific (I), e.g. for diagnosing a wide variety of diseases, sequencing, in forensic analysis etc., and generally to detect analytes other than (I). The oligonucleotide-derivatised nanoparticles are also useful for preparing nanostructures useful, for example, as biochips, biofilters, mechanical devices, separation membranes, chemical sensors, in computers, and for drug delivery. Very stable nanoparticle-oligonucleotide conjugates can be produced, allowing their direct use (as probes) in polymerase chain reaction, i.e. they survive multiple heating/cooling cycles so do not need to be added after amplification. (I) are detected by simple colour change, without the need for special equipment, making possible rapid field testing for e.g. pathogens. AAS63374-AAS63448 represent oligonucleotide-nanoparticle probes, and related sequences, used in the method of the invention

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 139

AAF28481

ID AAF28481 standard; DNA; 20 BP.

XX AAF28481;

DT 03-APR-2001 (first entry)

XX Random oligonucleotide, SEQ ID NO: 53.

KW Nucleic acid detection; nanoparticle-oligonucleotide conjugate;
KW disease diagnosis; forensic analysis; DNA sequencing; paternity testing;
KW cell line authentication; gene therapy; ss.

OS Synthetic.

PN WO200100876-A1.

XX 04-JAN-2001.

XX 26-JUN-2000; 2000WO-US017507.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

XX (MIRK/) MIRKIN C A.

PA (LETS/) LETSINGER R L.

PA (MUCI/) MUCIC R C.

PA (STOR/) STORHOFF J J.

PA (ELGH/) ELGHANIAN R.

PA (TATO/) TATON T A.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

DR WPI; 2001-061976/07.

XX Detecting nucleic acid, useful for e.g. diagnosis of diseases, forensics

PT and DNA sequencing, comprises observing detectable change brought about
PT by hybridization of nucleic acid with substrate or particle bound
PT oligonucleotides.

XX Disclosure; Page 199; 205pp; English.

XX The present sequence is an oligonucleotide used in a method for detecting
CC a nucleic acid having at least 2 portions. The method comprises
CC hybridising the nucleic acid with oligonucleotides, such as the present
CC sequence, attached to a substrate and/or particle and detecting a change
CC in colour, conductivity or optical density. The method is useful for the
CC diagnosis and/or monitoring of diseases, in forensics, in DNA sequencing,
CC for paternity testing, for cell line authentication and for monitoring
CC gene therapy. Detecting nucleic acids based upon observing a colour
CC change is cheap, fast, simple, and does not require specialised or
CC expensive equipment. The nanoparticle oligonucleotide conjugates remain
CC stable for at least 6 months. A single base mismatch and as little as 20
CC femtomoles (fM) of target can be detected using the conjugates

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 140

AAS10371

ID AAS10371 standard; DNA; 20 BP.

XX AAS10371;

DT 24-OCT-2001 (first entry)

XX Oligonucleotide-cyclic disulphide linker, d.

XX Nanoparticle; cyclic disulphide-oligonucleotide; DNA detection;
KW DNA isolation; genetic disease; bacterial disease; viral disease;
KW forensic science; paternity testing; gene therapy; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1

FT /*tag= a

FT /note= "A is covalently linked to a cyclic-disulphide moiety"

XX WO200151665-A2.

PN 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001190.

PR 13-JAN-2000; 2000US-0176409P.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

PR 12-JAN-2001; 2001US-00760500.

XX (NANO-) NANOSPHERE INC..

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA, Li Z;

XX WPI; 2001-451868/48.

XX Detecting a nucleic acid useful in e.g. diagnosing genetic, bacterial or
PT viral diseases, by contacting the nucleic acid with oligonucleotides
PT attached to nanoparticles and having sequences complementary a portion of

CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
 |||||
 DB 20 AAAAAAAAAAAAAAAAAA 1

RESULT 143
 AAF99431
 ID AAF99431 standard; DNA; 20 BP.
 AC AAF99431;
 XX
 DT 12-JUN-2001 (first entry)
 DE Immunostimulatory nucleic acid #547.
 XX
 KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
 KW immunostimulatory; tumour; viral infection; bacterial infection;
 KW fungal infection; parasitic infection; cancer; asthma;
 KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 PN WO200122972-A2.
 XX
 PD 05-APR-2001.
 XX
 PF 25-SEP-2000; 2000WO-US026383.
 XX
 PR 25-SEP-1999; 99US-0156113P.
 PR 27-SEP-1999; 99US-0156135P.
 PR 23-AUG-2000; 2000US-0227436P.
 XX
 PA (IOWA) UNIV IOWA RES FOUND.
 PA (COLE-) COLEY PHARM GMBH.
 XX
 PI Krieg AM, Schetter C, Vollmer J;
 DR WPI; 2001-273485/28.
 XX
 XX Vaccinating against tumors, infectious diseases, allergies and asthma
 PT using immunostimulatory Py-rich and TG nucleic acids.
 PS Claim 101; Page 49; 338pp; English.
 XX
 CC The present invention relates to a method for stimulating an immune
 CC response. The method comprises administering an immunostimulatory nucleic
 CC acid to a non-rodent subject in sufficient quantity to stimulate an
 CC immune response. The present sequence is one such immunostimulatory
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
 CC also useful for preventing cancer, asthma, infectious disease, allergy or
 CC immune deficiency. The present sequence can also be used to redirect a
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the
 CC present sequence may have a phosphorothioate backbone

XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
 |||||
 DB 1 AAAAAAAAAAAAAAAAAA 20

RESULT 144
 AAH46465/c
 ID AAH46465 standard; DNA; 20 BP.
 AC AAH46465;
 XX
 DT 14-SEP-2001 (first entry)
 DE Oligonucleotide #13.
 XX
 KW Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "All bases are phosphorothioate"
 FT modified_base 1
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "Modified with 2'-O-methyl"
 XX
 PN US6242591-B1.
 XX
 PD 05-JUN-2001.
 XX
 PF 11-JAN-2000; 2000US-00481486.
 XX
 PR 15-OCT-1997; 97US-00950779.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Cole DL, Ravikumar VT, Cheruvallath ZS;
 DR WPI; 2001-407218/43.
 XX
 XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides
 PT useful in biological research, comprises phosphorylating the 5'-hydroxyl
 PT of a nucleic acid having a nucleoside with a 2' modification.
 XX
 PS Example 23; Col 11; 7pp; English.
 XX
 CC The present invention relates to a method for preparing phosphorothioate
 CC oligonucleotides having at least one nucleoside with a 2' modification.
 CC The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid
 CC group having at least one nucleoside with a 2' modification in an
 CC acetonitrile. The present sequence was used to illustrate the method of
 CC the present invention. The method is useful for synthesising sulphurised
 CC 2' substituted phosphorothioate oligonucleotides, which may be used in
 CC molecular biological research, in applications such as anti-viral
 CC therapy, and for determining the stereochemical pathways of certain
 CC enzymes which recognise nucleic acids

XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 145
AAH78547
ID AAH78547 standard; cDNA; 20 BP.
XX AC
XX AAH78547;
XX 10-DEC-2001 (first entry)
XX DE Nucleotide sequence of a cDNA sequence.
XX KW Nucleic acid identification; DNA library screening; ss.
XX OS Synthetic.
XX US6274321-B1.
XX 14-AUG-2001.
XX PF 03-DEC-1999; 99US-00454704.
XX PR 03-DEC-1999; 99US-00454704.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Blumberg B;
XX DR WPI; 2001-588900/66.
XX PT Screening nucleic acids (NA) in pool of interest comprises pooling,
XX PT expressing NA to form expression product pool and identifying NA in NA
XX PT pool corresponding to expression product pool having interaction with
XX PT target moiety.
XX PS Disclosure; Col 22; 19pp; English.
XX CC The specification describes a method for identifying a nucleic acid in a
XX CC pool of interest. The method comprises pooling individually identifiable
XX CC nucleic acids into at least two pools of one nucleic acid each;
XX CC expressing nucleic acid pools to obtain protein expression product pools;
XX CC assaying protein expression product pools for products having interaction
XX CC with target molecule; selecting nucleic acid pools corresponding to
XX CC identified protein expression product pools; and identifying individual
XX CC nucleic acids in identified nucleic acid pools. The method is useful for
XX CC identifying a nucleic acid (e.g. cDNA) in a pool of interest and for
XX CC functionally screening several nucleic acids. The method is also useful
XX CC for screening genomic DNA libraries or other source of individual cDNAs,
XX CC mRNAs, synthetic libraries of nucleic acids e.g. combinatorial libraries.
XX CC The present sequence was used in the course of the invention
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 146
AAF28351
ID AAF28351 standard; DNA; 20 BP.
XX AC
XX AAF28351;
XX 02-APR-2001 (first entry)
XX DT
XX
```

```

DE DNA oligomer #1.
XX Deoxynucleic S-Methylthiouraea; DNmt; antisense therapy;
KW cardiovascular disease; inflammatory disease; neurocellular disease;
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW influenza; herpes; infection; ss.
XX OS Unidentified.
XX PN US6169176-B1.
XX PD 02-JAN-2001.
XX PF 28-SEP-1999; 99US-00407675.
XX PR 02-JUL-1998; 98US-0091481P.
XX PR 11-DEC-1998; 98US-0111800P.
XX PR 02-JUL-1999; 99US-00347443.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Dev AP, Bruice TC;
XX DR WPI; 2001-122276/13.
XX PT Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
XX PT antisense therapy, by synthesizing oligonucleotides comprising backbone
XX PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.
XX PS Example 7; Fig 16; 48pp; English.
XX CC The present sequence was used to demonstrate the ability of deoxynucleic
XX CC S-Methylthiouraea (DNmt) compounds to form triplexes with DNA oligomers. An
XX CC increase in the C content of the oligos resulted in a large decrease in
XX CC binding. This experiment was performed as an example of a method for
XX CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy
XX CC thiourea linkages. The method is useful for preparing oligonucleotides
XX CC for use in antisense or antigene therapy, to inhibit production of
XX CC proteins associated with genetic diseases, cardiovascular, inflammatory
XX CC and neurocellular diseases, and for antiviral therapy, e.g. to treat
XX CC human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
XX CC infections. The compounds are also useful as diagnostic reagents to
XX CC detect the presence or absence of the target DNA or RNA sequences to
XX CC which they specifically bind and by antagonising the normal biological
XX CC activity of a target protein, they can be used in the manipulation of
XX CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
XX CC cultures. The method provides an efficient and rapid solid-phase method
XX CC for the synthesis of thiourea and S-methylthiouraea
XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 147
ABS77742/c
ID ABS77742 standard; DNA; 20 BP.
XX AC ABS77742;
XX 13-DEC-2002 (first entry)
XX DE Angiogenesis inhibitory oligonucleotide #226.
XX KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
```

KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubrosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.
 XX
 PR 14-DEC-2000; 2000US-0255534P.
 XX
 PA (COLE-) COLEY PHARM GROUP INC.
 XX
 PI Bratzler RL;
 XX
 DR WPI; 2002-566690/60.
 XX
 PT Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 23; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubrosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 148
 ABS78072/c
 ID ABS78072 standard; DNA; 20 BP.
 AC ABS78072;
 XX
 DT 13-DEC-2002 (first entry)
 DE Angiogenesis inhibitory oligonucleotide #556.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubrosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.

XX WO200253141-A2.
 PN 11-JUL-2002.
 PD 14-DEC-2001; 2001WO-US048458.
 XX
 PF 14-DEC-2000; 2000US-0255534P.
 XX
 PR (COLE-) COLEY PHARM GROUP INC.
 XX
 PA Bratzler RL;
 XX
 DR WPI; 2002-566690/60.
 XX
 PT Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 29; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubrosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 149
 ABS78076
 ID ABS78076 standard; DNA; 20 BP.
 AC ABS78076;
 XX
 DT 13-DEC-2002 (first entry)
 DE Angiogenesis inhibitory oligonucleotide #560.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubrosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 PD 11-JUL-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048458.

PR 14-DEC-2000; 2000US-0255534P.
 PA (COLE-) COLEY PHARM GROUP INC.
 XX Bratzler RL;
 PI
 XX WPI; 2002-566690/60.
 DR
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 XX
 PS Claim 2; Page 29; 276pp; English.
 XX
 CC The invention relates to inhibiting angiogenesis in a subject, comprising
 CC administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Oster-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiodiroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 150
 ABL39402/c
 ID ABL39402 standard; DNA; 20 BP.
 XX
 AC ABL39402;
 XX
 DT 16-APR-2002 (first entry)
 XX
 DE Immunostimulatory nucleic acid SEQ ID NO: 838.
 XX
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 XX
 PN WO200197843-A2.
 XX
 XX 27-DEC-2001.
 PD
 PF 22-JUN-2001; 2001WO-US020154.
 XX
 XX 22-JUN-2000; 2000US-0213346P.
 PR
 XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX Weiner G, Hartmann G;
 PI
 XX WPI; 2002-154611/20.
 DR

XX Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of
 PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.
 XX
 PS Disclosure; Page 309; 312pp; English.
 XX
 CC The present invention relates to methods for treating or preventing
 CC cancer, involving administering to a subject having or at risk of
 CC developing cancer immunostimulatory nucleic acids that induce expression
 CC of cell surface antigens and antibodies. The methods are useful for
 CC treating or preventing cancer such as basal cell carcinoma, bladder
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
 CC breast cancer, cervical cancer, colon and rectum cancer, connective
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
 CC present sequence is an immunostimulatory oligonucleotide described in the
 CC exemplification of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 151
 ABL38648
 ID ABL38648 standard; DNA; 20 BP.
 XX
 AC ABL38648;
 XX
 DT 16-APR-2002 (first entry)
 XX
 DE Immunostimulatory nucleic acid SEQ ID NO: 2.
 XX
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; ss.
 XX
 OS Synthetic.
 XX
 PN WO200197843-A2.
 XX
 PD 27-DEC-2001.
 XX
 PF 22-JUN-2001; 2001WO-US020154.
 XX
 XX 22-JUN-2000; 2000US-0213346P.
 PR
 PA (IOWA) UNIV IOWA RES FOUND.
 XX
 PI Weiner G, Hartmann G;
 XX
 XX WPI; 2002-154611/20.
 DR
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of
 PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.
 XX
 PS Disclosure; Page 95; 312pp; English.
 XX
 CC The present invention relates to methods for treating or preventing
 CC cancer, involving administering to a subject having or at risk of
 CC developing cancer immunostimulatory nucleic acids that induce expression

CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 152
ABL39403/C
ID ABL39403 standard; DNA; 20 BP.
XX
AC ABL39403;
XX
DT 16-APR-2002 (first entry)
XX
DE Immunostimulatory nucleic acid SEQ ID NO: 839.
XX
KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; ss.
XX
OS Synthetic.
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
PT Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention

XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 153
ABL54775/C
ID ABL54775 standard; DNA; 20 BP.
XX
AC ABL54775;
XX
DT 10-JUN-2002 (first entry)
XX
DE CD14 receptor PCR primer SEQ ID NO 9.
XX
KW Angiotensin-I converting enzyme; ACE; CD14; receptor; SNP;
KW single-nucleotide polymorphism; PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2002034599-A.
XX
PD 05-FEB-2002.
XX
PF 26-JUL-2000; 2000JP-00225354.
XX
PR 26-JUL-2000; 2000JP-00225354.
XX
PA (TOYM) TOYOCO KK.
XX
DR WPI; 2002-275727/32.
XX
PT Detecting 1 base polymorphism on a sequence of a chromosome or it's
PT fragment.
XX
PS Example 2; Page 10; 10pp; Japanese.
XX
CC The invention relates to a method for detecting 1 base polymorphism on
CC the sequence of a chromosome or its fragment in which a sample nucleic
CC acid is reacted with a reaction liquor containing a nucleic acid primer
CC having a base adjacent to the polymorphic base at its 3'-end, one
CC dideoxynucleotide corresponding to a polymorphic base having a
CC distinguishable feature or its mixture, DNA polymerase and a composition
CC required for its activity expression to detect the presence of taking
CC dideoxynucleotide in the nucleic acid primer and to detect the type of
CC the base to be specified. The method is used for detecting 1 base
CC polymorphism on the sequence of a chromosome or its fragment. The present
CC sequence is that of a PCR primer, useful in examples of the invention
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 154
ABK65035
ID ABK65035 standard; DNA; 20 BP.
XX
AC ABK65035;
XX

```

DT 02-JUL-2002 (first entry)
DE Nanoparticle-oligonucleotide #55.
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
XX Synthetic.
OS WO200218643-A2.
PN 07-MAR-2002.
XX
XX 10-AUG-2001; 2001WO-US025237.
XX
XX 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
XX WPI; 2002-258024/30.
XX
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
XX Example 18; Page 410; 412pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 155
ABK65050
ID ABK65050 standard; DNA; 20 BP.
XX
AC ABK65050;

```

```

XX
DT 02-JUL-2002 (first entry)
DE Nanoparticle-oligonucleotide #70.
KW Nanoparticle-oligonucleotide; nanofabrication; nucleic acid detection;
KW ss.
XX Synthetic.
OS WO200218643-A2.
PN 07-MAR-2002.
XX
XX 10-AUG-2001; 2001WO-US025237.
XX
XX 11-AUG-2000; 2000US-0224631P.
PR 08-DEC-2000; 2000US-0254392P.
PR 11-DEC-2000; 2000US-0255235P.
PR 12-JAN-2001; 2001US-00760500.
PR 28-MAR-2001; 2001US-00820279.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA, Garimella V, Li Z, Park S;
XX
XX WPI; 2002-258024/30.
XX
XX Detecting nucleic acid, useful for diagnosis of genetic, viral or
PT bacterial disease, comprises hybridizing nanoparticles with attached
PT oligonucleotides to nucleic acid and detecting change brought about by
PT hybridization.
XX
XX Example 24; Fig 44; 412pp; English.
XX
XX The invention relates to a method of detecting a nucleic acid (NA) having
CC at least 2 portions comprising: (a) providing nanoparticles (NP) with
CC attached oligonucleotides (OGN), where OGN has a sequence complementary
CC to the sequence of NA; (b) contacting NA and NP under conditions
CC effective to allow hybridisation of OGN with NA; and (c) observing a
CC detectable change brought about by hybridisation of OGN with NA. The
CC method is useful for detecting a nucleic acid, separating a selected
CC nucleic acid from others and methods of nanofabrication. Detecting
CC analytes such as nucleic acids and proteins are useful for the diagnosis
CC of genetic, bacterial and viral diseases. The OGN-NP conjugates that use
CC cyclic disulphide linkers improve the sensitivity of diagnostic assays.
CC In particular assays using OGN-NP conjugates prepared using linkers
CC comprising a steroid residue attached to a cyclic disulphide have been
CC found to be approximately 10 times more sensitive than assays employing
CC conjugates prepared using alkanethiols or acyclic disulphides as the
CC linker. The OGN-NP conjugates are stable allowing them to be used
CC directly in PCR solutions. Therefore conjugates added as probes to a DNA
CC target to be PCR amplified can be carried through the 30 or 40 heating
CC cooling cycles of the PCR and are still able to detect the amplicons
CC without opening the tubes and causing contamination. ABK64981-ABK65055
CC represent nanoparticle-oligonucleotides of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 156
AAL45122/c
ID AAL45122 standard; DNA; 20 BP.
XX

```

```
AC AAL45122;
XX
XX 24-MAY-2002 (first entry)
XX
DE Oligonucleotide synthesis method related DNA #1.
XX
XX Oligonucleotide synthesis; polynucleotide array; protecting group;
KW oxidation; ss.
XX
OS Synthetic.
XX
XX EP1176151-A1.
XX
XX 30-JAN-2002.
XX
XX 27-JUL-2001; 2001EP-00118360.
XX
XX 28-JUL-2000; 2000US-00627249.
XX
XX (AGIL-) AGILENT TECHNOLOGIES INC.
XX
XX Dellinger DJ, Perbost MCM, Betley JR, Caruthers M;
XX
XX WPI; 2002-156732/21.
XX
XX Synthesis of polynucleotide useful during fabrication of an array
PT involves coupling nucleoside phosphoramidite and a solid-supported
PT nucleoside and treating the product with an oxidation/deprotection
XX composition.
XX
XX Example 1; Page 15; 36pp; English.
XX
XX The present invention relates to a method for the synthesis of a
CC polynucleotide which involves coupling a second nucleoside to a first
CC nucleoside through a phosphate linkage, where the second nucleoside has a
CC non-carbonate protecting group protecting a hydroxyl, and exposing the
CC product to a composition which concurrently oxidizes the phosphate formed
CC to a phosphate and deprotects the protected hydroxyl of the second
CC nucleoside. The method is useful for synthesizing the polynucleotides,
CC for carrying out either 3' to 5' or 5' to 3' synthesis and for
CC fabricating an addressable array of polynucleotides on a substrate. The
CC present sequence is an oligonucleotide produced to demonstrate the method
CC of the invention
XX
XX Sequence 20 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
XX ||||||||||||||||||
XX DB 20 AAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 157
XX ABL36232
XX ID ABL36232 standard; DNA; 20 BP.
XX
XX ABL36232;
XX
XX 08-APR-2002 (first entry)
XX
XX M tuberculosis rRNA probe SEQ ID NO: 83.
XX
XX Skin disorder; psoriasis; atopic dermatitis; allergic contact dermatitis;
KW alopecia areata; skin cancer; Mycobacterium vaccae; melanoma; cytostatic;
KW antipsoriatic; dermatological; antiinflammatory; antiallergic;
KW Th2 immune response; immunomodulatory; probe; ss.
XX
XX Mycobacterium tuberculosis.
XX
XX US6328978-B1.
XX
```

```
XX 11-DEC-2001.
XX
XX 02-JUN-1999; 99US-00324542.
XX
XX 23-DEC-1997; 97US-00997080.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Tan PLJ, Prestidge R;
XX
XX WPI; 2002-138361/18.
XX
XX Inhibiting skin inflammation associated with skin disorder e.g.
PT psoriasis, by administering composition comprising delipidated and
PT deglycolipidated Mycobacterium vaccae cells or Mycobacterium vaccae
PT culture filtrate.
XX
XX Example 5; Col 99-100; 116pp; English.
XX
XX The present invention relates to a method of inhibiting skin inflammation
CC associated with a skin disorder selected from psoriasis, atopic
CC dermatitis and allergic contact dermatitis, which involves administering
CC a composition containing delipidated and deglycolipidated Mycobacterium
CC vaccae cells or M. vaccae culture filtrate. The skin disorder to be
CC treated may also include alopecia areata, and skin cancers such as basal
CC cell carcinoma, squamous cell carcinoma and melanoma. The composition
CC acts by inhibiting the Th2 immune response. The present sequence is a
CC probe described in the exemplification of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
XX ||||||||||||||||||
XX DB 1 AAAAAAAAAAAAAAAAAAAAAA 20
XX
XX RESULT 158
XX ABS64673
XX ID ABS64673 standard; DNA; 20 BP.
XX
XX ABS64673;
XX
XX 15-NOV-2002 (first entry)
XX
XX Nucleic acid detection method associated polynucleotide #55.
XX
XX Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW nanoparticle; viral RNA detection; bacterial DNA detection;
KW fungal DNA detection; nanoprobe conjugate; ss.
XX
XX Synthetic.
XX
XX WO200246472-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-US046418.
XX
XX 08-DEC-2000; 2000US-0254392P.
XX
XX 08-DEC-2000; 2000US-0254418P.
XX
XX 11-DEC-2000; 2000US-0255235P.
XX
XX 11-DEC-2000; 2000US-0255236P.
XX
XX 12-JAN-2001; 2001US-00760500.
XX
XX 28-MAR-2001; 2001US-00820279.
XX
XX 09-APR-2001; 2001US-0282640P.
XX
XX 10-AUG-2001; 2001US-00927777.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX
```

```

XX  Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI  Taton TA, Garimella V, Li Z, Park S;
XX  WPI; 2002-608256/65.
XX
PT  Detecting nucleic acid having two portions, by providing nanoparticles
PT  having oligonucleotides attached to it, contacting nucleic acid and
XX  nanoparticles to allow hybridization, and observing detectable change.
XX
PS  Example 18; Page 437; 442pp; English.
XX
CC  The invention describes a method of detecting (M1) a nucleic acid having
CC  two portions, involving providing nanoparticles having oligonucleotides
CC  attached to it, which has a sequence complementary to sequence of two
CC  portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC  allow hybridisation of oligonucleotides with two or more portions of
CC  nucleic acid, and observing a detectable change brought about by
CC  hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC  conjugates (II) and the aggregate probe are useful for detecting two or
CC  more nucleic acids (from a biological source) having at least two
CC  portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC  with a disease, synthetic, or structurally-modified natural or synthetic
CC  RNA or DNA, or a product of a polymerase chain reaction amplification.
CC  (II) is useful for preparing a nanoprobe conjugate for detecting an
CC  analyte, and for detecting a nucleic acid bound to an electrode surface.
CC  (I) and (II) are useful for fabricating, and for separating a selected
CC  nucleic acid having two portions from other nucleic acids. (I), (II) and
CC  the aggregate probe are useful for detecting an analyte (especially
CC  polivalent analyte) in a sample. This sequence represents a
CC  polynucleotide used to demonstrate the method of the invention
XX
SQ  Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
    Query Match      1.1%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db  1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 159
AB564688
ID  ABS64688 standard; DNA; 20 BP.
XX
AC  ABS64688;
XX
DT  15-NOV-2002 (first entry)
XX
DE  Nucleic acid detection method associated polynucleotide #70.
XX
KW  Nucleic acid detection method; nanoparticle-oligonucleotide conjugate;
KW  nanoparticle; viral RNA detection; bacterial DNA detection;
KW  fungal DNA detection; nanoprobe conjugate; ss.
XX
OS  Synthetic.
XX
PN  WO200246472-A2.
XX
PD  13-JUN-2002.
XX
PF  07-DEC-2001; 2001WO-US046418.
XX
PR  08-DEC-2000; 2000US-0254392P.
PR  08-DEC-2000; 2000US-0254418P.
PR  11-DEC-2000; 2000US-0255235P.
PR  11-DEC-2000; 2000US-0255236P.
PR  12-JAN-2001; 2001US-00760500.
PR  28-MAR-2001; 2001US-00820279.
PR  09-APR-2001; 2001US-0282640P.
PR  10-AUG-2001; 2001US-00927777.

```

```

XX  (NANO-) NANOSPHERE INC.
XX  Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI  Taton TA, Garimella V, Li Z, Park S;
XX  WPI; 2002-608256/65.
XX
PT  Detecting nucleic acid having two portions, by providing nanoparticles
PT  having oligonucleotides attached to it, contacting nucleic acid and
XX  nanoparticles to allow hybridization, and observing detectable change.
XX
PS  Example 24; Fig 44; 442pp; English.
XX
CC  The invention describes a method of detecting (M1) a nucleic acid having
CC  two portions, involving providing nanoparticles having oligonucleotides
CC  attached to it, which has a sequence complementary to sequence of two
CC  portions of nucleic acid, contacting nucleic acid and nanoparticles, to
CC  allow hybridisation of oligonucleotides with two or more portions of
CC  nucleic acid, and observing a detectable change brought about by
CC  hybridisation. (M1), nanoparticles (I), nanoparticle-oligonucleotide
CC  conjugates (II) and the aggregate probe are useful for detecting two or
CC  more nucleic acids (from a biological source) having at least two
CC  portions, such as viral RNA, bacterial or fungal DNA, a gene associated
CC  with a disease, synthetic, or structurally-modified natural or synthetic
CC  RNA or DNA, or a product of a polymerase chain reaction amplification.
CC  (II) is useful for preparing a nanoprobe conjugate for detecting an
CC  analyte, and for detecting a nucleic acid bound to an electrode surface.
CC  (I) and (II) are useful for fabricating, and for separating a selected
CC  nucleic acid having two portions from other nucleic acids. (I), (II) and
CC  the aggregate probe are useful for detecting an analyte (especially
CC  polivalent analyte) in a sample. This sequence represents a
CC  polynucleotide used to demonstrate the method of the invention
XX
SQ  Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
    Query Match      1.1%; Score 20; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 1.6e+02;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db  1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 160
ABN87103/c
ID  ABN87103 standard; DNA; 20 BP.
XX
AC  ABN87103;
XX
DT  30-JUL-2002 (first entry)
XX
DE  Capture probe CP5' SEQ ID NO:23.
XX
KW  Protein scaffold; antibody; binding protein; immunoglobulin;
KW  tumour necrosis factor alpha; TNF-alpha; protein framework; probe; ss.
XX
OS  Synthetic.
XX
PN  WO200232925-A2.
XX
PD  25-APR-2002.
XX
PF  16-OCT-2001; 2001WO-US032233.
XX
PR  16-OCT-2000; 2000US-00688566.
XX  (PHYL-) PHYLLOS INC.
XX  Lipovsek D, Wagner RW, Kuimelis RG;
XX  WPI; 2002-444238/47.

```

XX New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.

PS Disclosure; Page 58; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 161

ID ABZ88267
XX ABZ88267 standard; DNA; 20 BP.

AC ABZ88267;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

PD 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

DR WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 3509; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: the sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 162

ID ABZ88565

XX ABZ88565 standard; DNA; 20 BP.

AC ABZ88565;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

PD 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

PA (EPIG-) EPIGENESIS PHARM INC.

PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX
 PS Disclosure; SEQ ID NO 4123; 872pp; English.
 XX
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, for reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 167
 ABZ89706
 ID ABZ89706 standard; DNA; 20 BP.
 XX
 AC ABZ89706;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 PN
 XX
 PD 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX
 PS Disclosure; SEQ ID NO 4948; 872pp; English.
 XX
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, for reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 |||||
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 168
 ABZ88620
 ID ABZ88620 standard; DNA; 20 BP.
 XX
 AC ABZ88620;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 PN
 XX
 PD 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX
 PS Disclosure; SEQ ID NO 3862; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 169
 ABZ88814
 ID ABZ88814 standard; DNA; 20 BP.
 XX
 AC ABZ88814;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX
 PS Disclosure; SEQ ID NO 4056; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 170
 ABZ89241
 ID ABZ89241 standard; DNA; 20 BP.
 XX
 AC ABZ89241;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

Disclosure; SEQ ID NO 5892; 872pp; English.

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 172

ABZ88618
ID ABZ88618 standard; DNA; 20 BP.

AC ABZ88618;

DT 17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antiseense; lung dysfunction; nasal airway dysfunction;
antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
antisthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
antiseense gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 3860; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 1 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1754
DB 1 CAAAAA...AAAAA 20

RESULT 173
ABZ88815
ID ABZ88815 standard; DNA; 20 BP.
XX
AC ABZ88815;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4057; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAA...AAAAA 1755
DB 1 AAAAAA...AAAAA 20

RESULT 174
ABZ85311/c
ID ABZ85311 standard; DNA; 20 BP.
XX
AC ABZ85311;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

```

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Claim 15; SEQ ID NO 553; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 175
ABZ85435/c
ID ABZ85435 standard; DNA; 20 BP.
XX
XX ABZ85435;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI

```

```

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Claim 15; SEQ ID NO 677; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 176
ABZ88817
ID ABZ88817 standard; DNA; 20 BP.
XX
XX ABZ88817;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI

```

PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 4059; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences)
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX

```

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
       ||| ||||| ||||| ||||| |||||
Db      1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 177
ABZ88939
ID ABZ88939 standard; DNA; 20 BP.
XX AC
XX AC
XX AC
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antischismatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
PI Nvce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

```

PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4181; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 XX
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 XX
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 DB 1 AAAAAAAAAAAAAAAAAAAAAA 20
 XX
 RESULT 178
 ABZ89302
 ID ABZ89302 standard; DNA; 20 BP.
 XX
 AC ABZ89302;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 FN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D;

```
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 4544; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
XX | | | | | | | | | | | | | | | |
XX Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
XX
XX RESULT 179
XX ABZ88566
XX ID ABZ88566 standard; DNA; 20 BP.
XX
XX AC ABZ88566;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX FN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
```

```
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 3808; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
XX | | | | | | | | | | | | | | | |
XX Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
XX
XX RESULT 180
XX ABZ89086
XX ID ABZ89086 standard; DNA; 20 BP.
XX
XX AC ABZ89086;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX FN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
```

Miller S, Tang L, Shahabuddin S;
WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(e) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 4328; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.

Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
    | | | | | | | | | | | | | | | |
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 181
ABZ85533
ID ABZ85533 standard; DNA; 20 BP.
XX AC ABZ85533;
XX XX
DT 17-OCT-2003 (first entry)
XX XX
DE Human oligonucleotide sequence.
XX XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX XX
OS Homo sapiens.
XX XX
PN WO200285308-A2.
XX XX
PD 31-OCT-2002.
XX XX
PP 23-APR-2002; 2002WO-US013135.
XX XX
PR 24-APR-2001; 2001US-0286137P.
XX XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

```

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Claim 15; SEQ ID NO 775; 872pp; English.
PS
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 182
ABZ89015
ID ABZ89015 standard; DNA; 20 BP.
XX
XX AC ABZ89015;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nvce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Disclosure; SEQ ID NO 4257; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 183
 ABZ89441
 ID ABZ89441 standard; DNA; 20 BP.
 XX
 AC ABZ89441;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 XX
 XX 24-APR-2001; 2001US-0286137P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Disclosure; SEQ ID NO 4683; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 184
 ABZ89016
 ID ABZ89016 standard; DNA; 20 BP.
 XX
 AC ABZ89016;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013135.
 XX
 XX 24-APR-2001; 2001US-0286137P.
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4946; 872pp; English.
 XX
 XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1755
 DB 1 AAAAAAAAAAAAAAAAAA 20
 RESULT 187
 ACD27320
 ID ACD27320 standard; DNA; 20 BP.
 XX
 AC ACD27320;
 XX
 DT 15-OCT-2003 (first entry)
 XX
 DE Nanotechnology nucleic acid detection method associated #54.
 XX
 KW Nanotechnology; ss; nucleic acid detection; nanoparticle;
 KW virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
 KW cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
 KW sexually transmitted disease; inherited disorder; forensic;
 KW paternity testing; cell line authentication.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 modified_base 1
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "OTHER= Thiol modified" "
 XX
 FN US2002155461-A1.
 XX
 PD 24-OCT-2002.
 XX
 XX 12-OCT-2001; 2001US-00976378.
 PF
 XX

PR 29-JUL-1996; 96US-0031809P.
 PR 21-JUL-1997; 97WO-US012783.
 PR 29-JAN-1999; 99US-00240755.
 PR 25-JUN-1999; 99US-00344667.
 PR 26-APR-2000; 2000US-0200161P.
 PR 26-JUN-2000; 2000US-00603830.
 XX
 PA (NANO-) NANOSPHERE INC.
 XX
 XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 PI Taton TA;
 XX
 XX WPI; 2003-228115/22.
 DR
 XX
 PT Detecting nucleic acids having 2 portions e.g. for detecting disease,
 PT comprises use of nanoparticles which have oligonucleotides attached to
 PT them that are complementary to portions of the nucleic acid sequence.
 XX
 FS Example 18; Page 44; 130pp; English.
 XX
 CC This invention relates to a novel method for detecting a nucleic acid
 CC having 2 portions. The method comprises providing nanoparticles having
 CC oligonucleotides attached, where the oligonucleotide on each nanoparticle
 CC has a sequence complementary to a sequence of 2 portions of nucleic acid.
 CC The nucleic acid and nanoparticle are contacted to allow hybridisation of
 CC the oligonucleotide on the nanoparticle with two or more portions of
 CC nucleic acid and observing a detectable change brought about by the
 CC hybridisation. The method of the invention is useful for separating a
 CC selected nucleic acid having 2 portions, from other nucleic acids, and
 CC for detecting nucleic acids having 2 portions. The method of the
 CC invention is useful for detecting any type of nucleic acids which may be
 CC used for diagnosis of disease and in sequencing of nucleic acids.
 CC Preferably, the method is useful for detecting nucleic acids for
 CC diagnosis and/or monitoring of viral diseases (human immunodeficiency
 CC virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
 CC virus), bacterial diseases, sexually transmitted diseases, inherited
 CC disorders, in forensics, in DNA sequencing, for paternity testing, for
 CC cell line authentication, for monitoring gene therapy, etc. This method
 CC involves detecting nucleic acids based on observing a colour change with
 CC the naked eye so is cheap, fast, simple and robust, and does not require
 CC specialised expensive equipment. The present sequence represents a thiol
 CC modified oligonucleotide sequence used to demonstrate the method of the
 CC invention
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1755
 DB 1 AAAAAAAAAAAAAAAAAA 20
 RESULT 188
 ACC82890/c
 ID ACC82890 standard; DNA; 20 BP.
 XX
 AC ACC82890;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198762.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1, phosphothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX

```

FH Key      Location/Qualifiers
FT modified_base 1..20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT modified_base 1..5
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN WO2003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 76; 11pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 124 TTCAGACCGCTGCTCGGAG 143
DB 20 TTCAGACCGCTGCTCGGAG 1
|||||
RESULT 189
ACC82896/c
ID ACC82896 standard; DNA; 20 BP.
XX
XX ACC82896;
XX
XX 27-AUG-2003 (first entry)
DE Human TRIP6 antisense oligonucleotide ISIS #198768.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW

```

```

KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX Homo sapiens.
OS Synthetic.
XX
FH Key      Location/Qualifiers
FT modified_base 1..20
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT modified_base 1..5
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN WO2003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 76; 11pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 8 G; 2 T; 0 U; 0 Other;
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 418 GGCCTTCGCCCTCGGAAGCCT 437
DB 20 GGCCTTCGCCCTCGGAAGCCT 1
|||||
RESULT 190
ACC82919/c
ID ACC82919 standard; DNA; 20 BP.
XX
XX ACC82919;
XX
XX 27-AUG-2003 (first entry)
DT
XX

```

DE Human TRIP6 antisense oligonucleotide ISIS #198791.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

OS Homo sapiens.
 OS Synthetic.

PH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone; All cytidine residues
 are 5-methylcytidines"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

PN 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

XX Example 15; Page 77; ilpp; English.

XX The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX Sequence 20 BP; 4 A; 7 C; 6 G; 3 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.1%; Score 20; DB 1; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1201 GACCGATCTCGGGCTAT 1220

DB 20 GACCGATCTCGGGCTAT 1

|||||

RESULT 191

ACC82889/c

ID ACC82889 standard; DNA; 20 BP.

XX ACC82889;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198761.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

OS Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT modified_base 1..20

FT /*tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone; All cytidine residues
 are 5-methylcytidines"

FT modified_base 1..5

FT /*tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /*tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

PN 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789;

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

XX Example 15; Page 76; ilpp; English.

XX The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX Sequence 20 BP; 8 A; 3 C; 3 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.1%; Score 20; DB 1; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 46 GCCAGAAAAAGTTTCTTTT 65

DB 20 GCCAGAAAAAGTTTCTTTT 1

|||||

```
RESULT 192
ACC82907/c
ID ACC82907 standard; DNA; 20 BP.
XX
XX ACC82907;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198779.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone; All cytidine residues
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 76; 11pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 973 AGCGGGGAGTACTTTGGCCA 992
DB 20 AGCGGGGAGTACTTTGGCCA 1.
RESULT 193
ACC82911/c
ID ACC82911 standard; DNA; 20 BP.
XX
XX ACC82911;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198783.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate backbone; All cytidine residues
XX modified_base 1..5
XX /tag= b
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX modified_base 16..20
XX /tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 11pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
```

XX SQ Sequence 20 BP; 9 A; 7 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1063 GTGGCTCCTTTGATGTC 1082
 |||||
 Db 20 GTGGCTCCTTTGATGTC 1

RESULT 194
 ACC82897/c
 ID ACC82897 standard; DNA; 20 BP.
 XX
 AC ACC82897;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198769.
 XX
 KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone; All cytidine residues
 FT /note= "5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 WO2003040328-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 05-NOV-2002; 2002WO-US035479.
 XX
 PR 08-NOV-2001; 2001US-00008789.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dobie K;
 XX
 DR WPI; 2003-430662/40.
 XX
 PS Example 15; Page 76; 11pp; English.
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.

CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 443 CCGAGATAGACTTGCTGAGC 462
 |||||
 Db 20 CCGAGATAGACTTGCTGAGC 1

RESULT 195
 ACC82900/c
 ID ACC82900 standard; DNA; 20 BP.
 XX
 AC ACC82900;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198772.
 XX
 KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone; All cytidine residues
 FT /note= "5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 WO2003040328-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 05-NOV-2002; 2002WO-US035479.
 XX
 PR 08-NOV-2001; 2001US-00008789.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dobie K;
 XX
 DR WPI; 2003-430662/40.
 XX
 PS New antisense oligonucleotides targetted to nucleic acids encoding thyroid
 CC hormone receptor interacto 6, useful for diagnosing or treating
 CC hyperproliferative disorders, such as cancer.
 XX
 PS Claim 3; Page 76; 11pp; English.
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.

CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targeted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 2 A; 3 C; 9 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 568 AAGCCAAATCCAGCTCGCC 587
DB 20 AAGCCAAATCCAGCTCGCC 1
RESULT 196
ACC82905/c
ID ACC82905 standard; DNA; 20 BP.
XX
AC ACC82905;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198777.
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
DR WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX

PS Example 15; Page 76; 11pp; English.
XX
CC The invention relates to antisense compounds targeted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targeted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 3 A; 9 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 830 AAGAGGAAGCTGCTGGGCTC 849
DB 20 AAGAGGAAGCTGCTGGGCTC 1
RESULT 197
ACC82909/c
ID ACC82909 standard; DNA; 20 BP.
XX
AC ACC82909;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198781.
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
DR WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
PS Example 15; Page 76; 111pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 6 A; 9 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1030 GCTGGGGTTGTGGCCCTTGA 1049
|||||
Db 20 GCTGGGGTTGTGGCCCTTGA 1
|||||

RESULT 198
ACCC82929/c
ID ACC82929 standard; DNA; 20 BP.
XX ACC82929;
XX
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198801.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
PN
XX
PD 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX

(ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX MPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
PS Example 15; Page 77; 111pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 1 A; 9 C; 4 G; 6 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1384 GAGCCAGGTCAGGAGGAGAC 1403
|||||
Db 20 GAGCCAGGTCAGGAGGAGAC 1
|||||

RESULT 199
ACCC82910/c
ID ACC82910 standard; DNA; 20 BP.
XX ACC82910;
XX
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198782.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
PN
XX
PD 15-MAY-2003.
XX

```
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PI Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 77; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 8 A; 6 C; 5 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1054 GTCCTTCACGTGGGCTGCTT 1073
DB 20 GTCCTTCACGTGGGCTGCTT 1
RESULT 200
ACC82921/c
ID ACC82921 standard; DNA; 20 BP.
XX
XX ACC82921;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198793.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides".
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT
```

```
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX PI Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 5 A; 8 C; 6 G; 1 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1255 GTGGTGTCACCGCGGCT 1274
DB 20 GTGGTGTCACCGCGGCT 1
RESULT 201
ACC82899/c
ID ACC82899 standard; DNA; 20 BP.
XX
XX ACC82899;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198771.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT
```

FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= C
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

PN 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

PS Claim 3; Page 76; 11pp; English.

XX The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX Sequence 20 BP; 2 A; 6 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 552 CCGCAGCGGCTCCCTGAAGC 571

Db 20 CCGCAGCGGCTCCCTGAAGC 1

RESULT 202

ACC82920/C

ID ACC82920 standard; DNA; 20 BP.

XX ACC82920;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198792.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

/*tag= a

FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= C
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

PS Claim 3; Page 77; 11pp; English.

XX The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX Sequence 20 BP; 6 A; 6 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1247 TCACCTCGGTGGTGTGCAC 1266

Db 20 TCACCTCGGTGGTGTGCAC 1

RESULT 203

ACC82922/C

ID ACC82922 standard; DNA; 20 BP.

XX ACC82922;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198794.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

```

OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX Claim 3; Page 77; 11lpp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
QY 1292 CAGTGGATGCTACGAGCCAG 1311
DB 20 CAGTGGATGCTACGAGCCAG 1
RESULT 204
ID ACC82951/c
XX ACC82951 standard; DNA; 20 BP.
XX ACC82951;
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198823.
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX chromosome 7q22; ZRP-1; phosphorothioate; ss.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX Claim 3; Page 77; 11lpp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX Sequence 20 BP; 7 A; 3 C; 6 G; 4 T; 0 U; 0 Other;
QY 1664 ACCTGTATGACTTTGTTCACC 1683
DB 20 ACCTGTATGACTTTGTTCACC 1
RESULT 205
ID ACC82952/c
XX ACC82952 standard; DNA; 20 BP.
XX ACC82952;
XX ACC82952;

```

DT 27-AUG-2003 (first entry)
DE Human TRIP6 antisense oligonucleotide ISIS #198824.
XX
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT
FT
PN WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 9 A; 2 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1683 CAATGCTGCTCTCTCTTC 1702
Db 20 CAATGCTGCTCTCTCTTC 1

RESULT 206

ACC82953/c
ID ACC82953 standard; DNA; 20 BP.
XX
AC ACC82953;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198825.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT
FT
PN WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 77; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 5 A; 1 C; 5 G; 9 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1708 TCAAGAAATAATATCCCTC 1727

```

DB      20 TCAAGAAATAATAATCCCTC 1
|||||
RESULT 207
ACC82881
ID      ACC82881 standard; DNA; 20 BP.
AC      ACC82881;
XX
XX      27-AUG-2003 (first entry)
XX
DE      Human TRIP6 DNA specific forward PCR primer.
KW      Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW      OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW      inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW      chromosome 7q22; ZRP-1; PCR; primer; ss.
OS      Homo sapiens.
XX
XX      WO2003040328-A2.
PN
XX
PD      15-MAY-2003.
XX
XX      05-NOV-2002; 2002WO-US035479.
PF
XX
XX      08-NOV-2001; 2001US-00008789.
PR
XX
XX      (ISIS-) ISIS PHARM INC.
PA
XX
XX      Bennett CF, Dobie K;
PI
XX
XX      WPI; 2003-430662/40.
DR
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT      hormone receptor interactor 6, useful for diagnosing or treating
PT      hyperproliferative disorders, such as cancer.
PS      Example 13; Page 74; 111pp; English.
XX
XX      The invention relates to antisense compounds targetted to a nucleic acid
CC      encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC      expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC      zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC      Antisense compounds of the invention are useful for modulating the
CC      expression of TRIP6 and for treating diseases or conditions associated
CC      with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC      cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC      to prevent or delay infection, inflammation or tumour formation, as
CC      research reagents and kits and in distinguishing between functions of
CC      various members of a biological pathway. The are also useful in antisense
CC      therapy. The present sequence is human TRIP6 DNA specific PCR primer,
CC      used in the exemplification of the invention
XX
XX      Sequence 20 BP; 4 A; 2 C; 9 G; 5 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1001 GCTGGGAGAGATGTGGTT 1020
|||||
DB      1 GCTGGGAGAGATGTGGTT 20
|||||

RESULT 208
ACC82901/c
ID      ACC82901 standard; DNA; 20 BP.
XX
XX      ACC82901;
AC
XX
XX      27-AUG-2003 (first entry)
DT

```

```

XX      Human TRIP6 antisense oligonucleotide ISIS #198773.
DE
XX
KW      Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW      OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW      inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW      chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX      Homo sapiens.
OS
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
FH      modified_base 1..20
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX      WO2003040328-A2.
PN
XX
XX      15-MAY-2003.
PD
XX
XX      05-NOV-2002; 2002WO-US035479.
PF
XX
XX      08-NOV-2001; 2001US-00008789.
PR
XX
XX      (ISIS-) ISIS PHARM INC.
PA
XX
XX      Bennett CF, Dobie K;
PI
XX
XX      WPI; 2003-430662/40.
DR
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT      hormone receptor interactor 6, useful for diagnosing or treating
PT      hyperproliferative disorders, such as cancer.
PS      Example 15; Page 76; 111pp; English.
XX
XX      The invention relates to antisense compounds targetted to a nucleic acid
CC      encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC      expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC      zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC      Antisense compounds of the invention are useful for modulating the
CC      expression of TRIP6 and for treating diseases or conditions associated
CC      with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC      cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC      to prevent or delay infection, inflammation or tumour formation, as
CC      research reagents and kits and in distinguishing between functions of
CC      various members of a biological pathway. The are also useful in antisense
CC      therapy. The present sequence is an antisense oligo targetted to human
CC      TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX      Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      714 GCGGGAGCCTCTCAGGCTT 733
|||||
DB      20 GCGGGAGCCTCTCAGGCTT 1
|||||

RESULT 209
ACC82904/c

```

ID ACC82904 standard; DNA; 20 BP.
 XX AC ACC82904;
 XX DT 27-AUG-2003 (first entry)
 XX DE Human TRIP6 antisense oligonucleotide ISIS #198776.
 XX KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX WO2003040328-A2.
 XX PN 15-MAY-2003.
 XX PD 05-NOV-2002; 2002WO-US035479.
 XX PF 08-NOV-2001; 2001US-00008789.
 XX PR (ISIS-) ISIS PHARM INC.
 XX PA Bennett CF, Dobie K;
 XX PI WPI; 2003-430662/40.
 XX DR New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 XX hormone receptor interactor 6, useful for diagnosing or treating
 XX hyperproliferative disorders, such as cancer.
 XX PS Claim 3; Page 76; 11pp; English.
 XX CC The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX Sequence 20 BP; 1 A; 7 C; 4 G; 8 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB-1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 797 ATAGGAGCCAGAGAGCCA 816
 ||||||||||||||||

Db 20 ATAGGAGCCAGAGAGCCA 1
 RESULT 210
 ACC82912/c
 ID ACC82912 standard; DNA; 20 BP.
 XX AC ACC82912;
 XX DT 27-AUG-2003 (first entry)
 XX DE Human TRIP6 antisense oligonucleotide ISIS #198784.
 XX KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX WO2003040328-A2.
 XX PN 15-MAY-2003.
 XX PD 05-NOV-2002; 2002WO-US035479.
 XX PF 08-NOV-2001; 2001US-00008789.
 XX PR (ISIS-) ISIS PHARM INC.
 XX PA Bennett CF, Dobie K;
 XX PI WPI; 2003-430662/40.
 XX DR New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 XX hormone receptor interactor 6, useful for diagnosing or treating
 XX hyperproliferative disorders, such as cancer.
 XX PS Claim 3; Page 77; 11pp; English.
 XX CC The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB-1; Length 20;

```
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1073 TTGTATGTTCTACATGCCGG 1092
    |||||
Db 20 TTGTATGTTCTACATGCCGG 1

RESULT 211
ACC82939/c
ID ACC82939 standard; DNA; 20 BP.
XX
AC ACC82939;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198811.
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
DR WPI; 2003-430662/40.
XX
PS New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
Example 15; Page 77; 11pp; English.
XX
The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present invention is an antisense oligo targetted to human
```

```
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1508 CGCTGGATGGGCACATCTTG 1527
    |||||
Db 20 CGCTGGATGGGCACATCTTG 1

RESULT 212
ACC82892/c
ID ACC82892 standard; DNA; 20 BP.
XX
AC ACC82892;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198764.
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
XX Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
DR WPI; 2003-430662/40.
XX
PS New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
Example 15; Page 76; 11pp; English.
XX
The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present invention is an antisense oligo targetted to human
```


CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 1 A; 5 C; 9 G; 5 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 259 CACGGAGCAGCACTCCAGCC 278
 Db 20 CACGGAGCAGCACTCCAGCC 1
 RESULT 213
 ACC82916/C
 ID ACC82916 standard; DNA; 20 BP.
 XX
 AC ACC82916;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198788.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FN WO2003040328-A2.
 XX
 PD 15-MAY-2003.
 XX
 PP 05-NOV-2002; 2002WO-US035479.
 XX
 PR 08-NOV-2001; 2001US-00008789.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Bennett CF, Dobie K;
 XX WPI; 2003-430662/40.
 DR
 XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.
 XX
 PS Example 15; Page 77; 11pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its

CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 3 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1156 GTGCCACCCCTGGAGAAATG 1175
 Db 20 GTGCCACCCCTGGAGAAATG 1
 RESULT 214
 ACC82925/C
 ID ACC82925 standard; DNA; 20 BP.
 XX
 AC ACC82925;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198797.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FN WO2003040328-A2.
 XX
 PD 15-MAY-2003.
 XX
 PP 05-NOV-2002; 2002WO-US035479.
 XX
 PR 08-NOV-2001; 2001US-00008789.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA Bennett CF, Dobie K;
 XX WPI; 2003-430662/40.
 DR
 XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

XX Claim 3; Page 77; 111pp; English.

XX The invention relates to antisense compounds targetted to a nucleic acid

CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its

CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and

CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.

CC Antisense compounds of the invention are useful for modulating the

CC expression of TRIP6 and for treating diseases or conditions associated

CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.

CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.

CC to prevent or delay infection, inflammation or tumour formation, as

CC research reagents and kits and in distinguishing between functions of

CC various members of a biological pathway. The are also useful in antisense

CC therapy. The present sequence is an antisense oligo targetted to human

CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX

SQ Sequence 20 BP; 6 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1328 ACTTTCACAGGAAGTTTGCC 1347

DB 20 ACTTTCACAGGAAGTTTGCC 1

RESULT 215

ACC82926/c

ID ACC82926 standard; DNA; 20 BP.

XX ACC82926;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198798.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;

XX OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;

XX inflammation; therapy; hyperproliferative disorder; infection; cancer;

XX chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

XX Synthetic.

PH Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT are 5-methylcytidines"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT are 5-methylcytidines"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX

DR WPI; 2003-430662/40.

XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid

PT hormone receptor interactor 6, useful for diagnosing or treating

PT hyperproliferative disorders, such as cancer.

XX Claim 3; Page 77; 111pp; English.

PS The invention relates to antisense compounds targetted to a nucleic acid

CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its

CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and

CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.

CC Antisense compounds of the invention are useful for modulating the

CC expression of TRIP6 and for treating diseases or conditions associated

CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.

CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.

CC to prevent or delay infection, inflammation or tumour formation, as

CC research reagents and kits and in distinguishing between functions of

CC various members of a biological pathway. The are also useful in antisense

CC therapy. The present sequence is an antisense oligo targetted to human

CC TRIP6 DNA. This oligo is used in the exemplification of the invention

XX

SQ Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 CAGTGTGCGTGGGCCCATTA 1377

DB 20 CAGTGTGCGTGGGCCCATTA 1

RESULT 216

ACC82938/c

ID ACC82938 standard; DNA; 20 BP.

XX ACC82938;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198810.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;

XX OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;

XX inflammation; therapy; hyperproliferative disorder; infection; cancer;

XX chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

XX Synthetic.

PH Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER

FT /note= "Phosphorothioate backbone; All cytidine residues

FT are 5-methylcytidines"

FT modified_base 1..5

FT /tag= b

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT /tag= c

FT /mod_base= OTHER

FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX

```
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dobie K;
XX PR WPI; 2003-430662/40.
XX DR
XX PA New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX PT hormone receptor interactor 6, useful for diagnosing or treating
XX PT hyperproliferative disorders, such as cancer.
XX PS Claim 3; Page 77; 111pp; English.
XX CC The invention relates to antisense compounds targetted to a nucleic acid
XX CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX CC Antisense compounds of the invention are useful for modulating the
XX CC expression of TRIP6 and for treating diseases or conditions associated
XX CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX CC to prevent or delay infection, inflammation or tumour formation, as
XX CC research reagents and kits and in distinguishing between functions of
XX CC various members of a biological pathway. They are also useful in antisense
XX CC therapy. The present sequence is an antisense oligo targetted to human
XX CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1507 CCGCTGGATGGGCACATCTT 1526
DB 20 CCGCTGGATGGGCACATCTT 1
RESULT 217
ACCG82941/C
ID ACC82941 standard; DNA; 20 BP.
XX AC ACC82941;
XX DT 27-AUG-2003 (first entry)
XX DE Human TRIP6 antisense oligonucleotide ISIS #198813.
XX KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT FT 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX FT
XX PN WO2003040328-A2.
XX FT
```

```
PD 15-MAY-2003.
XX 05-NOV-2002; 2002MO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dobie K;
XX DR WPI; 2003-430662/40.
XX PT New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX PT hormone receptor interactor 6, useful for diagnosing or treating
XX PT hyperproliferative disorders, such as cancer.
XX PS Claim 3; Page 77; 111pp; English.
XX CC The invention relates to antisense compounds targetted to a nucleic acid
XX CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX CC Antisense compounds of the invention are useful for modulating the
XX CC expression of TRIP6 and for treating diseases or conditions associated
XX CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX CC to prevent or delay infection, inflammation or tumour formation, as
XX CC research reagents and kits and in distinguishing between functions of
XX CC various members of a biological pathway. They are also useful in antisense
XX CC therapy. The present sequence is an antisense oligo targetted to human
XX CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX SQ Sequence 20 BP; 5 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;
QY 1523 TCTTGTGCAAGGCTGCAGC 1542
DB 20 TCTTGTGCAAGGCTGCAGC 1
RESULT 218
ACCG82945/C
ID ACC82945 standard; DNA; 20 BP.
XX AC ACC82945;
XX DT 27-AUG-2003 (first entry)
XX DE Human TRIP6 antisense oligonucleotide ISIS #198817.
XX KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT FT 16..20
FT /tag= c
FT modified_base
```

```
FT FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN WO2003040328-A2.
XX PD 15-MAY-2003.
XX PF 05-NOV-2002; 2002WO-US035479.
XX PR 08-NOV-2001; 2001US-00008789.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 77; 11lpp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 4 A; 4 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1571 CCGTCACCACTGACTGCTGA 1590
DB 20 CCGTCACCACTGACTGCTGA 1
RESULT 219
ACC82948/c
ID ACC82948 standard; DNA; 20 BP.
XX
XX ACC82948;
XX
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198820.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT FT /tag= a
FT FT /mod_base= OTHER
FT FT /note= "Phosphorothioate backbone; All cytidine residues
FT FT are 5-methylcytidines"
FT modified_base 1..5
```

```
FT FT /*tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX modified_base 15..20
XX FT /*tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX PD 15-MAY-2003.
XX PF 05-NOV-2002; 2002WO-US035479.
XX PR 08-NOV-2001; 2001US-00008789.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 77; 11lpp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 7 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1608 TGCTGGGTTCTCAGTTCAG 1627
DB 20 TGCTGGGTTCTCAGTTCAG 1
RESULT 220
ACC82928/c
ID ACC82928 standard; DNA; 20 BP.
XX
XX ACC82928;
XX
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198800.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT FT
```

```
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT      modified_base
FT      1. .5
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base
FT      16. .20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX      WO2003040328-A2.
XX
XX      15-MAY-2003.
XX
XX      05-NOV-2002; 2002WO-US035479.
XX
XX      08-NOV-2001; 2001US-00008789.
XX      (ISIS-) ISIS PHARM INC.
XX      Bennett CP, Dobie K;
XX      WPI; 2003-430662/40.
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX      hormone receptor interactor 6, useful for diagnosing or treating
XX      hyperproliferative disorders, such as cancer.
XX
XX      Claim 3; Page 77; 11pp; English.
XX
XX      The invention relates to antisense compounds targetted to a nucleic acid
XX      encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX      expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX      zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX      Antisense compounds of the invention are useful for modulating the
XX      expression of TRIP6 and for treating diseases or conditions associated
XX      with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX      cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX      to prevent or delay infection, inflammation or tumour formation, as
XX      research reagents and kits and in distinguishing between functions of
XX      various members of a biological pathway. The are also useful in antisense
XX      therapy. The present sequence is an antisense oligo targetted to human
XX      TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX      Sequence 20 BP; 3 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX
XX      Query Match      1.1%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      1372 GCCAATGCTGCTGAGCCAGG 1391
XX      Db      20 GCCAATGCTGCTGAGCCAGG 1
XX
XX      RESULT 221
XX      ACC82935/c
XX      ID      ACC82935 standard; DNA; 20 BP.
XX
XX      AC      ACC82935;
XX
XX      DT      27-AUG-2003 (first entry)
XX
XX      DE      Human TRIP6 antisense oligonucleotide ISIS #198807.
XX      KW      Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX      OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX      inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX      chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
```

```
OS      Homo sapiens.
OS      Synthetic.
FH      Key
FT      modified_base
FT      1. .20
FT      Location/Qualifiers
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT      modified_base
FT      1. .5
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base
FT      16. .20
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX      WO2003040328-A2.
XX
XX      15-MAY-2003.
XX
XX      05-NOV-2002; 2002WO-US035479.
XX
XX      08-NOV-2001; 2001US-00008789.
XX      (ISIS-) ISIS PHARM INC.
XX      Bennett CP, Dobie K;
XX      WPI; 2003-430662/40.
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX      hormone receptor interactor 6, useful for diagnosing or treating
XX      hyperproliferative disorders, such as cancer.
XX
XX      Example 15; Page 77; 11pp; English.
XX
XX      The invention relates to antisense compounds targetted to a nucleic acid
XX      encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX      expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX      zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX      Antisense compounds of the invention are useful for modulating the
XX      expression of TRIP6 and for treating diseases or conditions associated
XX      with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX      cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX      to prevent or delay infection, inflammation or tumour formation, as
XX      research reagents and kits and in distinguishing between functions of
XX      various members of a biological pathway. The are also useful in antisense
XX      therapy. The present sequence is an antisense oligo targetted to human
XX      TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX      Sequence 20 BP; 6 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
XX
XX      Query Match      1.1%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      1469 TGCTGCTCTCTCTCTGAGGGC 1488
XX      Db      20 TGCTGCTCTCTCTCTGAGGGC 1
XX
XX      RESULT 222
XX      ACC82906/c
XX      ID      ACC82906 standard; DNA; 20 BP.
XX
XX      AC      ACC82906;
XX
XX      DT      27-AUG-2003 (first entry)
XX
XX      DE      Human TRIP6 antisense oligonucleotide ISIS #198778.
XX
```

```
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;  
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;  
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;  
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified_base 1..20 /*tag= a  
FT /mod_base= OTHER  
FT /note= "Phosphorothioate backbone; All cytidine residues  
FT are 5-methylcytidines"  
FT modified_base 1..5 /*tag= b  
FT /mod_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified_base 16..20 /*tag= c  
FT /mod_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
PN WO2003040328-A2.  
XX  
PD 15-MAY-2003.  
XX  
XX 05-NOV-2002; 2002WO-US035479.  
PF  
XX 08-NOV-2001; 2001US-00008789.  
PR  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Bennett CF, Dobie K;  
XX WPI; 2003-430662/40.  
DR  
XX  
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid  
PT hormone receptor interactor 6, useful for diagnosing or treating  
PT hyperproliferative disorders, such as cancer.  
XX  
PS Claim 3; Page 76; 11pp; English.  
XX  
XX The invention relates to antisense compounds targetted to a nucleic acid  
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its  
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and  
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.  
CC Antisense compounds of the invention are useful for modulating the  
CC expression of TRIP6 and for treating diseases or conditions associated  
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.  
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.  
CC to prevent or delay infection, inflammation or tumour formation, as  
CC research reagents and kits and in distinguishing between functions of  
CC various members of a biological pathway. The are also useful in antisense  
CC therapy. The present sequence is an antisense oligo targetted to human  
CC TRIP6 DNA. This oligo is used in the exemplification of the invention  
XX  
SQ Sequence 20 BP; 2 A; 5 C; 9 G; 4 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 899 CCTGAGCCAGCCTCCAGAG 918  
DB 20 CCTGAGCCAGCCTCCAGAG 1  
  
RESULT 223  
ACC82924/c  
ID ACC82924 standard; DNA; 20 BP.  
XX  
AC ACC82924;
```

```
XX  
DT 27-AUG-2003 (first entry)  
XX  
DE Human TRIP6 antisense oligonucleotide ISIS #198796.  
XX  
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;  
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;  
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;  
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified_base 1..20 /*tag= a  
FT /mod_base= OTHER  
FT /note= "Phosphorothioate backbone; All cytidine residues  
FT are 5-methylcytidines"  
FT modified_base 1..5 /*tag= b  
FT /mod_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
FT modified_base 16..20 /*tag= c  
FT /mod_base= OTHER  
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"  
XX  
PN WO2003040328-A2.  
XX  
PD 15-MAY-2003.  
XX  
XX 05-NOV-2002; 2002WO-US035479.  
PF  
XX 08-NOV-2001; 2001US-00008789.  
PR  
XX (ISIS-) ISIS PHARM INC.  
XX  
XX Bennett CF, Dobie K;  
XX WPI; 2003-430662/40.  
DR  
XX  
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid  
PT hormone receptor interactor 6, useful for diagnosing or treating  
PT hyperproliferative disorders, such as cancer.  
XX  
PS Claim 3; Page 77; 11pp; English.  
XX  
XX The invention relates to antisense compounds targetted to a nucleic acid  
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its  
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and  
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.  
CC Antisense compounds of the invention are useful for modulating the  
CC expression of TRIP6 and for treating diseases or conditions associated  
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.  
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.  
CC to prevent or delay infection, inflammation or tumour formation, as  
CC research reagents and kits and in distinguishing between functions of  
CC various members of a biological pathway. The are also useful in antisense  
CC therapy. The present sequence is an antisense oligo targetted to human  
CC TRIP6 DNA. This oligo is used in the exemplification of the invention  
XX  
SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;  
  
Query Match 1.1%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1320 TATTGAGGACTTTCACAGGA 1339  
DB 20 TATTGAGGACTTTCACAGGA 1
```

RESULT 224
 ACC82931/c
 ID ACC82931 standard; DNA; 20 BP.
 XX
 AC ACC82931;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198803.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT
 FT
 PN WO2003040328-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035479.
 XX
 XX 08-NOV-2001; 2001US-00008789.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Dobie K;
 XX
 XX WPI; 2003-430662/40.
 XX
 XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.
 XX
 PS Claim 3; Page 77; 111pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 7 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 1..11; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1405 GTGAGAATTGTTGCTCTGGA 1424
 Db 20 GTGAGAATTGTTGCTCTGGA 1
 RESULT 225
 ACC82932/c
 ID ACC82932 standard; DNA; 20 BP.
 XX
 AC ACC82932;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198804.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT
 FT
 PN WO2003040328-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035479.
 XX
 XX 08-NOV-2001; 2001US-00008789.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Dobie K;
 XX
 XX WPI; 2003-430662/40.
 XX
 XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.
 XX
 PS Claim 3; Page 77; 111pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1410 AATTGTTGCTCGATCGAA 1429
    |||||
    20 AATTGTTGCTCGATCGAA 1
DB

RESULT 226
ACC82937/C
ID ACC82937 standard; DNA; 20 BP.
XX
AC ACC82937;
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198809.
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PP 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
WPI; 2003-430662/40.
XX
PS Claim 3; Page 77; 11pp; English.
XX
CC The invention relates to antisense compounds targeted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
```

```
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targeted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 4 A; 7 C; 7 G; 2 T; 0 U; 0 Other;
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1500 CTGCTACCCGCTGGATGGC 1519
    |||||
    20 CTGCTACCCGCTGGATGGC 1
DB

RESULT 227
ACC82891/C
ID ACC82891 standard; DNA; 20 BP.
XX
AC ACC82891;
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198763.
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PP 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
WPI; 2003-430662/40.
XX
PS Claim 3; Page 76; 11pp; English.
XX
CC The invention relates to antisense compounds targeted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
```


expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. They are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention

Sequence 20 BP; 3 A; 7 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 152 TCAGGCCATGTCGGGCC 171
 Db 20 TCAGGCCATGTCGGGCC 1

RESULT 228
 ACC82923/c

ID ACC82923 standard; DNA; 20 BP.

XX ACC82923;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198795.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"

FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid hormone receptor interactor 6, useful for diagnosing or treating hyperproliferative disorders, such as cancer.

XX Claim 3; Page 77; 11pp; English.

The invention relates to antisense compounds targetted to a nucleic acid encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22. Antisense compounds of the invention are useful for modulating the expression of TRIP6 and for treating diseases or conditions associated with the expression of TRIP6 such as hyperproliferative disorders (e.g. cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g. to prevent or delay infection, inflammation or tumour formation, as research reagents and kits and in distinguishing between functions of various members of a biological pathway. They are also useful in antisense therapy. The present sequence is an antisense oligo targetted to human TRIP6 DNA. This oligo is used in the exemplification of the invention

Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1308 CCAGATCCACTGTATTCGAGG 1327
 Db 20 CCAGATCCACTGTATTCGAGG 1

RESULT 229
 ACC82930/c

ID ACC82930 standard; DNA; 20 BP.

XX ACC82930;

XX 27-AUG-2003 (first entry)

XX Human TRIP6 antisense oligonucleotide ISIS #198802.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"

FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

XX 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

XX WPI; 2003-430662/40.

XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid

```

PT hormone receptor interacto 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
PS Claim 3; Page 77; 11pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 6 A; 7 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1397 AGGAGACTGTGAGATTGTT 1416
DB 20 AGGAGACTGTGAGATTGTT 1
RESULT 230
ACC82944/c
ID ACC82944 standard; DNA; 20 BP.
XX ACC82944;
DT 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198816.
XX
KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2003; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX

```

```

PI Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
PT New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interacto 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
PS Claim 3; Page 77; 11pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1567 GCCACCGTCACCACTGACTG 1586
DB 20 GCCACCGTCACCACTGACTG 1
RESULT 231
ACC82949/c
ID ACC82949 standard; DNA; 20 BP.
XX ACC82949;
XX
DT 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198821.
XX
KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX
PD 15-MAY-2003.
XX
PF 05-NOV-2002; 2002WO-US035479.
XX

```

XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX Claim 3; Page 77; 11pp; English.
XX The invention relates to antisense compounds targeted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targeted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1623 TCCAGTTCCTCCATCCTTGAT 1642
Db 20 TCCAGTTCCTCCATCCTTGAT 1
RESULT 232
ACC82918/C
ID ACC82918 standard; DNA; 20 BP.
XX ACC82918;
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198790.
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

PN W02003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX Claim 3; Page 77; 11pp; English.
XX The invention relates to antisense compounds targeted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targeted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX Sequence 20 BP; 3 A; 5 C; 8 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1190 AGCCCATCTGGACCGGATC 1209
Db 20 AGCCCATCTGGACCGGATC 1
RESULT 233
ACC82940/C
ID ACC82940 standard; DNA; 20 BP.
XX ACC82940;
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198812.
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

```
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 11lpp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 5 A; 6 C; 4 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1513 GATGGGCACATCTGTGCAA 1532
DB 20 GATGGGCACATCTGTGCAA 1
XX
RESULT 234
ACC82950/c
ID ACC82950 standard; DNA; 20 BP.
XX
XX ACC82950;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198822.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
```

```
FT modified_base are 5-methylcytidines"
FT 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX modified_base 16..20
XX /*tag= c
XX /mod_base= OTHER
XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 11lpp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 8 A; 2 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1636 CTTTGATTGATCACTCTCCC 1655
DB 20 CTTTGATTGATCACTCTCCC 1
XX
RESULT 235
ACC82895/c
ID ACC82895 standard; DNA; 20 BP.
XX
XX ACC82895;
XX
XX 27-AUG-2003 (first entry)
XX
XX Human TRIP6 antisense oligonucleotide ISIS #198767.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
```

```

PH Key      Location/Qualifiers
FT modified_base 1..20
FT OS Homo sapiens.
FT FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 76; 111pp; English.
XX
XX The invention relates to antisense compounds targeted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX SQ Sequence 20 BP; 2 A; 7 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 387 GCACACGCGAGGGCTCCCTG 406
XX Db 20 GCACACGCGAGGGCTCCCTG 1
XX
XX RESULT 236
XX ACC82908/c
XX ID ACC82908 standard; DNA; 20 BP.
XX
XX AC ACC82908;
XX
XX DT 27-AUG-2003 (first entry)
XX
XX DE Human TRIP6 antisense oligonucleotide ISIS #198780.
XX
XX KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX inflammation; therapy; hyperproliferative disorder; infection; cancer;

```

```

KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX OS Homo sapiens.
XX Synthetic.
XX
XX Key      Location/Qualifiers
FT modified_base 1..20
FT FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 76; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX SQ Sequence 20 BP; 7 A; 9 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 985 TTGGCCAGTGTGGTGGCTG 1004
XX Db 20 TTGGCCAGTGTGGTGGCTG 1
XX
XX RESULT 237
XX ACC82927/c
XX ID ACC82927 standard; DNA; 20 BP.
XX
XX AC ACC82927;
XX
XX DT 27-AUG-2003 (first entry)
XX
XX

```

```
DE Human TRIP6 antisense oligonucleotide ISIS #198799.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN WO2003040328-A2.
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 11pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 4 A; 8 C; 4 G; 4 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1367 GTGGGCCCATATGCTGTAG 1386
DB 20 GTGGGCCCATATGCTGTAG 1
RESULT 238
ACC82934/c
ID ACC82934 standard; DNA; 20 BP.
```

```
ACC82934;
27-AUG-2003 (first entry)
Human TRIP6 antisense oligonucleotide ISIS #198806.
Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
inflammation; therapy; hyperproliferative disorder; infection; cancer;
chromosome 7q22; ZRP-1; phosphorothioate; ss.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
modified_base 1..20
/*tag= a
/mod_base= OTHER
/note= "Phosphorothioate backbone; All cytidine residues
are 5-methylcytidines"
modified_base 1..5
/*tag= b
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
modified_base 16..20
/*tag= c
/mod_base= OTHER
/note= "2'-methoxyethyl (2'-MOE) nucleotides"
WO2003040328-A2.
15-MAY-2003.
05-NOV-2002; 2002WO-US035479.
08-NOV-2001; 2001US-00008789.
(ISIS-) ISIS PHARM INC.
Bennett CF, Dobie K;
WPI; 2003-430662/40.
New antisense oligonucleotides targetted to nucleic acids encoding thyroid
hormone receptor interactor 6, useful for diagnosing or treating
hyperproliferative disorders, such as cancer.
Claim 3; Page 77; 11pp; English.
The invention relates to antisense compounds targetted to a nucleic acid
encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
Antisense compounds of the invention are useful for modulating the
expression of TRIP6 and for treating diseases or conditions associated
with the expression of TRIP6 such as hyperproliferative disorders (e.g.
cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
to prevent or delay infection, inflammation or tumour formation, as
research reagents and kits and in distinguishing between functions of
various members of a biological pathway. The are also useful in antisense
therapy. The present sequence is an antisense oligo targetted to human
TRIP6 DNA. This oligo is used in the exemplification of the invention
Sequence 20 BP; 8 A; 5 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1427 GAAGTTTTCACATGGCTGT 1446
DB 20 GAAGTTTTCACATGGCTGT 1
```

RESULT 239
 ACC82954/c
 ID ACC82954 standard; DNA; 20 BP.
 XX
 AC ACC82954;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198826.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN WO2003040328-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 05-NOV-2002; 2002WO-US035479.
 XX
 PR 08-NOV-2001; 2001US-00008789.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dobie K;
 XX
 DR WPI; 2003-430662/40.
 XX
 PS New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.
 XX
 PS Example 15; Page 77; 11pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 5 A; 3 C; 4 G; 8 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1712 GAATAATAATCCCTCGAGT 1731
 |||||
 Db 20 GAATAATAATCCCTCGAGT 1
 RESULT 240
 ACC82894/c
 ID ACC82894 standard; DNA; 20 BP.
 XX
 AC ACC82894;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Human TRIP6 antisense oligonucleotide ISIS #198766.
 XX
 KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 XX
 PN WO2003040328-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 05-NOV-2002; 2002WO-US035479.
 XX
 PR 08-NOV-2001; 2001US-00008789.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Bennett CF, Dobie K;
 XX
 DR WPI; 2003-430662/40.
 XX
 PS New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.
 XX
 PS Claim 3; Page 76; 11pp; English.
 XX
 CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention

```
XX SQ Sequence 20 BP; 1 A; 6 C; 8 G; 5 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 381 ACTCCAGCACGCGAGGGGC 400
Db 20 ACTCCAGCACGCGAGGGGC 1

RESULT 241
ACC82914/c
ID ACC82914 standard; DNA; 20 BP.
AC ACC82914;
XX
XX
XX
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198786.
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate backbone; All cytidine residues
FT modified_base 1..5 are 5-methylcytidines"
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 15..20 /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX
XX
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.

CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 4 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1103 GCGGCCAGCATTTCTACGCC 1122
Db 20 GCGGCCAGCATTTCTACGCC 1

RESULT 242
ACC82936/c
ID ACC82936 standard; DNA; 20 BP.
AC ACC82936;
XX
XX
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198808.
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /*mod_base= OTHER
FT /*note= "phosphorothioate backbone; All cytidine residues
FT modified_base 1..5 are 5-methylcytidines"
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX
XX
XX
XX 15-MAY-2003.
XX
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 77; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
```


CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. They are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1497 GGGCTGCTACCCGCTGGATG 1516
 Db 20 GGGCTGCTACCCGCTGGATG 1
 RESULT 243
 ACC82946/C
 ID ACC82946 standard; DNA; 20 BP.
 XX
 AC ACC82946;
 XX
 XX 27-AUG-2003 (first entry)
 DT Human TRIP6 antisense oligonucleotide ISIS #198818.
 DE
 XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT
 XX WO2003040328-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035479.
 XX
 XX 08-NOV-2001; 2001US-00008789.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Dobie K;
 XX WPI; 2003-430662/40.
 XX
 XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 FT hyperproliferative disorders, such as cancer.
 FT
 XX

PS Claim 3; Page 77; 11pp; English.
 XX
 CC The invention relates to antisense compounds targeted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. They are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targeted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX
 SQ Sequence 20 BP; 7 A; 4 C; 6 G; 3 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1579 ACTGACTGCTGAGTCTTCCT 1598
 Db 20 ACTGACTGCTGAGTCTTCCT 1
 RESULT 244
 ACC82903/C
 ID ACC82903 standard; DNA; 20 BP.
 XX
 AC ACC82903;
 XX
 XX 27-AUG-2003 (first entry)
 DT Human TRIP6 antisense oligonucleotide ISIS #198775.
 DE
 XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..20
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT
 XX WO2003040328-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 05-NOV-2002; 2002WO-US035479.
 XX
 XX 08-NOV-2001; 2001US-00008789.
 XX
 XX (ISIS-) ISIS PHARM INC.
 XX Bennett CF, Dobie K;
 XX WPI; 2003-430662/40.
 XX

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interacto 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
PS Claim 3; Page 76; 11pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 3 A; 8 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 GGCCTGGCTATAGGAGCCAG 807
DB 20 GGCCTGGCTATAGGAGCCAG 1

RESULT 245
ACC82917/c
ID ACC82917 standard; DNA; 20 BP.
XX
AC ACC82917;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198789.
XX
KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
FN WO2003040328-A2.
PD 15-MAY-2003.
XX
PP 05-NOV-2002; 2002WO-US035479.
XX
PR 08-NOV-2001; 2001US-00008789.
XX

PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Dobie K;
XX
DR WPI; 2003-430662/40.
XX
PT New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interacto 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
PS Claim 3; Page 77; 11pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1164 CCTGGAGAAATGTGCCAGT 1183
DB 20 CCTGGAGAAATGTGCCAGT 1

RESULT 246
ACC82933/c
ID ACC82933 standard; DNA; 20 BP.
XX
AC ACC82933;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198805.
XX
KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
FN WO2003040328-A2.
PD 15-MAY-2003.
XX

```

XX PF 05-NOV-2002; 2002WO-US035479.
XX XX
XX PR 08-NOV-2001; 2001US-00008789.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dobie K;
XX PR WPI; 2003-430662/40.
XX DR
XX XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX PT hormone receptor interacto 6, useful for diagnosing or treating
XX FT hyperproliferative disorders, such as cancer.
XX XX
XX PS Claim 3; Page 77; 11lpp; English.
XX XX
XX CC The invention relates to antisense compounds targetted to a nucleic acid
XX CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
XX CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX CC Antisense compounds of the invention are useful for modulating the
XX CC expression of TRIP6 and for treating diseases or conditions associated
XX CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX CC to prevent or delay infection, inflammation or tumour formation, as
XX CC research reagents and kits and in distinguishing between functions of
XX CC various members of a biological pathway. The are also useful in antisense
XX CC therapy. The present sequence is an antisense oligo targetted to human
XX CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX XX
XX SQ Sequence 20 BP; 8 A; 5 C; 4 G; 3 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1416 TGCTCTGGATCGAAGTTTTC 1435
Db 20 TGCTCTGGATCGAAGTTTTC 1

RESULT 247
ACCS2943/C
ID ACC82943 standard; DNA; 20 BP.
XX
XX AC CCS2943;
XX
XX DT 27-AUG-2003 (first entry)
XX
XX DE Human TRIP6 antisense oligonucleotide ISIS #198815.
XX
XX KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
XX KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone; All cytidine residues
XX FT are 5-methylcytidines"
XX FT 1..5
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX FT 16..20
XX FT /tag= c
XX FT /mod_base= OTHER

```

```

FT XX /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX PF WO2003040328-A2.
XX XX
XX PD 15-MAY-2003.
XX XX
XX PF 05-NOV-2002; 2002WO-US035479.
XX XX
XX PR 08-NOV-2001; 2001US-00008789.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Dobie K;
XX PR WPI; 2003-430662/40.
XX DR
XX XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX PT hormone receptor interacto 6, useful for diagnosing or treating
XX FT hyperproliferative disorders, such as cancer.
XX XX
XX PS Claim 3; Page 77; 11lpp; English.
XX XX
XX CC The invention relates to antisense compounds targetted to a nucleic acid
XX CC encoding thyroid hormone receptor interacto 6 (TRIP6) to inhibit its
XX CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX CC Antisense compounds of the invention are useful for modulating the
XX CC expression of TRIP6 and for treating diseases or conditions associated
XX CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX CC to prevent or delay infection, inflammation or tumour formation, as
XX CC research reagents and kits and in distinguishing between functions of
XX CC various members of a biological pathway. The are also useful in antisense
XX CC therapy. The present sequence is an antisense oligo targetted to human
XX CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX XX
XX SQ Sequence 20 BP; 3 A; 4 C; 9 G; 4 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1558 GAGCTCTCAGCCACCGTCAC 1577
Db 20 GAGCTCTCAGCCACCGTCAC 1

RESULT 248
ACCS2947/C
ID ACC82947 standard; DNA; 20 BP.
XX
XX AC CCS2947;
XX
XX DT 27-AUG-2003 (first entry)
XX
XX DE Human TRIP6 antisense oligonucleotide ISIS #198819.
XX
XX KW Human; antisense; thyroid hormone receptor interacto 6; TRIP6; tumour;
XX KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
XX KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
XX KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone; All cytidine residues
XX FT are 5-methylcytidines"
XX FT 1..5
XX FT /tag= b

```

FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

PN 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

PA (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

PI WPI; 2003-430662/40.

XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

PS Claim 3; Page 77; 11lpp; English.

CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX Sequence 20 BP; 6 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1594 TTCTAGAGTACCTGCTGG 1613

DB 20 TTCTAGAGTACCTGCTGG 1

RESULT 249

ACC82955/c

ID ACC82955 standard; DNA; 20 BP.

XX ACC82955;

XX 27-AUG-2003 (first entry)

DE Human TRIP6 antisense oligonucleotide ISIS #198827.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..20

FT /tag= a

FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone; All cytidine residues
 FT are 5-methylcytidines"
 FT modified_base 1..5
 FT /tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
 FT modified_base 16..20
 FT /tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX WO2003040328-A2.

PN 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035479.

XX 08-NOV-2001; 2001US-00008789.

PA (ISIS-) ISIS PHARM INC.

XX Bennett CF, Dobie K;

PI WPI; 2003-430662/40.

XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
 PT hormone receptor interactor 6, useful for diagnosing or treating
 PT hyperproliferative disorders, such as cancer.

PS Claim 3; Page 77; 11lpp; English.

CC The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. The are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX Sequence 20 BP; 5 A; 2 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1721 ATCCCTCGAGTTTACAAAA 1740

DB 20 ATCCCTCGAGTTTACAAAA 1

RESULT 250

ACC82893/c

ID ACC82893 standard; DNA; 20 BP.

XX ACC82893;

XX 27-AUG-2003 (first entry)

DE Human TRIP6 antisense oligonucleotide ISIS #198765.

XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX Homo sapiens.

```

OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX Claim 3; Page 76; 111pp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX Sequence 20 BP; 5 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 365 TGGGTCCTCCATGGAGTACTC 384
DB 20 TGGGTCCTCCATGGAGTACTC 1
|||||
|||||

RESULT 251
ACC82898/c
XX ACC82898 standard; DNA; 20 BP.
XX ACC82898;
XX 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198770.
DE Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
XX

```

```

KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX Homo sapiens.
XX Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5
FT /tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX 15-MAY-2003.
XX 05-NOV-2002; 2002WO-US035479.
XX 08-NOV-2001; 2001US-00008789.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX hormone receptor interactor 6, useful for diagnosing or treating
XX hyperproliferative disorders, such as cancer.
XX Example 15; Page 76; 111pp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX Antisense compounds of the invention are useful for modulating the
XX expression of TRIP6 and for treating diseases or conditions associated
XX with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX to prevent or delay infection, inflammation or tumour formation, as
XX research reagents and kits and in distinguishing between functions of
XX various members of a biological pathway. The are also useful in antisense
XX therapy. The present sequence is an antisense oligo targetted to human
XX TRIP6 DNA. This oligo is used in the exemplification of the invention
XX Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 457 CTGAGCACCACGCTGGCCAA 476
DB 20 CTGAGCACCACGCTGGCCAA 1
|||||
|||||

RESULT 252
ACC82902/c
XX ACC82902 standard; DNA; 20 BP.
XX ACC82902;
XX

```

DT 27-AUG-2003 (first entry)
XX Human TRIP6 antisense oligonucleotide ISIS #198774.
XX
XX
KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX Key
FH modified_base Location/Qualifiers
FT 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
PN WO2003040328-A2.
XX
XX 15-MAY-2003.
PD
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Claim 3; Page 76; 111pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 5 A; 6 C; 7 G; 2 T; 0 U; 0 Other;
Query Match 1..1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 720 AGCCTCTCAGGCTTCGGGC 739
|||||
Db 20 AGCCTCTCAGGCTTCGGGC 1
RESULT 253

ACC82913/c
ID ACC82913 standard; DNA; 20 BP.
XX
AC ACC82913;
XX
DT 27-AUG-2003 (first entry)
XX
DE Human TRIP6 antisense oligonucleotide ISIS #198785.
XX
XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX Key
FH modified_base Location/Qualifiers
FT 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT 16..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
XX
XX 15-MAY-2003.
PD
XX 05-NOV-2002; 2002WO-US035479.
XX
XX 08-NOV-2001; 2001US-00008789.
XX
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Dobie K;
XX WPI; 2003-430662/40.
XX
XX New antisense oligonucleotides targetted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 77; 111pp; English.
XX
CC The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
SQ Sequence 20 BP; 2 A; 8 C; 8 G; 2 T; 0 U; 0 Other;
Query Match 1..1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1091 GGGCCCGAGCTTCGGCCAG 1110

```
Db      20 GGGCCACGCTTGGCGGCCAG 1
RESULT 254
ACC82915/c
ID      ACC82915 standard; DNA; 20 BP.
XX
AC      ACC82915;
XX
DT      27-AUG-2003 (first entry)
XX
DE      Human TRIP6 antisense oligonucleotide ISIS #198787.
XX
KW      Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW      OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW      inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW      chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN      WO2003040328-A2.
XX
PD      15-MAY-2003.
XX
PF      05-NOV-2002; 2002WO-US035479.
XX
PR      08-NOV-2001; 2001US-00008789.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Bennett CF, Dobie K;
XX
DR      WPI; 2003-430662/40.
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX      hormone receptor interactor 6, useful for diagnosing or treating
XX      hyperproliferative disorders, such as cancer.
XX
XX      Example 15; Page 77; 11pp; English.
XX
XX      The invention relates to antisense compounds targetted to a nucleic acid
XX      encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX      expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX      zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX      Antisense compounds of the invention are useful for modulating the
XX      expression of TRIP6 and for treating diseases or conditions associated
XX      with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX      cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX      to prevent or delay infection, inflammation or tumour formation, as
XX      research reagents and kits and in distinguishing between functions of
XX      various members of a biological pathway. The are also useful in antisense
XX      therapy. The present sequence is an antisense oligo targetted to human
XX      TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX      Sequence 20 BP; 3 A; 7 C; 7 G; 3 T; 0 U; 0 Other;
SQ
```

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1151 GCTACGTGGCCACCCCTGGAG 1170
      |||||
Db      20 GCTACGTGGCCACCCCTGGAG 1

RESULT 255
ACC82942/c
ID      ACC82942 standard; DNA; 20 BP.
XX
AC      ACC82942;
XX
DT      27-AUG-2003 (first entry)
XX
DE      Human TRIP6 antisense oligonucleotide ISIS #198814.
XX
KW      Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
KW      OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
KW      inflammation; therapy; hyperproliferative disorder; infection; cancer;
KW      chromosome 7q22; ZRP-1; phosphorothioate; ss.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1..20
FT      /tag= a
FT      /mod_base= OTHER
FT      /note= "Phosphorothioate backbone; All cytidine residues
FT      are 5-methylcytidines"
FT      modified_base 1..5
FT      /tag= b
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT      modified_base 16..20
FT      /tag= c
FT      /mod_base= OTHER
FT      /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN      WO2003040328-A2.
XX
PD      15-MAY-2003.
XX
PF      05-NOV-2002; 2002WO-US035479.
XX
PR      08-NOV-2001; 2001US-00008789.
XX
PA      (ISIS-) ISIS PHARM INC.
XX
PI      Bennett CF, Dobie K;
XX
DR      WPI; 2003-430662/40.
XX
XX      New antisense oligonucleotides targeted to nucleic acids encoding thyroid
XX      hormone receptor interactor 6, useful for diagnosing or treating
XX      hyperproliferative disorders, such as cancer.
XX
XX      Claim 3; Page 77; 11pp; English.
XX
XX      The invention relates to antisense compounds targetted to a nucleic acid
XX      encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
XX      expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
XX      zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
XX      Antisense compounds of the invention are useful for modulating the
XX      expression of TRIP6 and for treating diseases or conditions associated
XX      with the expression of TRIP6 such as hyperproliferative disorders (e.g.
XX      cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
XX      to prevent or delay infection, inflammation or tumour formation, as
XX      research reagents and kits and in distinguishing between functions of
XX      various members of a biological pathway. The are also useful in antisense
XX      therapy. The are also useful in antisense
```


RESULT 258

AAL61645
ID AAL61645 standard; DNA; 20 BP.

AC AAL61645;
XX

DT 22-SEP-2003 (first entry)

XX Thiol-modified oligo #4 used in the nucleic acid detection method.

DE Nucleic acid detection; fabrication; ss.

XX Unidentified.

OS WO2003035829-A2.

XX 01-MAY-2003.

XX 08-OCT-2002; 2002WO-US032088.

XX 09-OCT-2001; 2001US-0327864P.

XX 07-DEC-2001; 2001US-00008978.

XX (NANO-) NANOSPHERE INC.

XX Park S, Taton TA, Mirkin CA;

XX WPI; 2003-430409/40.

XX Detecting nucleic acid having two portions, by providing nanoparticles having oligonucleotides attached to it, contacting nucleic acid and nanoparticles to allow hybridization, and observing detectable change.
XX Example 18; Page 179; 467pp; English.

XX The invention relates to a method of detecting a nucleic acid having two portions. The method involves providing nanoparticles having oligonucleotides attached to it which has a sequence complementary to sequence of two portions of nucleic acid, contacting nucleic acid and nanoparticles to allow hybridization of oligonucleotides with two or more portions of nucleic acid and observing a detectable change brought about by hybridization. The method and aggregate probes are useful for detecting two or more nucleic acids (from a biological source) having at least two portions such as viral RNA, bacterial or fungal DNA, a gene associated with a disease, synthetic or structurally modified natural or synthetic RNA or DNA, or a product of a polymerase chain reaction amplification. The invention is useful for preparing a nanoprobe conjugate for detecting an analyte and for detecting a nucleic acid bound to an electrode surface. It is also useful for fabricating and for separating a selected nucleic acid having two portions from other nucleic acids. The present sequence is an oligo used to illustrate the method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 259

ABZ59815/c

ID ABZ59815 standard; RNA; 20 BP.

XX ABZ59815;

XX 01-APR-2003 (first entry)

XX Potato gene PCR primer dT20.

DE

XX

KW Potato; plant; mitochondrial carrier protein; elongation factor EF-2;
KW Transferrin binding protein; receptor-like protein kinase; helicase;
KW non-long terminal repeat retroelement reverse transcriptase;
KW overwatering; transgenic; reverse transcriptase; PCR; primer; ss.

OS Synthetic.

XX DE10114063-A1.

XX 10-OCT-2002.

XX 22-MAR-2001; 2001DE-01014063.

XX 22-MAR-2001; 2001DE-01014063.

XX (MPBC-) MPB COLOGNE GMBH MOLECULAR PLANT & PROTE.

XX Buelow L, Tscharncke M, Haussuehl K;

XX WPI; 2003-041808/04.

XX New DNA sequences from potato, useful for producing plants with altered properties, e.g. tolerance of flooding, also related proteins, antibodies and inhibitory sequences.

XX Example 1; Page 8; 26pp; German.

XX The invention relates to DNA sequences (I) that encode six specific plant proteins: (i) a protein (ABP60425) with mitochondrial carrier protein activity (IIa); (ii) a protein (ABP60426) with transferrin binding protein activity (IIb); (iii) a protein (ABP60427) with receptor-like protein kinase activity (IIc); (iv) a protein (ABP60428) with elongation factor EF-2 activity (IId); (v) a protein (ABP60429) with non-long terminal repeat retroelement reverse transcriptase activity (IIf); or (vi) a protein (ABP60430) with helicase activity (IIg). (I), also related sequences, derived ribozymes and antisense sequences, expression vectors, encoded proteins and antibodies against the proteins, are used to produce plants with altered properties, including tolerance of overwatering. The antibodies are also used for isolation of the proteins and in immunoassays. Also (I) or their primer or probe fragments are used to screen for terminators and constitutively, aerobically or anaerobically inducible plant promoters, specifically for use in potatoes and the sequence that encodes (IId) is used to alter the translation profile in plants. Since (I) are derived from potato, their promoters and terminators provide high level transgene expression in potato, with improved tissue specificity and inducibility, and can also be used to control endogenous genes. The present sequence is that of a PCR primer used in the first strand synthesis of cDNAs derived from potato

XX Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 260

ABX79181

ID ABX79181 standard; DNA; 20 BP.

XX ABX79181;

XX 15-APR-2003 (first entry)

XX Thio-modified 20da oligonucleotide.

XX Nanoparticle; ss; nucleic acid detection; viral disease; probe;
KW human immunodeficiency virus infection; hepatitis virus infection;

```

KW herpes virus infection; cytomegalovirus infection; forensic science;
KW Epstein-Barr virus infection; bacterial disease; gene therapy;
KW sexually transmitted disease; inherited disorder; DNA sequencing;
KW paternity testing; cell line authentication.
XX
OS Synthetic.
XX
XX US2002155462-A1.
XX
XX 24-OCT-2002.
XX
XX 12-OCT-2001; 2001US-00976577.
XX
XX 29-JUL-1996; 96US-0031809P.
XX
XX 21-JUL-1997; 97WO-US012783.
XX
XX 29-JAN-1999; 99US-00240755.
XX
XX 25-JUN-1999; 99US-00344667.
XX
XX 26-APR-2000; 2000US-0200161P.
XX
XX 26-JUN-2000; 2000US-00603830.
XX
XX (NANO-) NANOSPHERE INC.
XX
XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX Taton TA;
XX
XX WPI; 2003-198491/19.
XX
XX Detecting nucleic acids having at least 2 portions comprises use of
XX nanoparticles which have oligonucleotides attached to them that are
XX complementary to portions of the nucleic acid sequence.
XX
XX Example 18; Page 44; 130pp; English.
XX
XX The invention relates to detecting a nucleic acid (NA) having at least 2
XX portions, comprises providing a type of nanoparticles (NP) having
XX attached to oligonucleotides (O) (O) on each NP has a sequence
XX complementary to sequence of at least 2 portions of NA, contacting NA
XX and NP to allow hybridisation of (O) on NP with 2 or more portions of (O)
XX on NP with NA. The nanoparticle is useful for separating a selected
XX nucleic acid having at least 2 portions, from other nucleic acids, and
XX for detecting nucleic acids having at least 2 portions. The method of
XX using NP is useful for detecting any type of nucleic acids which may be
XX used for diagnosis of disease and in sequencing of nucleic acids.
XX Preferably, the method is useful for detecting nucleic acids for
XX diagnosis and/or monitoring of viral diseases (human immunodeficiency
XX virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
XX virus), bacterial diseases, sexually transmitted diseases, inherited
XX disorders, in forensics, in DNA sequencing, for paternity testing, for
XX cell line authentication and for monitoring gene therapy. The method is
XX useful in research and analytical laboratories in DNA sequencing and in
XX the field to detect the presence of specific pathogens. Detecting nucleic
XX acids based on observing a colour change with the naked eye is cheap,
XX fast, simple and robust, and do not require specialised expensive
XX equipment. The present sequence is a nanoparticle (e.g. gold particles)
XX labelled probe used to demonstrate the method of the invention
XX
XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 20; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1736 AAAAAAAAAAAAAAAAAA 1755
XX ||||||||||||||||||
XX 1 AAAAAAAAAAAAAAAAAA 20
XX
XX RESULT 261
XX ABX92177
XX ID ABX92177 standard; DNA; 20 BP.
XX
XX AC ABX92177;

```

```

Db      1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 262
ACD27255
ID      ACD27255 standard; DNA; 20 BP.
XX
AC      ACD27255;
XX
XX      15-OCT-2003 (first entry)
XX
XX      Nanotechnology nucleic acid detection method associated #54.
XX
XX      Nanotechnology; ss; nucleic acid detection; nanoparticle;
KW      virus detection; human immunodeficiency virus; HIV; hepatitis; herpes;
KW      cytomegalovirus; Epstein-Barr virus; bacterial disease; DNA sequencing;
KW      sexually transmitted disease; inherited disorder; forensic;
KW      paternity testing; cell line authentication.
XX
OS      Synthetic.
XX
FH      Key      Location/Qualifiers
FT      modified_base 1
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "OTHER= Thiol modified" "
XX
XX      US2002155459-A1.
XX
XX      24-OCT-2002.
XX
XX      11-OCT-2001; 2001US-00975062.
XX
XX      29-JUL-1996; 96US-0031809P.
XX      21-JUL-1997; 97WO-US012783.
XX      29-JAN-1999; 99US-00240755.
XX      25-JUN-1999; 99US-00344667.
XX      26-APR-2000; 2000US-0200161P.
XX      26-JUN-2000; 2000US-00603830.
XX
XX      (NANO-) NANOSPHERE INC.
XX
XX      Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX      Taton TA;
XX
XX      WPI; 2003-228114/22.
XX
XX      Detecting nucleic acids having 2 portions e.g. for detecting disease,
XX      comprises use of nanoparticles which have oligonucleotides attached to
XX      them that are complementary to portions of the nucleic acid sequence.
XX
XX      Example 18; Page 43; 129pp; English.
XX
XX      This invention relates to a novel method for detecting a nucleic acid
XX      having 2 portions. The method comprises providing nanoparticles having
XX      oligonucleotides attached, where the oligonucleotide on each nanoparticle
XX      has a sequence complementary to a sequence of 2 portions of nucleic acid.
XX      The nucleic acid and nanoparticle are contacted to allow hybridisation of
XX      the oligonucleotide on the nanoparticle with two or more portions of
XX      nucleic acid and observing a detectable change brought about by the
XX      hybridisation. The method of the invention is useful for separating a
XX      selected nucleic acid having 2 portions, from other nucleic acids, and
XX      for detecting nucleic acids having 2 portions. The method of the
XX      invention is useful for detecting any type of nucleic acids which may be
XX      used for diagnosis of disease and in sequencing of nucleic acids.
XX      Preferably, the method is useful for detecting nucleic acids for
XX      diagnosis and/or monitoring of viral diseases (human immunodeficiency
XX      virus, hepatitis virus, herpes virus, cytomegalovirus and Epstein-Barr
XX      virus), bacterial diseases, sexually transmitted diseases, inherited
XX      disorders, in forensics, in DNA sequencing, for paternity testing, for
XX      cell line authentication, for monitoring gene therapy, etc. This method
XX      involves detecting nucleic acids based on observing a colour change with
XX      the naked eye so is cheap, fast, simple and robust, and does not require

```

```

CC      specialised expensive equipment. The present sequence represents a thiol
CC      modified oligonucleotide sequence used to demonstrate the method of the
CC      invention
XX
XX      Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX      Query Match      1.1%; Score 20; DB 1; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 1.6e+02;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1736 AAAAAAAAAAAAAAAAAAAAAA 1755
XX      Db      1 AAAAAAAAAAAAAAAAAAAAAA 20
XX
XX      RESULT 263
XX      ACD27125
XX      ID      ACD27125 standard; DNA; 20 BP.
XX
XX      AC      ACD27125;
XX
XX      DT      15-OCT-2003 (first entry)
XX
XX      DE      Nanotechnology nucleic acid detection method oligonucleotide #54.
XX
XX      KW      Nanotechnology; nucleic acid detection; nanoparticle; ss; forensic;
XX      KW      DNA sequencing; paternity testing; cell line authentication.
XX
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      modified_base 1
XX      FT      /*tag= a
XX      FT      /mod_base= OTHER
XX      FT      /note= "OTHER= Thiol modified" "
XX
XX      PN      US2002164605-A1.
XX
XX      PD      07-NOV-2002.
XX
XX      PF      28-SEP-2001; 2001US-00966312.
XX
XX      PR      29-JUL-1996; 96US-0031809P.
XX      PR      21-JUL-1997; 97WO-US012783.
XX      PR      29-JAN-1999; 99US-00240755.
XX      PR      25-JUN-1999; 99US-00344667.
XX      PR      26-APR-2000; 2000US-0200161P.
XX      PR      26-JUN-2000; 2000US-00603830.
XX
XX      PA      (NANO-) NANOSPHERE INC.
XX
XX      PI      Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
XX      PI      Taton TA;
XX
XX      DR      WPI; 2003-247253/24.
XX
XX      PT      Detecting nucleic acid having two portions, by providing nanoparticles
XX      PT      having oligonucleotides attached to it, contacting nucleic acid and
XX      PT      nanoparticles to allow hybridization, and observing detectable change,
XX      PT      useful in forensics.
XX
XX      PS      Example 18; Page 44; 130pp; English.
XX
XX      CC      This invention relates to a novel method for detecting nucleic acid
XX      CC      sequences having two portions. The method involves providing
XX      CC      nanoparticles having oligonucleotides attached to them, which has a
XX      CC      sequence complementary to sequence of two portions of nucleic acid,
XX      CC      contacting nucleic acid and nanoparticles, to allow hybridisation of
XX      CC      oligonucleotides with two or more portions of nucleic acid, and observing
XX      CC      a detectable change brought about by hybridisation. The method of the
XX      CC      invention and the aggregate probes are useful for detecting two or more
XX      CC      nucleic acids (from a biological source) having at least two portions,
XX      CC      such as viral RNA or DNA, bacterial or fungal DNA, a gene associated with

```

CC a disease, synthetic, or structurally- modified natural or synthetic RNA
CC or DNA, or a product of a polymerase chain reaction amplification.
CC Nanoparticles and nanoparticle- oligonucleotide conjugates of the
CC invention are useful for nanofabrication, and for separating a selected
CC nucleic acid having two portions from other nucleic acids. The method of
CC the invention is useful in forensics, DNA sequencing, for paternity
CC testing, cell line authentication, and monitoring gene therapy.
CC Diagnostic assays employing the nanoparticle-oligonucleotide conjugates
CC of the invention improve the sensitivity of the nucleic acid detection
CC assay. The present sequence represents a thiol modified oligonucleotide
CC sequence used to demonstrate the method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 264

ACD27385
ID ACD27385 standard; DNA; 20 BP.

AC ACD27385;

DT 15-OCT-2003 (first entry)

XX Nanotechnology nucleic acid detection method associated #54.

DE Nanoparticle; ss; nucleic acid detection; DNA sequencing;
KW pathogen detection.

XX Synthetic.

Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "

US2002182611-A1.

PD 05-DEC-2002.

XX 28-SEP-2001; 2001US-00966491.

XX 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;

DR WPI; 2003-596264/56.

XX Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.

PS Example 18; Page 43; 109pp; English.

XX This invention relates to a novel method for detecting a nucleic acid by
CC contacting a nucleic acid with at least two types of nanoparticles having
CC oligonucleotides attached, allowing hybridisation of the oligonucleotides

CC on the nanoparticles, and observing a detectable change. The
CC oligonucleotides on each nanoparticle have a sequence complementary to
CC its respective portion of the sequence of the nucleic acid to be
CC detected. The method of the invention may be used for the detection of a
CC nucleic acid used in, e.g. research and analytical laboratories in DNA
CC sequencing, in the field to detect the presence of specific pathogens, in
CC the doctor's office for quick identification of an infection to assist
CC in prescribing a drug for treatment, and in homes and health centres for
CC inexpensive first-line screening. The method of the invention detects
CC nucleic acids based on observing a colour change with the naked eye. This
CC method is cheap, fast, simple, robust and does not require specialised or
CC expensive equipment. The present sequence represents a thiol modified
CC oligonucleotide sequence used to demonstrate the method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
|||||

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 265

ACD27190
ID ACD27190 standard; DNA; 20 BP.

AC ACD27190;

DT 15-OCT-2003 (first entry)

XX Nanotechnology nucleic acid detection method associated #54.

DE Nanoparticle; ss; nucleic acid detection; DNA sequencing.

XX Synthetic.

Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER= Thiol modified" "

US2002182613-A1.

XX 05-DEC-2002.

XX 12-OCT-2001; 2001US-00976971.

XX 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
PI Taton TA;

DR WPI; 2003-596265/56.

XX Detection of nucleic acid for, e.g. research and analytical laboratories
PT in deoxyribonucleic acid sequencing, involves contacting nucleic acid
PT with nanoparticles having oligonucleotides.

PS Example 18; Page 43; 107pp; English.

XX This invention relates to a novel method for detecting a nucleic acid by
CC contacting nucleic acid with at least two types of nanoparticles having

CC oligonucleotides, allowing hybridisation of the oligonucleotides on the
 CC nanoparticles, and observing a detectable change. The oligonucleotides on the
 CC each nanoparticle have a sequence complementary to its respective portion
 CC of the sequence of the nucleic acid. The method of the invention may be
 CC used for the detection of a nucleic acid used in, e.g. research and
 CC analytical laboratories in DNA sequencing, in the field to detect the
 CC presence of specific pathogens, in the doctor's office for quick
 CC identification of an infection to assist in prescribing a drug for
 CC treatment, and in homes and health centres for inexpensive first-line
 CC screening. The inventive method of detecting nucleic acids based on
 CC observing a colour change with the naked eye are cheap, fast, simple,
 CC robust (the reagents are stable), do not require specialised or expensive
 CC equipment, and little or no instrumentation is required. The present
 CC sequence represents a thiol modified oligonucleotide sequence used to
 CC demonstrate the method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 266

ID ACD27060 standard; DNA; 20 BP.

AC ACD27060;

DT 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method oligonucleotide #54.

XX Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

OS Synthetic.

Key modified_base 1 Location/Qualifiers

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= Thiol modified" "

PN US2003044805-A1.

XX 06-MAR-2003.

PF 15-OCT-2001; 2001US-00981344.

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;

PI Taton TA;

XX WPI; 2003-521746/49.

DR Detection of nucleic acid having -2 portions used to prepare biomaterials

XX and in nanofabrication methods, comprises providing nanoparticles,

PT contacting nucleic acid and nanoparticles, and observing change.

XX Example 18; Page 44; 130pp; English.

CC This invention relates to a novel method for detecting nucleic acids. The
 CC method comprises providing nanoparticles with oligonucleotides attached
 CC to them, which have a sequence complementary to a sequence of two
 CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
 CC to allow hybridisation of the oligonucleotides with two or more portions
 CC of the nucleic acid, and observing a detectable change brought about by
 CC the hybridisation. The nucleic acid to be detected must have at least two
 CC portions and the distances between these are chosen so that when the
 CC nanoparticle-oligonucleotide conjugate binds the target sequence a
 CC detectable change occurs. The method of the invention is useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic, or structurally- modified natural
 CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
 CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
 CC and for detecting a nucleic acid bound to an electrode surface.
 CC Nanoparticles and nanoparticle conjugates of the invention are useful for
 CC nanofabrication and for separating a selected nucleic acid having two
 CC portions from other nucleic acids. Diagnostic assays employing
 CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
 CC nucleic acid detection methods and can be used to detect nucleic acids
 CC that are present in only small amounts in a sample. The invention also
 CC provides highly desirable nanoparticle-oligonucleotide conjugates. These
 CC conjugates are stable with tailored hybridisation abilities. The present
 CC sequence represents a thiol modified oligonucleotide sequence used to
 CC demonstrate the method of the invention

XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 267

ACH00064

ID ACH00064 standard; DNA; 20 BP.

AC ACH00064;

DT 15-OCT-2003 (first entry)

DE Nanotechnology nucleic acid detection method oligonucleotide #54.

XX Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

OS Synthetic.

Key modified_base 1 Location/Qualifiers

FT /*tag= a

FT /mod_base= OTHER

FT /note= "OTHER= Thiol modified" "

PN US2003049631-A1.

XX 13-MAR-2003.

PF 10-OCT-2001; 2001US-00974500.

PR 29-JUL-1996; 96US-0031809P.

PR 21-JUL-1997; 97WO-US012783.

PR 29-JAN-1999; 99US-00240755.

PR 25-JUN-1999; 99US-00344667.

PR 26-APR-2000; 2000US-0200161P.

PR 26-JUN-2000; 2000US-00603830.

XX (NANO-) NANOSPHERE INC.

XX Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 PI Taton TA;
 XX WPI; 2003-634854/60.
 XX Detection of nucleic acid having at least two portions, by contacting
 PT nucleic acid and nanoparticles under conditions, which allows
 PT hybridization of oligonucleotides on nanoparticles with at least two
 PT portions of nucleic acid.
 XX Example 18; Page 44; 108pp; English.
 XX This invention relates to a novel method for detecting nucleic acids. The
 CC method comprises providing nanoparticles with oligonucleotides attached
 CC to them, which have a sequence complementary to a sequence of two
 CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
 CC to allow hybridisation of the oligonucleotides with two or more portions
 CC of the nucleic acid, and observing a detectable change brought about by
 CC the hybridisation. The nucleic acid to be detected must have at least two
 CC portions and the distances between these are chosen so that when the
 CC nanoparticle-oligonucleotide conjugate binds the target sequence a
 CC detectable change occurs. The method of the invention is useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic, or structurally- modified natural
 CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
 CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
 CC and for detecting a nucleic acid bound to an electrode surface.
 CC Nanoparticles and nanoparticle conjugates of the invention are useful for
 CC nanofabrication and for separating a selected nucleic acid having two
 CC portions from other nucleic acids. Diagnostic assays employing
 CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
 CC nucleic acid detection methods and can be used to detect nucleic acids
 CC that are present in only small amounts in a sample. The invention also
 CC provides highly desirable nanoparticle-oligonucleotide conjugates. These
 CC conjugates are stable with tailored hybridisation abilities. The present
 CC sequence represents a thiol modified oligonucleotide sequence used to
 CC demonstrate the method of the invention
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1755
 DB 1 AAAAAAAAAAAAAAAAAA 20
 RESULT 268
 ACD99851
 ID ACD99851 standard; DNA; 20 BP.
 XX ACD99851;
 AC ACD99851;
 DT 25-SEP-2003 (first entry)
 XX Immunostimulatory nucleic acid #537.
 DE Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX Synthetic.
 OS Synthetic.
 XX US2003050268-A1.
 PN US2003050268-A1.
 XX 13-MAR-2003.
 PD 13-MAR-2003.
 PF 29-MAR-2002; 2002US-00112653.
 XX 29-MAR-2001; 2001US-0279642P.
 PR (KRIE/) KRIEG A M.
 PA (BERG/) BERG D J.
 PI Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX

PF 29-MAR-2002; 2002US-00112653.
 XX 29-MAR-2001; 2001US-0279642P.
 XX (KRIE/) KRIEG A M.
 PA (BERG/) BERG D J.
 PI Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX Disclosure; Page 23; 229pp; English.
 XX The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid
 XX Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1755
 DB 1 AAAAAAAAAAAAAAAAAA 20
 RESULT 269
 ACD99847/c
 ID ACD99847 standard; DNA; 20 BP.
 XX ACD99847;
 AC ACD99847;
 DT 25-SEP-2003 (first entry)
 XX Immunostimulatory nucleic acid #533.
 DE Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
 XX Synthetic.
 OS Synthetic.
 XX US2003050268-A1.
 PN US2003050268-A1.
 XX 13-MAR-2003.
 PD 13-MAR-2003.
 PF 29-MAR-2002; 2002US-00112653.
 XX 29-MAR-2001; 2001US-0279642P.
 PR (KRIE/) KRIEG A M.
 PA (BERG/) BERG D J.
 PI Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.
 XX

CC or rhodamine B-labelled dye. Within the microarray the support is capable
 CC of accepting a charge. At least one hairpin sensor comprises two or more
 CC hairpin sensors. The two or more hairpin sensors include complementary
 CC probes that are the same or different and respective quenchable
 CC fluorescing agents that are the same or different. The two or more
 CC hairpin sensors are arranged in a spatially-defined pattern. The sensor
 CC and system are useful for detecting a target nucleotide sequence in a
 CC sample. Further, the method involves identifying the target nucleotide
 CC sequence by the location of the complementary probe to which the target
 CC nucleotide sequence binds. The two or more hairpin sensors include
 CC complementary probes or quenchable fluorescing agents, that are
 CC different. The sequence presented is the hairpin oligonucleotide target
 CC sequence, #2, used in an example of the invention.

XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 272

ADA06159
 ID ADA06159 standard; DNA; 20 BP.

XX AC ADA06159;

XX DT 06-NOV-2003 (first entry)

XX DE Nanoparticle labelled oligonucleotides, spacer DNA #2.

XX ss; nanoparticle; colloidal gold; semiconductor; nanomaterial;
 KW nanostructure; viral disease; human immunodeficiency virus infection;
 KW hepatitis virus infection; herpes virus infection;
 KW cytomegalovirus virus infection; Epstein-Barr virus; bacterial disease;
 KW sexually transmitted disease; inherited disorders; paternity testing;
 KW cell line authentication; gene therapy.

XX OS Synthetic.

XX PN US2003068622-A1.

XX PD 10-APR-2003.

XX PF 12-OCT-2001; 2001US-00976863.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

XX PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 PI Taton TA;

XX DR WPI; 2003-576420/54.

XX PT Detecting nucleic acids having at least 2 portions comprises use of
 PT nanoparticles which have oligonucleotides attached to them that are
 PT complementary to portions of the target nucleic acid sequence.

XX PS Example 18; Page 44; 130pp; English.

XX CC The invention relates to detecting a nucleic acid (NA) having at least 2
 CC portions comprising providing a type of nanoparticles (NP. e.g. colloidal
 CC gold) having oligonucleotides (O) attached (where (O) on each NP has a

CC sequence complementary to sequence of at least two portions of NA),
 CC contacting NA and NP to allow hybridisation of (O) on NP with 2 or more
 CC portions of NA, and observing a detectable change brought about by
 CC hybridization of (O) on NP with NA. Also included are aggregate probes,
 CC core probes, substrate having NP attached to it, a metallic or
 CC semiconductor NP having (O) attached to it, nanomaterials/nanostructures
 CC comprising nanoparticles and methods of nanofabrication utilising
 CC nanoparticles and satellite probes. The methods, probes nucleic acids,
 CC nanoparticles and oligonucleotides are useful for separating a selected
 CC nucleic acid having at least two portions, from other nucleic acids, and
 CC for detecting nucleic acids having at least two portions, for detecting
 CC NA having at least two portions. The method is useful for diagnosing any
 CC type of nucleic acids which may be used for diagnosis of disease and in
 CC detecting nucleic acids for diagnosis and/or monitoring of viral diseases
 CC (human immunodeficiency virus, hepatitis virus, herpes virus,
 CC cytomegalovirus and Epstein-Barr virus), bacterial diseases, sexually
 CC transmitted diseases, inherited disorders, in forensics, in DNA
 CC sequencing, for paternity testing, for cell line authentication, for
 CC monitoring gene therapy, etc. The method is useful in research and
 CC analytical laboratories in DNA sequencing, in the field to detect the
 CC presence of specific pathogens, etc. Detecting nucleic acids based on
 CC observing a colour change with the naked eye is cheap, fast, simple and
 CC robust, and do not require specialised expensive equipment. The present
 CC sequence is a spacer oligonucleotide used to illustrate the method of the
 CC invention.

XX SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAAAAAA 20

RESULT 273

ACD26995

ID ACD26995 standard; DNA; 20 BP.

XX AC ACD26995;

XX DT 15-OCT-2003 (first entry)

XX DE Nanotechnology nucleic acid detection method oligonucleotide #54.

XX KW Nanotechnology; nucleic acid detection; nanofabrication; nanoprobe; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT modified_base 1

XX FT /*tag= a

XX FT /mod base= OTHER

XX FT /note= "OTHER= Thiol modified" "

XX PN US2003049630-A1.

XX PD 13-MAR-2003.

XX PF 20-SEP-2001; 2001US-00957318.

XX PR 29-JUL-1996; 96US-0031809P.

XX PR 21-JUL-1997; 97WO-US012783.

XX PR 29-JAN-1999; 99US-00240755.

XX PR 25-JUN-1999; 99US-00344667.

XX PR 26-APR-2000; 2000US-0200161P.

XX PR 26-JUN-2000; 2000US-00603830.

XX PA (NANO-) NANOSPHERE INC.

PI Mirkin CA, Letsinger RL, Mucic RC, Storhoff JJ, Elghanian R;
 PI Taton TA;
 XX
 DR WPI; 2003-615795/58.
 XX
 PT Detecting nucleic acid having two portions, by providing nanoparticles
 PT having oligonucleotides attached to it, contacting nucleic acid and
 PT nanoparticles to allow hybridization, and observing detectable change.
 XX
 PS Example 18; Page 43; 129pp; English.
 XX
 CC This invention relates to a novel method for detecting nucleic acids. The
 CC method comprises providing nanoparticles with oligonucleotides attached
 CC to them, which have a sequence complementary to a sequence of two
 CC portions of nucleic acid, contacting the nucleic acid and nanoparticles
 CC to allow hybridization of the oligonucleotides with two or more portions
 CC of the nucleic acid, and observing a detectable change brought about by
 CC the hybridization. The nucleic acid to be detected must have at least two
 CC portions and the distances between these are chosen so that when the
 CC nanoparticle-oligonucleotide conjugate binds the target sequence a
 CC detectable change occurs. The method of the invention is useful for
 CC detecting two or more nucleic acids (from a biological source) having at
 CC least two portions, such as viral RNA, bacterial or fungal DNA, a gene
 CC associated with a disease, synthetic, or structurally-modified natural
 CC or synthetic RNA or DNA, or a product of a polymerase chain reaction
 CC amplification. Nanoparticle-oligonucleotide conjugates of the invention
 CC are useful for preparing a nanoprobe conjugate for detecting an analyte,
 CC and for detecting a nucleic acid bound to an electrode surface.
 CC Nanoparticles and nanoparticle conjugates of the invention are useful for
 CC nanofabrication and for separating a selected nucleic acid having two
 CC portions from other nucleic acids. Diagnostic assays employing
 CC nanoparticle-oligonucleotide conjugates improve the sensitivity of
 CC nucleic acid detection methods and can be used to detect nucleic acids
 CC that are present in only small amounts in a sample. The present sequence
 CC represents a thiol modified oligonucleotide sequence used to demonstrate
 CC the method of the invention
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 274
 ADB36933
 ID ADB36933 standard; DNA; 20 BP.
 XX
 AC ADB36933;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #547.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 FN US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-00776479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 DR WPI; 2003-657977/62.
 XX
 PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 8; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 275
 ADB36601/C
 ID ADB36601 standard; DNA; 20 BP.
 XX
 AC ADB36601;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #215.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 FN US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-00776479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 DR WPI; 2003-657977/62.
 XX
 PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 8; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 DR WPI; 2003-657977/62.
 XX
 PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 13; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 1 AAAAAAAAAAAAAAAAAAAAAA 20
 RESULT 275
 ADB36601/C
 ID ADB36601 standard; DNA; 20 BP.
 XX
 AC ADB36601;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #215.
 XX
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX
 OS Synthetic.
 XX
 FN US2003087848-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 02-FEB-2001; 2001US-00776479.
 XX
 PR 03-FEB-2000; 2000US-0179991P.
 XX
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 XX
 PI Bratzler RL, Petersen DM, Fouron Y;
 XX
 DR WPI; 2003-657977/62.
 XX
 PT Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 XX
 PS Disclosure; Page 8; 221pp; English.
 XX
 CC The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 20 BP; 20 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

```
Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 276
ADB36929/c
ID ADB36929 standard; DNA; 20 BP.
XX
AC ADB36929;
XX
DT 04-DEC-2003 (first entry)
XX
DE Immunostimulatory nucleic acid #543.
XX
KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
KW hypo-responsive subject; immunostimulatory.
XX
OS Synthetic.
XX
XX US2003087848-A1.
XX
XX 08-MAY-2003.
XX
XX 02-FEB-2001; 2001US-00776479.
XX
XX 03-FEB-2000; 2000US-0179991P.
XX
XX (BRAT/) BRATZLER R L.
PA (PETE/) PETERSEN D M.
PA (FOUR/) FOURON Y.
XX
PI Bratzler RL, Petersen DM, Fouron Y;
XX
XX WPI; 2003-657977/62.
XX
PT Treating and/or preventing allergy or asthma using an immunostimulatory
PT nucleic acid alone or in combination with an asthma/allergy medicament.
XX
PS Disclosure; Page 13; 221pp; English.
XX
CC The invention relates to a method of treating or preventing allergy or
CC asthma which comprises administering to a subject a poly-G nucleic acid
CC in an aerosol formulation. The methods and compositions of the present
CC invention are useful for diagnosing and/or treating asthma and allergy
CC especially in a hypo-responsive subject. The present sequence represents
CC an immunostimulatory nucleic acid of the invention.
XX
SQ Sequence 20 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 0 Other;

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 277
AAQ75643/c
ID AAQ75643 standard; DNA; 21 BP.
XX
AC AAQ75643;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX

Query Match      1.1%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 278
AAQ75646/c
ID AAQ75646 standard; DNA; 21 BP.
XX
AC AAQ75646;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX

Query Match      1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAAAAAA 1752
DB 20 TACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 279
AAQ75647/c
ID AAQ75647 standard; DNA; 21 BP.
XX
AC AAQ75647;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
```

PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1752

Db 20 TACAAAAA 1

RESULT 279

AAQ75645/c

ID AAQ75645 standard; DNA; 21 BP.

XX AC AAQ75645;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; Gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1752

Db 20 TACAAAAA 1

RESULT 280

AAQ90391

ID AAQ90391 standard; DNA; 21 BP.

XX AC AAQ90391;

XX 08-JAN-1996 (first entry)

XX CP-1 (synthetic DNA probe with 3' ribonucleoside terminal #2).

XX CP-1; HLA; dQa; 3' ribonucleoside; self-addressable electronic device;
KW SAED; hybridisation; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_feature 21

FT /*tag= a

FT /note= "3' ribonucleoside terminal"

XX WO9512808-A1.

XX 11-MAY-1995.

XX 26-OCT-1994; 94WO-US012270.

XX 01-NOV-1993; 93US-00146504.

XX (NANO-) NANOGEN INC.

XX Heller MJ, Tu E;

XX WPI; 1995-185870/24.

XX New self-addressable electronic devices - used for multi-step and
PT multiplex reactions such as DNA hybridisation(s), clinical diagnostics
PT and bio:polymer synthesis.

XX Example 1; Page 40; 86pp; English.

XX The sequences represented by, AAQ90390-90401 are synthetic DNA probes
CC containing 3' ribonucleoside termini. The sequences shown in AAQ90402-15
CC are synthetic DNA probes with 5' amino termini. These sequences were
CC specific for the polymorphisms of HLA gene dQa. The sequences were used
CC in the device of the invention. This is a self-addressable electronic
CC device (SAED) that can be used to carry out multi-step and multiplex
CC reactions, such as nucleic acid hybridisations. The advantages of this
CC method are that these reactions can be carried out with complete and
CC precise electronic control, and that the rate, specificity and
CC sensitivity of these reactions are greatly improved at micro-locations
XX

SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 281

AAT10743

ID AAT10743 standard; RNA; 21 BP.

XX AC AAT10743;

XX 09-SEP-1996 (first entry)

XX Oligonucleotide probe, CP-1.

XX

```

KW Electronically self-addressable device; ED; electrode; current source;
KW attachment layer; permeable; counterion; genetic typing; probe;
KW detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 21
FT /*tag= a
FT /note= '3'-ribonucleoside terminus"
XX
PN WO9601836-A1.
XX
PD 25-JAN-1996.
XX
PF 05-JUL-1995; 95WO-US008570.
XX
PR 07-JUL-1994; 94US-00271882.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
XX WPI; 1996-097582/10.
XX
XX Electronically self-addressable device - used for electronic control of,
XX e.g. nucleic acid hybridisation.
XX
XX Example 1; Page 60; 155pp; English.
XX
XX The sequences given in AAT10742-67 are synthetic oligonucleotides which
XX are used in the construction of the electronically self-addressable
XX device (ED) of the invention. The ED comprises a substrate, an electrode
XX or opt. a number of electrodes supported by the substrate, a current
XX source operatively connected to the electrode and an attachment layer
XX adjacent to the electrode which is permeable to a counterion but not
XX permeable to a molecule capable of insulating or binding to the
XX electrode. The attachment layer is capable of attaching a macromolecule.
XX The ED is used for genetic typing and comprises a number of
XX electronically addressable locations each comprising an electrode, and a
XX binding entity, such as one of these probes, attached to each of the
XX locations capable of detecting the presence of a genetic sequence
XX
XX Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 1 AAAAAAAAAAAAAAAAAAAAAA 20
RESULT 282
AAV35395
ID AAV35395 standard; DNA; 21 BP.
XX
AC AAV35395;
XX
DT 13-OCT-1998 (first entry)
XX
DE HIV-1 gag protein DNA primer #8.
XX
XX Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX
OS Synthetic.
XX
XX WO9822596-A1.
XX
PD 28-MAY-1998.
XX

```

```

PF 19-NOV-1997; 97WO-JP004216.
XX
PR 19-NOV-1996; 96JP-00323412.
XX
PA (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
PA (JAPG) NIPPON ZEON KK.
XX
PI Kojima A, Kurata T, Yasuda A;
XX
XX WPI; 1998-312481/27.
XX
XX Recombinant vaccinia virus containing fusion H1B gag gene - for
XX production in host cells of gag protein for use as vaccine.
XX
PS Example 1; Page 66; 84pp; Japanese.
XX
XX AAV35388-V35414 are primers used in a method which results in a
XX recombinant vaccinia virus comprising of a gag gene from a retrovirus
XX such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
XX region (30-300 bases in length) of a retroviral gene other than the gag
XX gene. The gag gene may be altered so as to produce a gag protein modified
XX from the natural sequence by the addition, deletion or substitution of at
XX least 1 amino acid residue. The fusion gene is inserted into a region of
XX a vaccinia virus not essential to its propagation, to give a recombinant
XX vaccinia virus vector which is used to transform a host cell (such as
XX HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
XX culturing the host cell produces particulate structures containing the
XX fusion gag protein. The recombinant vaccinia virus or the fusion gag
XX protein particles may be used in the production of vaccines for
XX protecting against infection with retroviruses such as HIV
XX
XX Sequence 21 BP; 19 A; 2 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 2 CAAAAAAAAAAAAAAAAAAAAA 21
RESULT 283
AAV35395
ID AAV35395 standard; DNA; 21 BP.
XX
AC AAV35395;
XX
DT 20-AUG-1999 (first entry)
XX
XX 3' ribonucleoside oligonucleotide probe CP-1.
XX
XX Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control; transport;
KW attachment; binding; DNA/RNA hybrid; probe; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 21
XX /*tag= a
XX
XX WO9929711-A1.
XX
PD 17-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025475.
XX
PR 05-DEC-1997; 97US-00986065.
XX
PA (NANO-) NANOGEN INC.
XX
PI Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;

```

```

XX DR WPI; 1999-385567/32.
XX PT New microelectronic device designed to carry out and control multi-step
XX and multiplex molecular biological reactions in microscopic format.
XX Example 1; Page 89; 179pp; English.
XX The specification describes a self-addressable, self-assembling
XX microelectronic device which is designed to actively carry out and
XX control multi-step and multiplex molecular biological reactions in
XX microscopic formats. A key aspect of this invention is played by the ion
XX permeable permeation layer which overlies the electrode. This permeation
XX layer allows attachment of nucleic acids to permit immobilization but
XX also separates the attached oligonucleotides and hybridized target DNA
XX sequences from the highly reactive electrochemical environment generated
XX immediately at the electrode surface. The microelectronic device is
XX designed and fabricated to actively carry out and control reactions such
XX as nucleic acid hybridizations, antibody/antigen reactions, sample
XX preparation, diagnostics and biopolymer synthesis. The device can
XX electronically control the transport and attachment of specific binding
XX entities, such as nucleic acids and polypeptides, to specific micro-
XX locations. The device can subsequently control the transport and reaction
XX of analytes or reactants at the addressed specific micro-locations. The
XX device is able to concentrate analytes and reactants, remove non-
XX specifically bound molecules, provide stringency control for DNA
XX hybridization reactions and improve the detection of analytes. The
XX present sequence represents a probe used to exemplify the invention
XX SQ Sequence 21 BP; 20 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 284
AAX26973/C
ID AAX26973 standard; cDNA; 21 BP.
XX AC AAX26973;
XX DT 25-JUN-1999 (first entry)
XX DE Primer used to reverse transcribe mamaglobin RNA.
XX KW Human; mammary-specific protein; mamaglobin; antigen; vaccine;
XX KW mamaglobin-expressing cancer; breast cancer;
XX KW autologous tumor lymphocyte; diagnosis; marker; primer; ss.
XX OS Synthetic.
XX PN WO9914230-A1.
XX PD 25-MAR-1999.
XX PF 18-SEP-1998; 98WO-US017991.
XX PR 18-SEP-1997; 97US-00933149.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Watson MA, Fleming TP;
XX DR WPI; 1999-244021/20.
XX PT Mamaglobin, secreted protein overexpressed in breast cancer.
XX PS Example 2; Page 55; 60pp; English.

```

```

XX CC The present primer was used to reverse transcribe RNA encoding a human
XX CC mammary-specific protein, designated mamaglobin. The specification
XX CC describes a protein comprising a mamaglobin antigen that is recognized
XX CC by B and/or Tc cells specific for the natural, secreted and glycosylated
XX CC form of mamaglobin polypeptide. This protein, or recombinant vectors
XX CC that express it, are used in vaccines for treating mamaglobin-
XX CC expressing cancers, specifically of the breast. Such cancers can also be
XX CC treated using autologous tumor lymphocytes activated ex vivo with an
XX CC mamaglobin antigen, then returned to the patient. Expression of
XX CC mamaglobin is elevated in 2% of stage I primary breast cancers, so it
XX CC represents a marker useful for diagnosis of this disease
XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAA 2

RESULT 285
AAX44350/C
ID AAX44350 standard; DNA; 21 BP.
XX AC AAX44350;
XX DT 04-APR-2000 (first entry)
XX DE Protein kinase inhibiting primer #12.
XX KW Antimicrobial; cytostatic; immunosuppressive; protein kinase;
XX KW prophylactic; therapy; treatment; cancer; autoimmune disease;
XX KW pathogenic microorganism; primer; ss.
XX OS Unidentified.
XX PN US5998596-A.
XX PD 07-DEC-1999.
XX PF 04-APR-1995; 95US-00416214.
XX PR 04-APR-1995; 95US-00416214.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Bergan R, Neckers L;
XX KW WPI; 2000-104623/09.
XX DR Oligonucleotides inhibiting protein kinase, useful for treating diseases
XX PT such as cancer and autoimmune disease.
XX PS Example 8; Col 27-28; 26pp; English.
XX CC This invention describes novel purified aptameric oligonucleotides which
XX CC have antimicrobial, cytostatic and immunosuppressive activity. The
XX CC oligonucleotides are useful for binding to and preventing or inhibiting
XX CC the biological function of a protein kinase or a target molecule and for
XX CC detecting the presence or absence of a target molecule in biological
XX CC samples. The oligonucleotides are also useful for prophylactic and
XX CC therapeutic treatment of diseases such as cancer, autoimmune diseases and
XX CC diseases caused by pathogenic microorganisms. This sequence represents a
XX CC primer used in the method of the invention
XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 286
AAF99707/c
ID AAF99707 standard; DNA; 21 BP.
XX
AC AAF99707;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #823.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 287
```

```
AAH42480/c
ID AAH42480 standard; DNA; 21 BP.
XX
AC AAH42480;
XX
DT 01-OCT-2001 (first entry)
XX
DE Oligonucleotide used to produce branched chain compounds.
XX
KW Branched chain compound; nucleic acid synthesis; primer extension;
KW reverse transcription; nucleic acid hybridization;
KW nucleic acid amplification; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*note= "NH2-C6 attached"
FT modified_base 4 /*tag= b
FT /*note= "NH2-C6 attached"
FT misc_feature 6..7 /*tag= c
FT /*note= "branch present"
XX
PN EP1111068-A1.
XX
PD 27-JUN-2001.
XX
PF 21-DEC-1999; 99EP-00125484.
XX
PR 21-DEC-1999; 99EP-00125484.
XX
PA (LION-) LION BIOSCIENCE AG.
PA (VBCG-) VBC GENOMICS GMBH.
XX
PI Schmidt W, Hiller R, Huber M, Mueller M;
XX
DR WPI; 2001-466959/51.
XX
PT Branched compounds useful in e.g. nucleic acid synthesis reaction
PT comprises nucleic acid moieties optionally extended by a polymerase.
XX
PS Example 1; Page 10; 31pp; English.
XX
CC The specification describes branched compounds containing nucleic acid
CC moieties optionally extended by a polymerase. The branched chain
CC compounds of the invention are used in nucleic acid synthesis reaction,
CC primer extension reaction, reverse transcription reaction of RNA into
CC DNA, nucleic acid hybridization experiment (for identifying sequence of a
CC nucleic acid), and nucleic acid amplification experiment (for analysing
CC the expression pattern of genes). The compounds are also used in solid-
CC phase enzymatic reactions. The present sequence was used in the course of
CC the invention to produce branched chain compounds
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 288
ABS78428/c
ID ABS78428 standard; DNA; 21 BP.
XX
AC ABS78428;
XX
```

DT 13-DEC-2002 (first entry)
DE Angiogenesis inhibitory oligonucleotide #912.
XX
KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
KW plaque neovascularisation; telangiectasia; haemophilic joint;
KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
KW scleroderma; hypertrophic scar.
XX
OS Synthetic.
XX
PN WO200253141-A2.
XX
PD 11-JUL-2002.
XX
PF 14-DEC-2001; 2001WO-US048458.
XX
PR 14-DEC-2000; 2000US-0255534P.
XX
PA (COLE-) COLEY PHARM GROUP INC.
XX
PI Bratzler RL;
XX
DR WPI; 2002-566690/60.
XX
XX Inhibiting angiogenesis in a subject, involves administering at least one
PT antiangiogenic nucleic acid molecule to the subject.
XX
PS Claim 2; Page 35; 276pp; English.
XX
CC The invention relates to inhibiting angiogenesis in a subject, comprising
CC administering at least one antiangiogenic nucleic acid molecule. Also
CC included is a kit comprising a first container housing the antiangiogenic
CC nucleic acids, and instructions for administering them to a subject
CC having a condition characterised by unwanted angiogenesis. The method is
CC useful for inhibiting angiogenesis associated with solid tumour growth,
CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
CC acid of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 289
ABL39404/c
ID ABL39404 standard; DNA; 21 BP.
XX
AC ABL39404;
XX
XX 16-APR-2002 (first entry)
DT Immunostimulatory nucleic acid SEQ ID NO: 840.
DE Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
KW angiogenesis; metastasis; cytostatic; phosphorothioate backbone; ss.
XX

OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..21
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate backbone"
XX
PN WO200197843-A2.
XX
PD 27-DEC-2001.
XX
PF 22-JUN-2001; 2001WO-US020154.
XX
PR 22-JUN-2000; 2000US-0213346P.
XX
PA (IOWA) UNIV IOWA RES FOUND.
XX
PI Weiner G, Hartmann G;
XX
DR WPI; 2002-154611/20.
XX
XX Treating or preventing cancer, such as basal cell carcinoma, comprises
PT administering immunostimulatory nucleic acids that induce expression of
PT cell surface antigens and antibodies to a subject having or at risk of
PT developing cancer.
XX
PS Disclosure; Page 309; 312pp; English.
XX
CC The present invention relates to methods for treating or preventing
CC cancer, involving administering to a subject having or at risk of
CC developing cancer immunostimulatory nucleic acids that induce expression
CC of cell surface antigens and antibodies. The methods are useful for
CC treating or preventing cancer such as basal cell carcinoma, bladder
CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
CC breast cancer, cervical cancer, colon and rectum cancer, connective
CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
CC present sequence is an immunostimulatory oligonucleotide described in the
CC exemplification of the invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
Query Match 1.1%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.6e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 290
AAD51323/c
ID AAD51323 standard; DNA; 21 BP.
XX
AC AAD51323;
XX
XX 16-APR-2003 (first entry)
DT Regular oligo dT primer used to illustrate the method of the invention.
DE Laminitis; viral disease; vaccine; bacterial disease; primer; epistaxis;
KW gastritis; gastric ulcer; respiratory ailment; fracture; joint disease;
KW musculoskeletal damage; ss.
XX
OS Unidentified.
XX
PN WO200290579-A1.
XX

PD 14-NOV-2002.
 XX
 PF 03-MAY-2002; 2002WO-AU000553.
 XX
 PR 04-MAY-2001; 2001AU-00004809.
 XX
 PR 29-JUN-2001; 2001US-00896941.
 XX
 PA (GENO-) GENOMICS RES PARTNERS PTY LTD.
 XX
 PI Brandon RB;
 XX
 XX WPI; 2003-120558/11.

XX Assessing condition e.g. athletic ability, stage of disease, presence of
 PT drugs, response to exercise, response to vaccines, therapies, nutritional
 PT states, of performance animal involves analyzing nucleic acid expression.
 XX
 PS Disclosure; Page 46; 87pp; English.

XX The invention relates to a method for assessing a condition of a
 CC performance animal. The method involves determining in sample abundance
 CC of expressed target nucleic acid; transmitting digital sample signal to
 CC remote diagnostic server; processing digital sample signal at remotely
 CC located database to correlate digital signal with digital information and
 CC returning report of particular condition of animal. The method is useful
 CC for assessing a condition of a performance animal preferably human, dog
 CC or camel. The condition can be an athletic ability and a condition that
 CC enhances, hinders, impedes or does not change an expected ability of the
 CC performance animal; and also normal, pre-clinical, overt progress and/or
 CC stage of disease, undiagnosed or unclassified conditions, presence of
 CC drugs, response to exercise, response to vaccines, therapies, nutritional
 CC states and response to environmental conditions. Diseases assessed by the
 CC invention include laminitis, lameness, viral or bacterial disease,
 CC gastritis, gastric ulcers, respiratory ailments, fractures, epistaxis,
 CC musculoskeletal damage or disorders and joint diseases. The present
 CC sequence is a primer used to illustrate the method of the invention

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 DB 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 291
 ACH03246/c
 ID ACH03246 standard; DNA; 21 BP.

XX ACH03246;
 XX
 DT 25-SEP-2003 (first entry)
 XX
 DE Immunostimulatory nucleic acid #881.

XX Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.

XX Synthetic.

XX US2003050268-A1.

XX 13-MAR-2003.

XX 29-MAR-2002; 2002US-00112653.

XX 29-MAR-2001; 2001US-0279642P.

XX

PA (KRIE/) KRIEG A M.
 XX (BERG/) BERG D J.
 PI Krieg AM, Berg DJ;
 XX WPI; 2003-521815/49.

XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel
 PT disease by administering an immunostimulatory nucleic acid.

XX Disclosure; Page 33; 229pp; English.

XX The invention describes a method of treating non-allergic inflammatory
 CC disease comprising administering to a subject having or at risk of
 CC developing a non-allergic inflammatory disease an immunostimulatory
 CC nucleic acid for prevention or treatment of the disease. The method is
 CC useful for treating non-allergic inflammatory diseases, such as
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
 CC This sequence represents an immunostimulatory nucleic acid

XX SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 DB 21 AAAAAAAAAAAAAAAAAAAAAA 2

RESULT 292
 ADB37209/c
 ID ADB37209 standard; DNA; 21 BP.

XX ADB37209;

XX 04-DEC-2003 (first entry)

XX Immunostimulatory nucleic acid #823.

XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.

XX Synthetic.

XX US2003087848-A1.

XX 08-MAY-2003.

XX 02-FEB-2001; 2001US-00776479.

XX 03-FEB-2000; 2000US-0179991P.

XX (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 XX (FOUR/) FOURON Y.

XX Bratzler RL, Petersen DM, Fouron Y;

XX WPI; 2003-657977/62.

XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.

XX Disclosure; Page 17; 221pp; English.

XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy

CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX
 SQ Sequence 21 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 21 AAAAAAAAAAAAAAAAAAAAAA 2
 RESULT 293
 ID AAQ30432/C
 XX AAQ30432 standard; DNA; 23 BP.
 AC AAQ30432;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-DEC-1992 (first entry)
 XX
 DE Oligomer IL6805 for forming triplex with HUMIL6 target duplex.
 XX Human interleukin-6 gene; herpes simplex; AIDS; modified; HIV; RSV; HPV;
 KW malignancy; hepatitis; inflammation; ss.
 KW
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1
 FT /tag= a
 FT /mod base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 FT 11..12
 FT misc_feature
 FT /tag= d
 FT /note= "o-xyloso dimer synthon linkage"
 FT 12..23
 FT misc_feature
 FT /tag= c
 FT /label= inverted_polarity_region
 FT /note= "see comments"
 FT 23
 FT modified_base
 FT /tag= b
 FT /mod base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 FT
 XX WO209705-A1.
 XX
 XX 11-JUN-1992.
 XX
 XX 25-NOV-1991; 91WO-US008811.
 XX
 XX 23-NOV-1990; 90US-00617907.
 XX 18-JAN-1991; 91US-00643382.
 XX 08-APR-1991; 91US-00683420.
 XX 17-APR-1991; 91US-00686544.
 XX 17-APR-1991; 91US-00686546.
 XX 17-APR-1991; 91US-00686547.
 XX 27-SEP-1991; 91US-00766733.
 XX
 PA (GILE-) GILEAD SCI INC.
 XX
 XX Froehner B, Krawczyk S, Matteucci MD, Milligan J;
 PI WPI; 1992-217083/26.
 XX
 DR New oligomers contg. modified bases - which form a triplex with G-C
 XX doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
 PT herpes malignancy and inflammation.
 PT
 XX Claim 12; Page 71; 77pp; English.
 PS
 XX

CC The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a purine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC interleukin 6 gene untranslated sequence contg. a purine rich sequence
 CC concd. on one strand of the duplex. The oligomer, and others like it are
 CC useful in diagnosis and therapy of diseases characterised by specific DNA
 CC duplex targets, e.g. HPV, HER, HIV, hepatitis B, herpes, malignant
 CC tumours and inflammation. The triple helices form under mild conditions
 CC thus assays may be carried out without subjecting the test specimen to
 CC harsh conditions. The oligomer contains an inverted polarity region
 CC formed from an o-xyloso dimer synthon. The linking gp. is o-xyloso
 CC (nucleotides have the 3'positions of xylose sugars linked via the o-
 CC xylene ring). Two nucleotides are coupled through a xylene residue to
 CC form the dimer synthon. This additional modifications may render the
 CC oligomer stable to nuclease activity. The oligomer is able to inhibit
 CC gene expression, as verified by in vitro systems. See also AAQ25452-25501
 CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 23 BP; 0 A; 2 C; 0 G; 21 T; 0 U; 0 Other;
 Query Match 1.1%; Score 20; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 Db 22 AAAAAAAAAAAAAAAAAAAAAA 3
 RESULT 294
 ID AAF16627/C
 XX AAF16627 standard; DNA; 23 BP.
 AC AAF16627;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 114.
 KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;
 KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;
 KW DNA-RNA hybrid; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200071164-A1.
 XX
 XX 30-NOV-2000.
 XX
 XX 24-MAY-2000; 2000WO-AU000498.
 XX
 XX 24-MAY-1999; 99AU-00000510.
 XX
 XX (TACH/) TACHAS G.
 XX
 XX Tachas G;
 PI
 XX WPI; 2001-025093/03.
 DR
 XX
 XX Treating gastric acid disturbance by administering an oligonucleotide
 XX which modulates the activity of a polypeptide involved in gastric acid
 XX production or secretion.
 XX
 XX Example 3; Page 152; 164pp; English.
 XX
 XX The present invention provides oligonucleotides, and methods for their
 XX use, which are useful in modulating the action of proteins involved in
 XX gastric acid production. The target protein is preferably the histamine
 XX H2 receptor or one of the proteins which form part of the gastric proton
 XX pump. The sequences and methods of the invention are useful in the
 XX treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
 XX duodenal ulcers and other gastric acid disturbances, most of which are
 XX caused by Helicobacter pylori

```
XX Sequence 23 BP; 1 A; 0 C; 0 G; 22 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 20; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 23 AAAAAAAAAAAAAAAAAAAAAA 4

RESULT 295
AAI64873/C
ID AAI64873 standard; DNA; 24 BP.
XX
AC AAI64873;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human serine/threonine protein kinase 48 cDNA PCR primer #2.
XX
KW Human; serine/threonine protein kinase 48; cancer; HIV infection;
KW gene therapy; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN CN1300831-A.
XX
PD 27-JUN-2001.
XX
PF 22-DEC-1999; 99CN-00125686.
XX
PR 22-DEC-1999; 99CN-00125686.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PI Mao Y, Xie Y;
XX
WPI; 2001-530471/59.
XX
New human serine/threonine protein kinase 48 and its encoding
PT polynucleotide, useful for treating cancer and human immunodeficiency
PT virus infection.
XX
PS Example 3; Page 17(Disclosure); 33pp; Chinese.
XX
The present invention provides the protein and coding sequences of human
CC serine/threonine protein kinase 48. The sequences can be used in the
CC treatment of cancer and HIV infection. The present sequence is a PCR
CC primer for the coding sequence of the invention
XX
SQ Sequence 24 BP; 3 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1731 TTACAAAAAAAAAAAAAAAA 1750
DB 20 TTACAAAAAAAAAAAAAAAA 1

RESULT 296
ABL55130/C
ID ABL55130 standard; DNA; 24 BP.
XX
AC ABL55130;
XX
DT 31-MAY-2002 (first entry)
XX
DE Human gonadotropin-releasing hormone 10 RT-PCR primer, SEQ ID NO:4.
XX
```

```
KW Human; gonadotropin-releasing hormone 10; recombinant production; cancer;
KW HIV infection; human immunodeficiency virus; gene therapy; cytostatic;
XX anti-HIV; reverse transcription-PCR; RT-PCR; primer; ss.
OS Homo sapiens.
XX
PN CN1325900-A.
XX
PD 12-DEC-2001.
XX
PF 31-MAY-2000; 2000CN-00116266.
XX
PR 31-MAY-2000; 2000CN-00116266.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PI Mao Y, Xie Y;
XX
WPI; 2002-196660/26.
XX
Polypeptide-human gonadotropin-releasing hormone 10 and polynucleotide
PT encoding it.
XX
PS Example 2; Page 17 (Disclosure); 32pp; Chinese.
XX
The invention relates to human gonadotropin-releasing hormone 10
CC (AM49158) and to nucleic acids encoding it (ABL55128). The protein has a
CC molecular weight of 10 kD. The invention also relates to a method for the
CC recombinant production of the protein, an antagonist of the protein, and
CC the use of the protein, gene and antagonist in therapeutic applications.
CC Gonadotropin-releasing hormone 10 can be used in the treatment of a
CC variety of diseases such as cancer and HIV (human immunodeficiency virus)
CC infection. Sequences ABL55129-ABL55130 represent reverse transcription-
CC PCR (RT-PCR) primers used in an exemplification of the invention to
CC isolate human gonadotropin-releasing hormone 10 cDNA
XX
SQ Sequence 24 BP; 1 A; 1 C; 3 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 297
ABK86172/C
ID ABK86172 standard; DNA; 24 BP.
XX
AC ABK86172;
XX
DT 24-SEP-2002 (first entry)
XX
DE Oligo dT primer #4 used in method to study gene expression.
XX
KW Oligo dT primer; gene expression analysis; primer; ss.
XX
OS Synthetic.
XX
PN WO200236828-A2.
XX
PD 10-MAY-2002.
XX
PF 01-NOV-2001; 2001WO-US045401.
XX
PR 01-NOV-2000; 2000US-0244933P.
XX
PA (GENO-) GENOMIC SOLUTIONS INC.
XX
PI Kane MD, Dombkowski AA, Nagel AC;
XX
```

DR WPI; 2002-508123/54.
XX
PT Identifying and characterizing gene expression in samples, for
PT identifying mRNAs expressed at different levels, comprises employing an
PT identifier having an oligo-dT primer of a specific sequence and a
PT detectable marker at its 5' end.
XX
PS Example 1; Page 15; 45pp; English.
XX
CC The invention relates to systems for identification and characterization
CC of gene expression in one or more samples, comprising an identifier having
CC a specific oligo-dT primer sequence, where the identifier comprises a
CC detectable marker at its 5' end. The system is useful for identifying any
CC or all genes expressed in a given in vivo or in vitro RNA sample, as well
CC as the relative differences in mRNA between 2 or more samples, where
CC desired, for supporting discovery of new genes, and for identifying mRNAs
CC that are expressed at different levels between 2 or more samples. The new
CC system or method addresses limitations of prior methods by comprising
CC compositions and systems that incorporate new strategies where molecular
CC or biochemical assay compositions and systems are linked to DNA or RNA
CC sequence databases for optimal resource efficiency in assaying gene
CC expression. The system has the following advantages over existing
CC methods: (a) prior sequence information or clone library construction is
CC not needed to enable the assay; (b) provides immediate sequence
CC information in addition to information concerning changes or differences
CC in mRNA level; (c) determines mRNA expression level and mRNA identification
CC in one assay; (d) generates cDNA fragments from all mRNAs present in the
CC sample for subsequent investigation by common molecular biology
CC techniques; and (d) does not require prior knowledge of the sequence of
CC the genome of the organism under investigation and can be employed in
CC organisms lacking significant genomic sequence information. The present
CC sequence represents an oligo dT primer used in the method of the
XX invention
XX
SQ Sequence 24 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 4 Other;
Query Match 1.1%; Score 20; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAAAAAA 5
RESULT 298
ABS56855
ID ABS56855 standard; DNA; 24 BP.
AC ABS56855;
XX
DT 29-JAN-2003 (first entry)
XX
DE Human PDZ protein 11.99 cDNA RT-PCR primer #1.
XX
KW Human; PDZ protein 11.99; ss; malignant tumour; haemopathy; cancer;
KW HIV infection; human immunodeficiency virus; immunological disease;
KW inflammation; primer; RT-PCR; reverse transcriptase.
XX
OS Homo sapiens.
XX
FN CN1345800-A.
XX
PD 24-APR-2002.
XX
PF 26-SEP-2000; 2000CN-00125416.
XX
PR 26-SEP-2000; 2000CN-00125416.
XX
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI Mao Y, Xie Y;
XX

DR WPI; 2002-539316/58.
XX
PT Novel polypeptide-human PDZ protein 11.99 and polynucleotide for encoding
PT said polypeptide.
XX
PS Example 2; Page 16 (Disclosure); 32pp; Chinese.
XX
CC The invention relates to the human PDZ protein 11.99, a polynucleotide
CC encoding the polypeptide and a method for producing the polypeptide using
CC DNA recombination technology. The polypeptide is used for curing several
CC diseases such as malignant tumours, haemopathy, HIV infection,
CC immunological disease and various inflammations. This sequence represents
CC a reverse transcriptase PCR (RT-PCR) primer used in isolation of cDNA
CC encoding the human PDZ protein 11.99
XX
SQ Sequence 24 BP; 15 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
Query Match 1.1%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 28 GGAAGAGGAGGAAAAAAAAAAGCCAG 50
Db 2 GGAAGAGGAGGAAAAAAAAAAGGAG 24
RESULT 299
AAL47515/c
ID AAL47515 standard; DNA; 24 BP.
XX
AC AAL47515;
XX
DT 13-SEP-2002 (first entry)
XX
DE Human cyclophilin-40-12-54 coding sequence PCR primer #2.
XX
KW Human; cyclophilin-40-12.54; immunopathy; cancer; PCR; primer; ss.
XX
OS Homo sapiens.
XX
FN CN1331162-A.
XX
PD 16-JAN-2002.
XX
PF 28-JUN-2000; 2000CN-00116823.
XX
PR 28-JUN-2000; 2000CN-00116823.
XX
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-305482/35.
XX
PT Polypeptide-human cyclophilin-40-12.54 and polynucleotide for coding it.
XX
PS Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC The present invention provides the protein and coding sequences of human
CC cyclophilin-40-12.54. The sequences can be used in the treatment of
CC immunopathy and cancer. The present sequence is a PCR primer for the
CC coding sequence of the invention
XX
SQ Sequence 24 BP; 2 A; 1 C; 2 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1755
Db 23 TACTAAAAAAAAAAAAAAAAAAAAA 1

AA01577 standard; DNA; 26 BP.
AA01577;
18-JUL-2001 (first entry)
Human T-type calcium channel CACNA1G R6 3'-bisulfite PCR primer.
Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
cellular proliferative disorder; colorectal cancer; age related disease;
apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBNI;
G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
chromosome 17; PCR primer; ss.
Homo sapiens.
WO200119845-A1.
22-MAR-2001.
14-SEP-2000; 2000WO-US025479.
15-SEP-1999; 99US-00398522.
(UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Issa J;
WPI; 2001-244777/25.
New nucleic acid molecule for use as a marker for screening cancer.
comprises the coding region for a T-type calcium channel and regulatory
sequences associated with the channel.
Claim 21; Page 34; 125pp; English.
The present sequence for 3'-bisulfite PCR primer is used to study the
methylation state of region R6 in a novel human T-type calcium channel
CACNA1G which maps to chromosome 17. The methylation state of specific
regions within CpG islands associated with the CACNA1G gene correlate
with several cancerous phenotypes involving various tissue and cell
types. Since aberrant methylation of normally unmethylated CpG islands is
often observed in immortalised and transformed cells, CACNA1G is
implicated in cellular proliferative disorders e.g. leukaemia,
colorectal, lung, breast and other cancers. The nucleic acid coding for
CACNA1G is useful as a marker for screening cancer and age related
diseases. A diagnostic kit containing primers (AA01574-AA01623) for
amplification of a CpG-containing nucleic acid, where the primer
hybridises with a target polynucleotide sequence (AA01627-AA01676), can
be used for detecting aberrant methylation. The CpG island sequences
(AA01677-AA01692) are selected from genes encoding CACNA1G,
apolipoprotein B (APOB), caudal type homeobox transcription factor 2
(CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBNI), G
protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
activated receptor 2 (PAR2), paired-like homeodomain transcription factor
2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
SDC4) or a MINT31 sequence
Sequence 26 BP; 18 A; 3 C; 0 G; 4 T; 0 U; 1 Other;

Query Match 1.1%; Score 19.6; DB 1; Length 26;
Best Local Similarity 95.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1753

DB 1 ACRAAAAAAAAAAAAAAAAAA 20

RESULT 303
AA01670/C
ID AA01670 standard; DNA; 26 BP.
XX
XX AA01670;
AC AA01670;
XX
XX 18-JUL-2001 (first entry)
DT
XX
XX Human MINT31/CACNA1G region 6 reverse target sequence for bisulfite PCR.
DE
XX
XX Human; T-type calcium channel; CACNA1G; cytosine methylation; CpG island;
cellular proliferative disorder; colorectal cancer; age related disease;
apolipoprotein B; APOB; caudal type homeobox transcription factor 2;
CDX2; epidermal growth factor receptor; EGFR; fibrillin-1; FBNI;
G protein-coupled receptor 37; GPR37; heat shock 70kD protein 6; HSP70B';
HSPA6; RasGAP-related protein; IQGAP2; proteinase-activated receptor 2;
PAR2; paired-like homeodomain transcription factor 2; PITX2; klotho; KL;
patched A; patched B; PTCHA; PTCHB; syndecan 1; syndecan 4; SDC1; SDC4;
chromosome 17; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200119845-A1.
PN
XX
XX 22-MAR-2001.
PD
XX
XX 14-SEP-2000; 2000WO-US025479.
PF
XX
XX 15-SEP-1999; 99US-00398522.
PR
XX
XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA
XX
XX Issa J;
PI
XX
XX WPI; 2001-244777/25.
DR
XX
XX New nucleic acid molecule for use as a marker for screening cancer,
comprises the coding region for a T-type calcium channel and regulatory
sequences associated with the channel.
PT
XX
XX Claim 20; Page 36; 125pp; English.
PS
XX
XX The present sequence for human MINT31/T-type calcium channel CACNA1G
region 6 reverse target sequence is used to study the methylation state
of region 6 in MINT31/CACNA1G which map to chromosome 17. The methylation
state of specific regions within CpG islands associated with the CACNA1G
gene correlate with several cancerous phenotypes involving various tissue
and cell types. Since aberrant methylation of normally unmethylated CpG
islands is often observed in immortalised and transformed cells, CACNA1G
is implicated in cellular proliferative disorders e.g. leukaemia,
colorectal, lung, breast and other cancers. The nucleic acid coding for
CACNA1G is useful as a marker for screening cancer and age related
diseases. A diagnostic kit containing primers (AA01574-AA01623) for
amplification of a CpG-containing nucleic acid, where the primer
hybridises with a target polynucleotide sequence (AA01627-AA01676), can
be used for detecting aberrant methylation. The CpG island sequences
(AA01677-AA01692) are selected from genes encoding CACNA1G,
apolipoprotein B (APOB), caudal type homeobox transcription factor 2
(CDX2), epidermal growth factor receptor (EGFR), fibrillin-1 (FBNI), G
protein-coupled receptor 37 (GPR37), heat shock 70kD protein 6 (HSP70B';
HSPA6), RasGAP-related protein (IQGAP2), klotho (KL), proteinase-
activated receptor 2 (PAR2), paired-like homeodomain transcription factor
2 (PITX2), patched A and B (PTCHA; PTCHB) and syndecan 1 and 4 (SDC1;
SDC4) or a MINT31 sequence
XX
XX Sequence 26 BP; 4 A; 0 C; 3 G; 18 T; 0 U; 1 Other;

Query Match 1.1%; Score 19.6; DB 1; Length 26;

Best Local Similarity 95.0%; Pred. No. 2.2e+02;

Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAAAA 1753

```
Db      26 ACRAAAAAAAAAAAAAAAAAAAA 7
|||||
RESULT 304
AAQ75648/c
ID AAQ75648 standard; DNA; 21 BP.
XX
AC AAQ75648;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAAAAAA 1752
Db 21 TTATAAAAAAAAAAAAAAAAAAAA 1

RESULT 306
AAQ75660/c
ID AAQ75660 standard; DNA; 21 BP.
XX
AC AAQ75660;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAAAAAA 1752
Db 21 TAACAAAAAAAAAAAAAAAAAAAA 1

RESULT 305
AAQ75676/c
ID AAQ75676 standard; DNA; 21 BP.
XX
AC AAQ75676;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
```



```
PT by digestion with restriction enzymes.
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1754
||| |||||
Db 21 ACACAAAAA 1754

RESULT 310
AAQ75769/c
ID AAQ75769 standard; DNA; 21 BP.
XX
AC AAQ75769;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1754
||| |||||
Db 21 ACACAAAAA 1754

RESULT 310
AAQ75769/c
ID AAQ75769 standard; DNA; 21 BP.
XX
AC AAQ75769;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1754
||| |||||
Db 21 ACACAAAAA 1754

RESULT 311
AAQ75628/c
ID AAQ75628 standard; DNA; 21 BP.
XX
AC AAQ75628;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1752
||| |||||
Db 21 TTACAAAAA 1752

RESULT 312
AAQ75726/c
ID AAQ75726 standard; DNA; 21 BP.
XX
AC AAQ75726;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
XX
PD 01-NOV-1994.
```



```

XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1730 GTTTACAAAAA 1750
Db 21 GTTTAAAAA 1

RESULT 313
AAQ75712/C
ID AAQ75712 standard; DNA; 21 BP.
XX AC AAQ75712;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX FA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1730 GTTTACAAAAA 1750
Db 21 GTTTAAAAA 1

RESULT 314
AAQ75775/C
ID AAQ75775 standard; DNA; 21 BP.
XX AC AAQ75775;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX FA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1753
Db 21 TACTAAAAA 1

RESULT 315
AAQ75673/C
ID AAQ75673 standard; DNA; 21 BP.
XX AC AAQ75673;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX

```

```

CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1753
Db 21 TACTAAAAA 1

RESULT 314
AAQ75775/C
ID AAQ75775 standard; DNA; 21 BP.
XX AC AAQ75775;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX FA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily.
XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAGAAAAA 1755
Db 21 CAAGAAAAA 1

RESULT 315
AAQ75673/C
ID AAQ75673 standard; DNA; 21 BP.
XX AC AAQ75673;
XX XX
XX DT 04-AUG-1995 (first entry)
XX XX

```


RESULT 318

AAQ75616/c

ID AAQ75616 standard; DNA; 21 BP.

XX

AC AAQ75616;

XX

DT 04-AUG-1995 (first entry)

XX

DE Reverse transcription primer used in cDNA analysis technique.

XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX

OS aggregate; restriction enzyme; ss.

XX

PN JP06303997-A.

XX

PD 01-NOV-1994.

XX

PF '16-APR-1993; 93JP-00112515.

XX

PR 16-APR-1993; 93JP-00112515.

XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX

XX WPI; 1995-018287/03.

DR

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

PT

XX by digestion with restriction enzymes.

XX

PS Disclosure; Page 6; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

CC

CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)

CC

CC and using the aggregate of mRNAs as the template for each reverse

CC

CC transcription primer; (b) digesting each of the prepared aggregates of

CC

CC the double-stranded cDNAs with restriction enzyme and; (c)

CC

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC

CC method can be used to analyse gene expression rapidly and easily

XX

SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

XX

XX Query Match 1.1%; Score 19.4; DB 1; Length 21;

XX

XX Best Local Similarity 95.2%; Pred. No. 2e+02; 1; Indels 0; Gaps 0;

XX

XX Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

Qy 1733 TACAAAAA 1753

Db 21 TACAAAAA 1

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

PF

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

16-APR-1993; 93JP-00112515.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

16-APR-1993; 93JP-00112515.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

16-APR-1993; 93JP-00112515.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

```
XX SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAGAAAAA 1755
||| ||||| ||||| |||||
DB 21 CAACAAAAA 1

RESULT 321
AAQ75744/C
ID AAQ75744 standard; DNA; 21 BP.
XX AC AAQ75744;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 21;
Best Local Similarity 95.2%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1753
||| ||||| ||||| |||||
DB 21 TACGAAAAA 1

RESULT 322
AAT68615/C
ID AAT68615 standard; DNA; 24 BP.
XX AC AAT68615;
XX DT 20-FEB-1998 (first entry)
XX DE DNA probe used in fingerprinting technique.

XX probe; screening; fingerprinting; assay; 3' termini; hybridisation; ss.
XX Synthetic.
XX PN EP778351-A2.
XX PD 11-JUN-1997.
XX PF 26-NOV-1996; 96EP-00118921.
XX PR 30-NOV-1995; 95JP-00311949.
XX PA (HITA) HITACHI LTD.
XX PI Kambara H, Okano K, Uematsu C;
XX DR WPI; 1997-300347/28.
XX PT Nucleic acid assay methods - based on restriction fragment length
XX PT determination.
XX PS Example 1; Page 7; 21pp; English.
XX CC The present sequence is a DNA probe used in a novel method of analysis or
XX CC assay for nucleotides, which comprises: (i) digesting DNA with a
XX CC restriction enzyme; (ii) discriminating a difference in sequences of the
XX CC DNA fragments obtained around the 3' termini with a DNA probe and
XX CC extending the DNA probe by a complementary strand synthesis to
XX CC fractionate the DNA fragments into groups; and (iii) measuring lengths of
XX CC the DNA fragments which belong to the groups, or length of the extended
XX CC DNA probe, and using the lengths obtained for the fragments around the 3'
XX CC termini as fingerprints. Where polyA is present, the presence of
XX CC recognition sequence GCG is critical for clarifying the terminal site,
XX CC this is because the length of polyA cannot be controlled. The method is
XX CC useful for assaying a large number of cDNA molecules or DNA fragments and
XX CC for assaying long DNA sequences
XX SQ Sequence 24 BP; 0 A; 2 C; 1 G; 19 T; 0 U; 2 Other;

Query Match 1.1%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 2.2e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1755
||| ||||| ||||| |||||
DB 21 CGAAAAA 1

RESULT 323
ABZ23536
ID ABZ23536 standard; DNA; 24 BP.
XX AC ABZ23536;
XX DT 07-APR-2003 (first entry)
XX DE fragment of a plasmid used to detect somatic instability.
XX KW Replication error; drug development; somatic instability; ss.
XX OS Synthetic.
XX FH Key misc_feature 4 Location/Qualifiers
XX FT /tag= a
XX FT /note= "this base represents an unspecified number of
XX FT bases"
XX FT 21
XX FT misc_feature 21
XX FT /tag= b
XX FT /note= "this base represents an unspecified number of
XX FT bases"
XX FT 21
```



```

PI Kim BH, Kim SJ;
XX WPI; 2003-627375/59.
XX
XX New calix(4)arene-nucleoside hybrid useful in gene therapy has at least
PT one nucleoside attached to a calix(4)arene group through amide bonding,
PT and is derived from a calix(4)arene having amino groups.
XX
XX Claim 7; Page 20; 16pp; English.
XX
CC The present sequence is that of a calix(4)arene-oligonucleotide hybrid of
CC the invention, which includes a calix(4)arene-nucleoside (preferably
CC thymidine) derivative. The calix(4)arene-oligonucleotide hybrid functions
CC as a DNA hairpin structure mimic. It effectively recognises DNA or RNA
CC through triplex formation by bonding between the calix(4)arene-containing
CC cavity and a biologically active substance. The hybrid has a certain
CC level of both rigidity and flexibility, is stable in vivo, has high cell
CC permeability and can be mass-produced. It can be used as a DNA sensor or
CC for gene therapy
XX
XX Sequence 25 BP; 0 A; 0 C; 0 G; 24 T; 0 U; 1 Other;
SQ
Query Match 1.1%; Score 19.4; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 2.3e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACCAAAAA1755
DB 25 AAAAAAAAAAAAAAAAAAAAAA 4
RESULT 326
ACC48482/c
ID ACC48482 standard; DNA; 21 BP.
XX
XX ACC48482;
XX
XX 11-AUG-2003 (first entry)
XX
XX Locked nucleic acid anchored oligo(I) primer ON12.
XX
XX Locked nucleic acid; LNA; gene therapy; primer; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 3
FT /*tag= b
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 5
FT /*tag= c
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 7
FT /*tag= d
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 9
FT /*tag= e
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 11
FT /*tag= f
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 13
FT /*tag= g
FT /*mod_base= OTHER

```

```

FT modified_base 15
FT /*tag= h
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 17
FT /*tag= i
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 19
FT /*tag= j
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 21
FT /*tag= k
FT /*mod_base= OTHER
FT /*note= "OTHER= locked nucleic acid"
FT modified_base 22
FT /*tag= l
FT /*mod_base= OTHER
FT /*note= "OTHER= Compound 17d"
XX
XX WO2003020739-A2.
XX
XX 13-MAR-2003.
XX
XX 04-SEP-2002; 2002WO-1B003911.
XX
XX 04-SEP-2001; 2001US-0317034P.
XX
XX 22-SEP-2001; 2001US-0323967P.
XX
XX (EXIQ-) EXIQON AS.
XX
XX Wengel J, Kauppinen S;
XX
XX WPI; 2003-363021/34.
XX
XX Novel nucleic acid comprising a locked nucleic acid unit having a
PT modified base that comprises an optionally substituted carbocyclic aryl
PT moiety, or modified nucleobase or nucleosidic base other than
PT oxazole/imidazole.
XX
XX Example 24a; Page 90; 119pp; English.
XX
XX The present sequence is that of pyrene-anchored locked nucleic acid (LNA)
CC oligo(dT) primer ON12, which was used in first-strand cDNA synthesis from
CC eukaryotic mRNA. It includes compound '17d' at its 3' end, which is based
CC on an LNA-type 2'-O,4'-C-methylene- beta-D-ribofuranosyl moiety. It is
CC one of a set of such primers (see also ACC48483-85) that were used in an
CC example from the invention to demonstrate improved reverse transcription
CC of mRNA using pyrene-LNA anchored oligo(T) primers. The following results
CC were observed: efficient priming on mRNAs with short poly(A) tails;
CC efficient anchoring of the oligo(T) primer by pyrene-LNA and LNA-C/G/T
CC units resulting in an improved T20-VN anchor primer and thus avoiding
CC reverse transcription of long poly(A) tracts; and improved reverse
CC transcription of eukaryotic poly(A)+RNA directly from total RNA extracts
CC due to increased specificity. The invention relates to modified LNA units
CC that comprise unique base groups. Desirable nucleobase and nucleosidic
CC base substitutions can mediate universal hybridisation when incorporated
CC into nucleic acid strands. The novel LNA compounds can be used e.g. as
CC PCR primers, in sequencing, the synthesis of antisense oligonucleotides,
CC and in diagnostics
XX
XX Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;
SQ
Query Match 1.1%; Score 19.2; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAA1754
DB 20 BAAAAA1

```

```

RESULT 327
ACC99729/c
ID ACC99729 standard; DNA; 21 BP.
XX
AC ACC99729;
XX
DT 02-SEP-2003 (first entry)
XX
DE Oligonucleotide.
XX
KW Multiplex real-time quantitative PCR; PCR primer; copy number;
KW Alzheimer's disease; ss.
XX
OS Synthetic.
XX
FN WO2003048377-A2.
XX
PD 12-JUN-2003.
XX
PF 02-DEC-2002; 2002WO-US038806.
XX
PR 30-NOV-2001; 2001US-0336095P.
XX
PR 19-JUL-2002; 2002US-0337475P.
XX
PA (UVRP ) UNIV ROCHESTER.
XX
PA (THER/) THERIANOS S.
XX
PI Zhu M, Coleman P;
XX
WPI; 2003-532841/50.
XX
PT Determining the relative copy number of a group of target nucleic acid
PT molecules present in a sample by performing a first or second PCR in a
PT PCR mixture and quantifying the number of copies of the second target
PT nucleic acid product.
XX
PS Example 1; Page 68; 118pp; English.
XX
CC The present invention describes a multiplex real-time quantitative PCR
CC method for determining the relative copy number of a group of target
CC nucleic acid molecules present in a sample. The method comprises: (1)
CC performing a first PCR in a PCR mixture; (2) performing a second PCR in a
CC PCR mixture; and (3) quantifying the number of copies of the second
CC target nucleic acid product present in the sample containing the target
CC nucleic acid molecule. Also described: (1) quantifying the copy number of
CC a group of target nucleic acids in a sample; and (2) determining whether
CC a subject is at risk of acquiring Alzheimer's disease. The method is
CC useful for determining the relative copy number of a group of target
CC nucleic acid molecules present in a sample for determining whether a
CC subject is at risk of acquiring Alzheimer's disease. ACC99620 to ACC99730
CC represent PCR primer used in the exemplification of the present invention
XX
SQ Sequence 21 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 2 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
:|||||
Db 20 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 328
AAQ73376
ID AAQ73376 standard; DNA; 24 BP.
XX
AC AAQ73376;
XX
DT 25-MAR-2003 (revised)
DT 02-MAY-1995 (first entry)
XX

```

```

DE Anti-HSV-1 G4 oligo #5651.
XX
KW Hybridise; herpes simplex virus; HSV; open reading frame;
KW translation initiation site; coding region; 5' UTR; ss.
XX
OS Synthetic.
XX
FN WO9419945-A1.
XX
PD 15-SEP-1994.
XX
PF 07-MAR-1994; 94WO-US002471.
XX
PR 12-MAR-1993; 93US-00031147.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Draper KG, Crooke ST, Mirabelli CK, Ecker DJ, Hanecak R;
PI Anderson KP, Brown-Driver VL, Wyatt JR;
XX
WPI; 1994-302552/37.
XX
PT New oligonucleotide(s) hybridising with DNA or RNA of herpesvirus gene -
PT cytomagalovirus, Epstein Barr virus and varicella zoster infections.
XX
PS Claim 12; Page 35; 72pp; English.
XX
CC The sequences given in AAQ73325-81 represent oligonucleotides which
CC hybridise specifically with DNA or RNA from a herpes virus gene
CC corresponding to one of the open reading frames UL5, -8, -9, -20, -27-
CC 29, -30, -42, -52 or IE175 of herpes simplex virus type 1 (HSV-1). These
CC oligos pref. hybridise with a translation initiation site, a coding
CC region or a 5' untranslated region. These oligos may be used in
CC compositions for the treatment and diagnosis of herpes viral infection,
CC by contacting the virus or the animal, or its cells, tissues or body
CC fluids with the oligo. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGGCTGGGGTTGGTGG 1042
|||||
Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24

RESULT 329
AAQ61902
ID AAQ61902 standard; DNA; 24 BP.
XX
AC AAQ61902;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
DE HSV replication inhibiting oligomer, ISIS no 5649.
XX
KW Inhibition; replication; herpes simplex virus; HSV; HIV;
KW human cytomegalovirus; influenza virus; inflammation;
KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy;
KW telomere length; retard; aging; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..24 /*tag= a
FT /note= "Phosphorothionate intersugar linkages"
XX

```

```
PN WO9408053-A1.
XX
PD 14-APR-1994.
XX
PF 29-SEP-1993; 93WO-US009297.
XX
PR 29-SEP-1992; 92US-00954185.
XX
XX (ISIS-) ISIS PHARM INC.
PA Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
DR
XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT of chromosomes.
XX
XX Disclosure; Page 19; 144pp; English.
XX
XX The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides
CC which contain a G4 or two G3 stretches and which may be used for
CC inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
CC such as these may also be used for inhibiting activity of HIV, human
CC cytomegalovirus or influenza virus, or for treating inflammatory and
CC neurological disorders caused by phospholipase A2 activity in cases of
CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
CC They may also be used for inhibiting division of malignant cells by
CC modulating telomere length, which may also retard aging. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGCGTGGGTTGTGG 1042
||||| ||||| ||||| ||||| ||
Db 1 TTGGGGTTGGGTTGGGTTGGG 24
RESULT 330
AAQ61990
ID AAQ61990 standard; DNA; 24 BP.
XX
XX AAQ61990;
AC
XX 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
XX Guanine quartet containing oligomer, #1.
DE
XX Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
KW human cytomegalovirus; influenza virus; inflammation; telomere length;
KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Key 1.24
FT misc_feature 1.24
FT /*tag= a
FT /note= "Phosphorothionate intersugar linkages"
XX
XX WO9408053-A1.
PN
XX 14-APR-1994.
XX
XX 29-SEP-1993; 93WO-US009297.
XX
XX 29-SEP-1992; 92US-00954185.
XX
XX (ISIS-) ISIS PHARM INC.
PA Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
DR
XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT of chromosomes.
XX
XX Disclosure; Page 105; 144pp; English.
XX
XX The sequences given in AAQ61990-2001 are oligonucleotides which contain
CC G4 or G3 stretches and which may be used for inhibiting replication of
CC herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
CC influenza virus, or for treating inflammatory and neurological disorders
CC caused by phospholipase A2 activity in cases of hyper- proliferation,
CC malignancy, cardiovascular disease and snake bite. Oligonucleotides such
CC as these, may be used for inhibiting division of malignant cells by
CC modulating telomere length, which may also retard aging. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGCGTGGGTTGTGG 1042
||||| ||||| ||||| ||||| ||
Db 1 TTGGGGTTGGGTTGGGTTGGG 24
RESULT 331
AAQ61894
ID AAQ61894 standard; DNA; 24 BP.
XX
XX AAQ61894;
AC
XX 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
XX HSV replication inhibiting oligomer, ISIS no 5651.
DE
XX Inhibition; replication; herpes simplex virus; HSV; HIV;
KW human cytomegalovirus; influenza virus; inflammation;
KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy;
KW telomere length; retard; aging; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Key 1.24
FT misc_feature 1.24
FT /*tag= a
FT /note= "Phosphorothionate intersugar linkages"
XX
XX WO9408053-A1.
PN
XX 14-APR-1994.
XX
XX 29-SEP-1993; 93WO-US009297.
XX
XX 29-SEP-1992; 92US-00954185.
XX
XX (ISIS-) ISIS PHARM INC.
PA Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
DR
```

```
XX
XX (ISIS-) ISIS PHARM INC.
XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
XX Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
XX
XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
XX of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
XX of chromosomes.
XX
XX Disclosure; Page 105; 144pp; English.
XX
XX The sequences given in AAQ61990-2001 are oligonucleotides which contain
XX G4 or G3 stretches and which may be used for inhibiting replication of
XX herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
XX influenza virus, or for treating inflammatory and neurological disorders
XX caused by phospholipase A2 activity in cases of hyper- proliferation,
XX malignancy, cardiovascular disease and snake bite. Oligonucleotides such
XX as these, may be used for inhibiting division of malignant cells by
XX modulating telomere length, which may also retard aging. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 2.3e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1019 TTGGGGATGGCGTGGGTTGTGG 1042
||||| ||||| ||||| ||||| ||
Db 1 TTGGGGTTGGGTTGGGTTGGG 24
RESULT 331
AAQ61894
ID AAQ61894 standard; DNA; 24 BP.
XX
XX AAQ61894;
AC
XX 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
XX HSV replication inhibiting oligomer, ISIS no 5651.
DE
XX Inhibition; replication; herpes simplex virus; HSV; HIV;
KW human cytomegalovirus; influenza virus; inflammation;
KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy;
KW telomere length; retard; aging; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Key 1.24
FT misc_feature 1.24
FT /*tag= a
FT /note= "Phosphorothionate intersugar linkages"
XX
XX WO9408053-A1.
PN
XX 14-APR-1994.
XX
XX 29-SEP-1993; 93WO-US009297.
XX
XX 29-SEP-1992; 92US-00954185.
XX
XX (ISIS-) ISIS PHARM INC.
PA Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
DR
```


XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 PT of chromosomes.
 XX
 PS Claim 5; Page 19; 144pp; English.
 XX
 CC The sequences given in AAQ61825-50 and AAQ61896-906 are oligonucleotides
 CC which contain a G4 or two G3 stretches and which may be used for
 CC inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
 CC such as these may also be used for inhibiting activity of HIV, human
 CC cytomegalovirus or influenza virus, or for treating inflammatory and
 CC neurological disorders caused by phospholipase A2 activity in cases of
 CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
 CC They may also be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1019 TTGGGGATGGGGCTGGGCTGTGG 1042
 ||||| ||||| ||||| ||||| ||
 Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
 RESULT 332
 AAQ61997
 ID AAQ61997 standard; DNA; 24 BP.
 AC AAQ61997;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX
 DE Guanine quartet containing oligomer, #8.
 XX
 KW Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..24
 FT /tag= a
 FT /note= "Phosphorothionate intersugar linkages"
 XX
 PN WO9408053-A1.
 XX
 PD 14-APR-1994.
 XX
 PF 29-SEP-1993; 93WO-US009297.
 XX
 PR 29-SEP-1992; 92US-00954185.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX
 DR WPI; 1994-135613/16.
 XX
 PT New modified oligo-nucleotide contg guanine quartet - inhibits activity
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 PT of chromosomes.
 XX
 PS Disclosure; Page 107; 144pp; English.

CC The sequences given in AAQ61990-2001 are oligonucleotides which contain
 CC G4 or G3 stretches and which may be used for inhibiting replication of
 CC herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
 CC influenza virus, or for treating inflammatory and neurological disorders
 CC caused by phospholipase A2 activity in cases of hyper- proliferation,
 CC malignancy, cardiovascular disease and snake bite. Oligonucleotides such
 CC as these, may be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 24 BP; 0 A; 0 C; 16 G; 8 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19.2; DB 1; Length 24;
 Best Local Similarity 87.5%; Pred. No. 2.3e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1019 TTGGGGATGGGGCTGGGCTGTGG 1042
 ||||| ||||| ||||| ||||| ||
 Db 1 TTGGGGTTGGGGTTGGGGTTGGGG 24
 RESULT 333
 AAQ97981
 ID AAQ97981 standard; DNA; 24 BP.
 AC AAQ97981;
 XX
 DT 25-MAR-2003 (revised)
 DT 19-OCT-1995 (first entry)
 XX
 DE Peptide nucleic acid oligomer targeting HIV gene.
 XX
 KW Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
 KW antiviral; antisense; triple helix; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..24
 FT /tag= a
 FT /note= "at least one (and preferably all) of the backbone
 subunits are composed of N-acetyl N-(2-aminoethyl)glycine
 peptide residues, the nucleobase being attached
 covalently to the acetyl group and the peptide linkage
 being formed by condensation of the glycine carboxy group
 of one residue with the amino group of the 2-aminoethyl
 moiety in the next residue"
 XX
 PN WO9504068-A1.
 XX
 PD 09-FEB-1995.
 XX
 PF 28-JUL-1994; 94WO-US008517.
 XX
 PR 29-JUL-1993; 93US-00099718.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Ecker DJ;
 XX
 DR WPI; 1995-082179/11.
 XX
 PT Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid
 PT sub:unit - binds in complementary manner to DNA and RNA, and useful for
 PT modulating HIV viral activity, e.g. in treating AIDS.
 XX
 PS Claim 2; Page 176; 186pp; English.
 XX
 CC New peptide nucleic acid (PNA) oligomers are provided which (a) consist
 CC of naturally occurring nucleobases covalently bound to a polyamide
 CC backbone and (b) hybridise to the translation initiation AUG region, 5'
 CC untranslated region (5' UTR), 3' untranslated region (3' UTR), splice
 CC junctions or coding sequence of a human immunodeficiency virus gene

Query Match 1.1%; Score 19.2; DB 1; Length 25;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGGTTGGG 1042
 ||||| ||||| ||||| ||||| |||||
 Db 1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 336
 AAQ61893
 ID AAQ61893 standard; DNA; 25 BP.
 XX AAQ61893;
 XX 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX HSV replication inhibiting oligomer, ISIS no 5367.
 DE
 XX Inhibition; replication; herpes simplex virus; HSV; HIV;
 KW human cytomegalovirus; influenza virus; inflammation;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy;
 KW telomere length; retard; aging; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH misc_feature 1..25
 FT /*tag= a
 FT /note= "Phosphorothionate intersugar linkages"
 FT
 XX WO9408053-A1.
 XX 14-APR-1994.
 XX 29-SEP-1993; 93WO-US009297.
 XX 29-SEP-1992; 92US-00954185.
 XX (ISIS-) ISIS PHARM INC.
 PA Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX WPI; 1994-135613/16.
 DR
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 FT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 FT of chromosomes.
 XX Disclosure; Page 19; 144pp; English.
 PS
 XX The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides
 CC which contain a G4 or two G3 stretches and which may be used for
 CC inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
 CC such as these may also be used for inhibiting activity of HIV, human
 CC cytomegalovirus or influenza virus, or for treating inflammatory and
 CC neurological disorders caused by phospholipase A2 activity in cases of
 CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
 CC They may also be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX Sequence 25 BP; 0 A; 0 C; 17 G; 8 T; 0 U; 0 Other;

Query Match 1.1%; Score 19.2; DB 1; Length 25;
 Best Local Similarity 87.5%; Pred. No. 2.4e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGGTTGGG 1042
 ||||| ||||| ||||| ||||| |||||

Db 1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 337
 AAQ97978
 ID AAQ97978 standard; DNA; 25 BP.
 XX AAQ97978;
 XX 25-MAR-2003 (revised)
 DT 19-OCT-1995 (first entry)
 XX Peptide nucleic acid oligomer targetting HIV gene.
 DE
 XX Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
 KW antiviral; antisense; triple helix; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH misc_feature 1..25
 FT /*tag= a
 FT /note= "at least one (and preferably all) of the backbone
 FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine
 FT peptide residues, the nucleobase being attached
 FT covalently to the acetyl group and the peptide linkage
 FT being formed by condensation of the glycine carboxy group
 FT of one residue with the amino group of the 2-aminoethyl
 FT moiety in the next residue"
 XX
 XX WO9504068-A1.
 XX 09-FEB-1995.
 XX 28-JUL-1994; 94WO-US008517.
 XX 29-JUL-1993; 93US-00099718.
 XX (ISIS-) ISIS PHARM INC.
 PA Ecker DJ;
 PI WPI; 1995-082179/11.
 DR
 XX Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid
 FT sub:unit - binds in complementary manner to DNA and RNA, and useful for
 FT modulating HIV viral activity, e.g. in treating AIDS.
 PT
 XX Claim 2; Page 176; 186pp; English.
 PS
 XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist
 CC of naturally occurring nucleobases covalently bound to a polyamide
 CC backbone and (b) hybridise to the translation initiation AUG region, 5'
 CC untranslated region (5' UTR), 3' untranslated region (3' UTR), splice
 CC junctions or coding sequence of a human immunodeficiency virus gene
 CC chosen from env, gag, pol, rev and tat. The PNAs can be used to target
 CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene
 CC regulation moieties. They have utility as gene-targeted drugs for
 CC modulating HIV processes. Hence they can be used to treat AIDS and other
 CC viral infections. They are also useful in diagnostic applications and as
 CC research tools. PNA oligomers have high affinity for complementary single
 CC stranded DNA. They are also able to form triple helices in which a first
 CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the
 CC resulting double helix or with the first PNA strand. The PNAs possess no
 CC significant charge and are water soluble, which facilitates cellular
 CC uptake. Further, since they contain amides of non-biological amino acids,
 CC they are biostable and resistant to enzymatic degradation by proteases.
 CC The present sequence is a specifically claimed PNA sequence (represented
 CC by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 25 BP; 0 A; 0 C; 17 G; 8 T; 0 U; 0 Other;

```
Query Match      1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1019 TTGGGATCGGCTGGGTTGGG 1042
DB 1 TTGGGTTGGGTTGGGTTGGG 24

RESULT 338
AAC96251/c
ID AAC96251 standard; DNA; 25 BP.
XX
AC AAC96251;
XX
DT 26-FEB-2001 (first entry)
XX
DE HLA DPA1 gene PCR primer #8.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 48; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 3 C; 3 G; 16 T; 0 U; 0 Other;

Query Match      1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1727 CGAGTTTACAAAAA 1750
DB 24 CGTCTGTACAAAAA 1

RESULT 339
AAC96074/c
ID AAC96074 standard; DNA; 25 BP.
XX
AC AAC96074;
XX
DT 26-FEB-2001 (first entry)
XX
DE (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
```

```
DE 16S rRNA gene PCR primer #41.
XX
KW DNA sequence analysis; sequencing; protein sequence; protein structure;
KW gene typing; organ donation; bacteria identification; 16S rRNA; HLA;
KW human leukocyte antigen; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200065088-A2.
XX
PD 02-NOV-2000.
XX
PF 20-APR-2000; 2000WO-EP003636.
XX
PR 26-APR-1999; 99EP-00303215.
XX
PA (AMSH ) AMERSHAM PHARMACIA BIOTECH AB.
XX
PI Ulfendahl P, Wong K;
XX
DR WPI; 2000-679677/66.
XX
PT Identifying extendible primers for use in identification, or
PT classification of a nucleic acid of an organism, allele or gene such as
PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
PT specific length.
XX
PS Claim 14; Page 45; 66pp; English.
XX
CC The present invention provides a method for identifying a set of
CC extendible primers which can be used in the identification, typing and
CC classification of genes. This can then be used to predict protein
CC sequence and structure, in organ donation to match the organ with the
CC receiver, and to identify bacteria in a sample. The method can be used to
CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
CC particular
XX
SQ Sequence 25 BP; 3 A; 3 C; 5 G; 14 T; 0 U; 0 Other;

Query Match      1.1%; Score 19.2; DB 1; Length 25;
Best Local Similarity 87.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1724 CCTCGAGTTTACAAAAA 1747
DB 24 CCTCGGCTACAAAAA 1

RESULT 340
AAQ75549/c
ID AAQ75549 standard; DNA; 19 BP.
XX
AC AAQ75549;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
```

DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAA 1752
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 341
AAT10757/c
ID AAT10757 standard; RNA; 19 BP.
XX
AC AAT10757;
XX
DT 09-SEP-1996 (first entry)
XX
DE Oligonucleotide probe, T-2.
XX
KW Electronically self-addressable device; ED; electrode; current source;
KW attachment layer; permeable; counterion; genetic typing; probe;
KW detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1
FT /*tag= a
FT /note= "5'-amino terminus"
XX
PN WO9601836-A1.
XX
PD 25-JAN-1996.
XX
PF 05-JUL-1995; 95WO-US008570.
XX
PR 07-JUL-1994; 94US-00271882.
XX
PA (NANO-) NANOGEN INC.
XX
PI Heller MJ, Tu E, Evans GA, Sosnowski RG;
XX
DR WPI; 1996-097582/10.
XX
PT Electronically self-addressable device - used for electronic control of,
PT e.g. nucleic acid hybridisation.
XX
PS Example 1; Page 61; 155pp; English.
XX
CC The sequences given in AAT10742-67 are synthetic oligonucleotides which
CC are used in the construction of the electronically self-addressable
CC device (ED) of the invention. The ED comprises a substrate, an electrode
CC or opt. a number of electrodes supported by the substrate, a current
CC source operatively connected to the electrode and an attachment layer
CC adjacent to the electrode which is permeable to a counterion but not

CC permeable to a molecule capable of insulating or binding to the
CC electrode. The attachment layer is capable of attaching a macromolecule.
CC The ED is used for genetic typing and comprises a number of
CC electronically addressable locations each comprising an electrode, and a
CC binding entity, such as one of these probes, attached to each of the
CC locations capable of detecting the presence of a genetic sequence
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 342
AAV07878/c
ID AAV07878 standard; DNA; 19 BP.
XX
AC AAV07878;
XX
DT 14-DEC-1998 (first entry)
XX
DE Aminoxy-modified oligonucleotide.
XX
KW phosphorothioate; ras gene; malignant cell growth; aminoxy-modified;
KW nuclease resistance; reporter group; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /*tag= a
FT /note= "5-methyl, 2'-aminoxyethoxy-thymidine"
XX
PN WO9835978-A1.
XX
PD 20-AUG-1998.
XX
PF 13-FEB-1998; 98WO-US002405.
XX
PR 14-FEB-1997; 97US-0037143P.
PR 30-JAN-1998; 98US-00016520.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Cook PD, Manoharan M, Kawasaki AM;
XX
DR WPI; 1998-568232/48.
XX
PT New aminoxy-modified oligonucleotides - which can show improved binding
PT to complementary strands and improved resistance to nuclease.
XX
PS Disclosure; Page 84; 131pp; English.
XX
CC The invention relates to aminoxy-modified(oligo)nucleotides or
CC nucleosides which are useful as therapeutics, diagnostics, and research
CC reagents. They may be used, e.g., for modulation of the ras gene and may
CC be able to modulate the process of transformation from normal to
CC malignant cell growth. They may be prepared using known methods.
CC Inclusion of the aminoxy moieties can improve binding of
CC oligonucleotides to complementary strands. The moieties can also provide
CC conjugation sites useful for conjugation of useful ligands (e.g. reporter
CC groups and groups for modifying uptake, distribution or other
CC pharmacodynamic properties) to oligonucleotides. The present sequence
CC represents an example of an aminoxy-modified oligonucleotide disclosed
CC in the specification
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

```
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 343
AAV06820/c
ID AAV06820 standard; DNA; 19 BP.
XX
XX AAV06820;
AC
XX 13-OCT-1998 (first entry)
DT
XX
DE Oligonucleotide containing modified internucleotide linkage.
XX
XX oligonucleotide; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16..18
FT /*tag= a
FT /note= these T residues are formed as part of a
FT conventional phosphoramidite oligonucleotide synthesis
FT process but using as the reactant a thymosine nucleoside
FT having at the 3'-position a group of formula -CH2-
FT P(OCH2CH2CN)-N(iPr)2"
XX
XX W09747636-A2.
PN
XX
XX 18-DEC-1997.
PD
XX
XX 03-JUN-1997; 97WO-GB001490.
PF
XX
XX 13-JUN-1996; 96GB-00012600.
PR
XX (NOVS ) NOVARTIS AG.
XX
XX Collingwood SP, Moser HE, Altmann K, Douglas ME;
PI
XX WPI; 1998-052233/05.
DR
XX New tetra:hydro:furan derivatives - useful in the synthesis of
PT oligo:nucleotide(s).
XX
XX Example 12; Page 29; 37pp; English.
PS
XX The invention relates, inter alia, to a method of preparing an
CC oligonucleotide by coupling (1) a new nucleoside having a protected 5'-
CC hydroxy group and at the 3'-position a group of formula -CH2-P(OR3)-
CC NR4R5, with (2) a nucleoside or oligonucleotide having a free 5'-hydroxy
CC group, to give (3) a precursor having an internucleoside linkage of
CC formula -CH2-P(OR3)-O-; and converting this to a linkage of formula -CH2-
CC P(OR3)(-X)-O- (where X = S or O). The present sequence is a specific
CC example of an oligonucleotide so prepared
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 0 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 344
AAV06820/c
ID AAV06820 standard; DNA; 19 BP.
XX
XX AAV06820;
AC
XX 20-AUG-1999 (first entry)
DT
XX
XX 5' amino oligonucleotide probe T-2.
DE
XX Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control; transport;
KW attachment; binding; DNA/RNA hybrid; probe; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1
FT /*tag= a
FT /note= "amino group attached at 5' terminal"
XX
XX W09929711-A1.
PN
XX
XX 17-JUN-1999.
PD
XX
XX 01-DEC-1998; 98WO-US025475.
PF
XX
XX 05-DEC-1997; 97US-00986065.
PR
XX (NANO-) NANOGEN INC.
PA
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
PI
XX WPI; 1999-385567/32.
DR
XX
XX New microelectronic device designed to carry out and control multi-step
PT and multiplex molecular biological reactions in microscopic format.
XX
XX Example 1; Page 90; 179pp; English.
PS
XX The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the ion
CC permeable permeation layer which overlies the electrode. This permeation
CC layer allows attachment of nucleic acids to permit immobilization but
CC also separates the attached oligonucleotides and hybridized target DNA
CC sequences from the highly reactive electrochemical environment generated
CC immediately at the electrode surface. The microelectronic device is
CC designed and fabricated to actively carry out and control reactions such
CC as nucleic acid hybridizations, antibody/antigen reactions, sample
CC preparation, diagnostics and biopolymer synthesis. The device can
CC electronically control the transport and attachment of specific binding
CC entities, such as nucleic acids and polypeptides, to specific micro-
CC locations. The device can subsequently control the transport and reaction
CC of analytes or reactants at the addressed specific micro-locations. The
CC device is able to concentrate analytes and reactants, remove non-
CC specifically bound molecules, provide stringency control for DNA
CC hybridization reactions and improve the detection of analytes. The
CC present sequence represents a probe used to exemplify the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 0 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 345
AAV06820/c
ID AAV06820 standard; DNA; 19 BP.
XX
XX AAV06820;
AC
XX 20-AUG-1999 (first entry)
DT
XX
XX 5' amino oligonucleotide probe T-2.
DE
XX Microelectronic device; multi-step reaction; microscopic format;
KW ion-permeable permeation layer; electrode; electrical control; transport;
KW attachment; binding; DNA/RNA hybrid; probe; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_feature 1
FT /*tag= a
FT /note= "amino group attached at 5' terminal"
XX
XX W09929711-A1.
PN
XX
XX 17-JUN-1999.
PD
XX
XX 01-DEC-1998; 98WO-US025475.
PF
XX
XX 05-DEC-1997; 97US-00986065.
PR
XX (NANO-) NANOGEN INC.
PA
XX Sosnowski RG, Butler WF, Tu E, Nerenberg MI, Heller MJ, Edman CF;
PI
XX WPI; 1999-385567/32.
DR
XX
XX New microelectronic device designed to carry out and control multi-step
PT and multiplex molecular biological reactions in microscopic format.
XX
XX Example 1; Page 90; 179pp; English.
PS
XX The specification describes a self-addressable, self-assembling
CC microelectronic device which is designed to actively carry out and
CC control multi-step and multiplex molecular biological reactions in
CC microscopic formats. A key aspect of this invention is played by the ion
CC permeable permeation layer which overlies the electrode. This permeation
CC layer allows attachment of nucleic acids to permit immobilization but
CC also separates the attached oligonucleotides and hybridized target DNA
CC sequences from the highly reactive electrochemical environment generated
CC immediately at the electrode surface. The microelectronic device is
CC designed and fabricated to actively carry out and control reactions such
CC as nucleic acid hybridizations, antibody/antigen reactions, sample
CC preparation, diagnostics and biopolymer synthesis. The device can
CC electronically control the transport and attachment of specific binding
CC entities, such as nucleic acids and polypeptides, to specific micro-
CC locations. The device can subsequently control the transport and reaction
CC of analytes or reactants at the addressed specific micro-locations. The
CC device is able to concentrate analytes and reactants, remove non-
CC specifically bound molecules, provide stringency control for DNA
CC hybridization reactions and improve the detection of analytes. The
CC present sequence represents a probe used to exemplify the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 0 U; 0 T; 0 U; 0 Other;
SQ
Query Match      1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 345
AAV06820/c
ID AAV06820 standard; DNA; 19 BP.
```

XX AC AAX81927;
XX DT 07-SEP-1999 (first entry)
XX DE Polynucleotide strand with amino groups.
XX KW Enzyme-specific cleavable polynucleotide substrate;
XX KW quenched fluorescent moiety; biological assay; detection; identification;
XX KW microorganism; sterilization assurance; nuclease; ss.
XX OS Synthetic.
XX FH Key
XX FT modified_base 7 Location/Qualifiers
XX FT /tag= a
XX FT /note= "amine-modified C6 derivative of deoxythymidine
XX FT (dT)"
XX FT modified_base 9
XX FT /tag= b
XX FT /note= "amine-modified C6 derivative of deoxythymidine
XX FT (dT)"
XX FT modified_base 11
XX FT /tag= c
XX FT /note= "amine-modified C6 derivative of deoxythymidine
XX FT (dT)"
XX FT modified_base 13
XX FT /tag= d
XX FT /note= "amine-modified C6 derivative of deoxythymidine
XX FT (dT)"
XX PN WO9935288-A1.
XX PD 15-JUL-1999.
XX PF 20-AUG-1998; 98WO-US017311.
XX PR 09-JAN-1998; 98US-00005260.
XX PA (MINN) MINNESOTA MINING & MFG CO.
XX PI Wei A, Mach PA;
XX PI WPI; 1999-419356/35.
XX DR An enzyme-specific cleavable polynucleotide substrate bearing quenched
XX PT fluorescent moieties.
XX PS Example 2; Page 20; 34pp; English.
XX CC The specification describes an enzyme-specific cleavable polynucleotide
XX CC substrate bearing quenched fluorescent moieties. The enzyme-specific
XX CC cleavable polynucleotide substrate is useful in biological assays for
XX CC detection and identification of microorganisms, sterilization assurance,
XX CC pharmaceutical discovery, enzyme assays, immunoassays and other
XX CC biological assays. The method provides a rapid and convenient approach
XX CC for detection and identification of microorganisms. It can be adapted to
XX CC sequence-dependent or sequence-independent tests. The invention provides
XX CC improved accuracy, faster detection, and overall lower cost in detection
XX CC and identification of microorganisms. The presence of nuclease is
XX CC measured more accurately and sensitively by red-shifting the emission
XX CC wavelength from far UV region (350-400 nm) to the 500-600 nm region of
XX CC the electromagnetic spectrum and reducing the effect of background signal
XX CC levels of intact reagents. The present sequence is used in the course of
XX CC the invention
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 346
AAZ01358/C
ID AAZ01358 standard; DNA; 19 BP.
XX AC AAZ01358;
XX DT 27-SEP-1999 (first entry)
XX DE PCR primer for PGI biallelic marker 4-4-187.
XX KW PGI gene; biallelic marker; PCR primer; PGI-related biallelic marker;
XX KW cancer; prostate cancer; diagnosis; therapy; prostate specific antigen;
XX KW PSA; human; ss.
XX OS Synthetic.
XX OS Homo sapiens.
XX PN WO9932644-A2.
XX PD 01-JUL-1999.
XX PF 22-DEC-1998; 98WO-IB002133.
XX PR 22-DEC-1997; 97US-00996306.
XX PR 09-SEP-1998; 98US-0099658P.
XX PA (GEST) GENSET.
XX PI Cohen D, Blumenfeld M, Chumakov I, Bougueleret L;
XX PI WPI; 1999-405178/34.
XX PT Use of a prostate cancer associated gene and biallelic markers derived
XX PT from it.
XX PS Claim 4; Page 374; 385pp; English.
XX CC The invention relates to a mammalian PGI gene and protein, and a set of
XX CC PGI biallelic markers. The PGI polynucleotide and biallelic markers are
XX CC used in a hybridisation assay, a sequencing assay, or in an allele-
XX CC specific amplification assay for determining the identity of a nucleotide
XX CC at a PGI-related biallelic marker. The methods can be used to detect and
XX CC to assess the risk of developing cancer or prostate cancer. Early-stage
XX CC diagnosis of prostate cancer relies on prostate specific antigen (PSA)
XX CC dosage. However, the effectiveness of this is limited due to its
XX CC inability to discriminate between malignant and non-malignant affections
XX CC of the organ. A need exists for both a reliable diagnostic procedure
XX CC which would enable early-stage diagnosis, and for preventative and
XX CC curative treatments of the disease. The PGI gene can be used for
XX CC detection of prostate cancer, and the risk of developing it in the
XX CC future, and can also be used to determine therapies for the disease
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 347
AAZ61390/C
ID AAZ61390 standard; DNA; 19 BP.
XX AC AAZ61390;
XX XX

```
DT 19-JUN-2000 (first entry)
XX Uniform phosphodiester oligonucleotide.
XX
XX
KW Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW nuclease resistance; phosphodiester; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16
FT /tag= a
FT /note= "2'-modified T"
FT modified_base 17
FT /tag= b
FT /note= "2'-modified T"
FT modified_base 18
FT /tag= c
FT /note= "2'-modified T"
FT modified_base 19
FT /tag= d
FT /note= "2'-modified T"
XX
PN WO200008044-A1.
XX
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99WO-US017895.
XX
XX 07-AUG-1998; 98US-00130566.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX WPI; 2000-205668/18.
XX
XX Novel 2'-O-aminoethyloxethyl modified nucleosides and oligonucleotides
XX used in diagnostic, therapeutic and research reagents.
XX
XX Disclosure; Page 44; 60pp; English.
XX
XX The present sequence represents an uniform phosphodiester
XX oligonucleotide. The specification describes oligomeric compounds
XX containing 2'-O-modified ribosyl nucleosides. The 2'-O-modified
XX nucleosides include ring structures that position the sugar moiety of the
XX nucleosides preferentially in 3' endo geometries. The modified oligomeric
XX compounds have increased binding affinity and increased nuclease
XX resistance. The oligomeric compounds can be used in diagnostic,
XX therapeutic and research reagents
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 348
AAZ61404/c
ID AAZ61404 standard; DNA; 19 BP.
XX
XX AAZ61404;
XX
XX 19-JUN-2000 (first entry)
XX
XX 2'-O-modified ribosyl oligonucleotide with phosphodiester linkages.
DE Oligomeric compound; 2'-O-modified ribosyl nucleoside; 3' endo geometry;
KW
```

```
KW nuclease resistance; phosphorothioate; ss.
XX
XX Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..19
FT /tag= a
FT /note= "nucleosides linked by phosphodiester linkages"
FT modified_base 16..19
FT /tag= b
FT /note= "2'-O-[2-N,N-dimethylaminoethyl]oxyethyl-5- methyl
FT uridine"
XX
XX WO200008044-A1.
XX
XX 17-FEB-2000.
XX
XX 06-AUG-1999; 99WO-US017895.
XX
XX 07-AUG-1998; 98US-00130566.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Cook PD;
XX WPI; 2000-205668/18.
XX
XX Novel 2'-O-aminoethyloxethyl modified nucleosides and oligonucleotides
XX used in diagnostic, therapeutic and research reagents.
XX
XX Disclosure; Page 51; 60pp; English.
XX
XX The present sequence represents an oligomeric compound containing 2'-O-
XX modified ribosyl nucleosides. The oligomeric compound contains
XX phosphodiester linkages. The 2'-O-modified nucleosides include ring
XX structures that position the sugar moiety of the nucleosides
XX preferentially in 3' endo geometries. The modified oligomeric compounds
XX have increased binding affinity and increased nuclease resistance. The
XX oligomeric compounds can be used in diagnostic, therapeutic and research
XX reagents
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 349
AAC62422/c
ID AAC62422 standard; DNA; 19 BP.
XX
XX AAC62422;
XX
XX 07-FEB-2001 (first entry)
XX
XX T19 diester for use in nuclease stability assay.
XX
XX T19 diester; nuclease stability assay; polymerase chain reaction; PCR;
KW molecular cloning; disease diagnosis; disease treatment; ss.
XX
XX Synthetic.
XX
XX US6127124-A.
XX
XX 03-OCT-2000.
XX
XX 20-JAN-1999; 99US-00234237.
XX
XX
```


PR 20-JAN-1999; 99US-00234237.
XX (ISIS-) ISIS PHARM INC.
XX Leeds JM, Cummins LL;
XX WPI; 2000-637737/61.
XX Determining the nuclease stability and relative binding affinity of an
FT oligomeric compound comprises capillary gel electrophoresis using laser-
PT induced fluorescence.
XX Example 3; Col 19-20; 14pp; English.
XX The present invention is concerned with methods of determining the
CC nuclease stability of oligomeric compounds using capillary-gel
CC electrophoresis and laser-induced fluorescence. The methods are useful in
CC the polymerase chain reaction (PCR), molecular cloning and disease
CC diagnosis and treatment. The present sequence was used in a demonstration
CC of the methods of the invention.
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 350
AAZ95241/C
ID AAZ95241 standard; DNA; 19 BP.
XX AC AAZ95241;
XX 05-JUN-2000 (first entry)
XX Modified oligonucleotide #3 ISIS # 22111.
XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22111;
KW research reagent; therapeutic; ss.
XX Synthetic.
FH Key Location/Qualifiers
FT misc_feature 1..15
FT /tag= a
FT /note= "Phosphorothioate internucleotide linkage"
FT misc_feature 15..19
FT /tag= d
FT /note= "Optionally all phosphorothioate internucleotide
FT linkages"
FT modified_base 16..19
FT /tag= c
FT /mod_base= OTHER
FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT 19
FT misc_RNA /tag= d
XX WO200004189-A1.
XX 27-JAN-2000.
XX 13-JUL-1999; 99WO-US015886.
XX 14-JUL-1998; 98US-00115043.
XX (ISIS-) ISIS PHARM INC.
XX

PI Manoharan M, Cook PD;
XX WPI; 2000-182445/16.
XX Novel modified oligonucleotides, useful in antisense methodologies,
FT diagnostics, therapeutics and as research reagents.
XX Example 54; Page 59; 75pp; English.
XX This sequence represents a modified oligonucleotide used in the course of
CC the invention. The invention relates to oligonucleotides comprising
CC nucleotides covalently linked together by internucleotide linkages where
CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC can be used in gene therapy and are also useful in antisense
CC methodologies, diagnostics, therapeutics and as research reagents
XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;
SQ Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 351
AAZ95240/C
ID AAZ95240 standard; DNA; 19 BP.
XX AC AAZ95240;
XX 05-JUN-2000 (first entry)
XX Modified oligonucleotide #3 ISIS # 22110.
XX Antisense oligonucleotide; phosphorothioate; gene therapy; ISIS # 22110;
KW research reagent; therapeutic; ss.
XX Synthetic.
FH Key Location/Qualifiers
FT misc_feature 1..15
FT /tag= a
FT /note= "Phosphorothioate internucleotide linkage"
FT misc_feature 15..19
FT /tag= d
FT /note= "Optionally all phosphorothioate internucleotide
FT linkages"
FT modified_base 16..19
FT /tag= c
FT /mod_base= OTHER
FT /note= "Optionally all 3'-O-(2-methoxyhexyl) or all 2'-O-
FT (2-methoxyethyl)"
XX WO200004189-A1.
XX 27-JAN-2000.
XX 13-JUL-1999; 99WO-US015886.
XX 14-JUL-1998; 98US-00115043.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Cook PD;
XX WPI; 2000-182445/16.
XX Novel modified oligonucleotides, useful in antisense methodologies,
FT diagnostics, therapeutics and as research reagents.

XX Example 54; Page 59; 75pp; English.
PS This sequence represents a modified oligonucleotide used in the course of
XX the invention. The invention relates to oligonucleotides comprising
CC nucleotides covalently linked together by internucleotide linkages where
CC at least 1 nucleotide is linked to adjacent nucleotide by a 2',5'-
CC internucleotide linkage and bears a 3'-substituent. The oligonucleotides
CC can be used in gene therapy and are also useful in antisense
CC methodologies, diagnostics, therapeutics and as research reagents
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 352
AAA06839/c
ID AAA06839 standard; DNA; 19 BP.
XX
AC AAA06839;
XX
DT 19-JUN-2000 (first entry)
XX
DE Modified T-containing oligonucleotide, SEQ ID NO:14.
XX
KW Modified nucleoside; aminoxy group;
KW 2'-deoxy-erythro-pentofuranosyl sugar moiety; nuclease resistant;
KW hybridisation; binding affinity; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /*tag= a
FT /note= "These nucleotides are substituted with 2'-O-{2-
FT [N-(2-amino)ethyl-N-(methyl)aminoxyethyl} group"
XX
PN WO200008042-A1.
XX
PD 17-FEB-2000.
XX
PF 09-AUG-1999; 99WO-US017988.
XX
PR 07-AUG-1998; 98US-00130973.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Cook PD, Prakash TP, Kawasaki AM;
XX WPI; 2000-224020/19.
XX
XX Aminoxy-modified nucleosides and oligonucleotides useful in diagnostic,
PT therapeutic and research reagents and for modulating the expression of
PT protein in organisms.
PS Example 99; Page 120; 195pp; English.
XX
XX The invention relates to aminoxy-modified nucleosides and
CC oligonucleotides and to oligonucleotides that elicit RNase H for cleavage
CC in a complementary nucleic acid strand. It also relates to
CC oligonucleotides wherein at least some of the nucleotides are
CC functionalised to be nuclease resistant, at least some of the nucleotides
CC include a substituent that potentiates hybridisation of the
CC oligonucleotide to a complementary strand, and at least some of the
CC nucleotides include a 2'-deoxy-erythro-pentofuranosyl sugar moiety. The
CC inclusion of one or more aminoxy moieties in such oligonucleotides

CC provides for improved binding of such oligonucleotides to a complementary
CC strand. The oligonucleotides of the invention are used as diagnostic,
CC therapeutic or research reagents, and can be used to modulate gene
CC expression in organisms. The oligonucleotides containing the modified
CC nucleosides have increased nuclease resistance and increased binding
CC affinity to a complementary strand. The present sequence represents an
CC oligonucleotide containing nucleotides substituted with a 2'-O-{2- [N-(2-
CC amino)ethyl-N-(methyl)aminoxyethyl} group
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 353
AAA88952/c
ID AAA88952 standard; DNA; 19 BP.
XX
AC AAA88952;
XX
DT 05-MAR-2001 (first entry)
XX
DE Oligonucleotide ISIS 22115.
XX
KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
KW diagnosis; DNA-RNA hybrid; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= f
FT /note= "phosphorothioate linkage"
FT modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) thymidine"
FT misc_RNA 19
FT /*tag= e
FT /label= RNA
FT modified_base 19
FT /*tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl) uridine"
XX
PN WO200066609-A1.
XX
PD 09-NOV-2000.
XX
PF 03-MAY-2000; 2000WO-US011913.
XX
PR 03-MAY-1999; 99US-00303586.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX
DR

XX New oligonucleotides containing sequences with A and B geometry, used to
 PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
 PT bacterial infections, bind to single stranded RNA or DNA.
 XX
 PS Example 54; Page 69; 132pp; English.
 XX
 CC Oligonucleotide ISIS 22115 contains a mixed phosphodiester and
 CC phosphorothioate backbone and has 2'-O-(2-methoxyethyl) chemistry. It was
 CC used in experiments to determine the effects of snake venom
 CC phosphodiesterase and liver homogenate on the stability of
 CC oligonucleotides. Novel oligonucleotides of the invention have both A-
 CC and B-form conformational geometry. The A-form geometry modulates the
 CC binding affinity and nuclease resistance of the oligonucleotide. The B-
 CC form geometry allows the oligonucleotide to serve as substrate for RNase-
 CC H when bound to a target nucleic acid strand. The oligonucleotides can be
 CC used to treat psoriasis and other inflammatory skin conditions, skin
 CC cancers and viral, bacterial and fungal infections, and in various
 CC diagnostic applications
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1754
 Db 19 AAAAAAAAAAAAAAAAAA 1
 RESULT 354
 AAA88965/c
 ID AAA88965 standard; DNA; 19 BP.
 XX
 AC AAA88965;
 XX
 DT 05-MAR-2001 (first entry)
 XX
 DE 2'-Modified chimeric oligonucleotide.
 XX
 KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
 KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
 KW diagnosis; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT modified_base 16
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
 FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
 FT modified_base 17
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
 FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
 FT modified_base 18
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
 FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
 FT modified_base 19
 FT /*tag= d
 FT /mod_base= OTHER
 FT /note= "2'-modified thymidine, i.e. -S-Me, -Me, 2'-ara-
 FT (F), 2'-ara-(OH), -2'-ara-(OMe)"
 PN W0200066609-A1.
 XX
 PD 09-NOV-2000.
 XX

PF 03-MAY-2000; 2000WO-US011913.
 XX
 PR 03-MAY-1999; 99US-00303586.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Manoharan M, Mohan V;
 XX
 DR WPI; 2000-672833/65.
 XX
 PT New oligonucleotides containing sequences with A and B geometry, used to
 PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
 PT bacterial infections, bind to single stranded RNA or DNA.
 XX
 PS Example 86; Page 102; 132pp; English.
 XX
 CC This sequence represents 2'-modified chimeric oligonucleotides containing
 CC 2'-modified T. The nucleotides were used to examine the effects of the
 CC modifications on nuclease resistance. Novel oligonucleotides of the
 CC invention have both A- and B-form conformational geometry. The A-form
 CC geometry modulates the binding affinity and nuclease resistance of the
 CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
 CC as substrate for RNase-H when bound to a target nucleic acid strand. The
 CC oligonucleotides can be used to treat psoriasis and other inflammatory
 CC skin conditions, skin cancers and viral, bacterial and fungal infections,
 CC and in various diagnostic applications
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1754
 Db 19 AAAAAAAAAAAAAAAAAA 1
 RESULT 355
 AAA88949/c
 ID AAA88949 standard; DNA; 19 BP.
 XX
 AC AAA88949;
 XX
 DT 05-MAR-2001 (first entry)
 XX
 DE Oligonucleotide ISIS 22112.
 XX
 KW Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
 KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
 KW diagnosis; ss.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT modified_base 16
 FT /*tag= e
 FT /mod_base= OTHER
 FT /note= "phosphorothioate linkage"
 FT modified_base 17
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "3'-O-(2-methoxyethyl)thymidine"
 FT modified_base 18
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "3'-O-(2-methoxyethyl)thymidine"
 FT modified_base 19
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "3'-O-(2-methoxyethyl)thymidine"
 FT modified_base 20
 FT /*tag= d
 FT /mod_base= OTHER


```

FT      /*tag= e
FT      /note= "phosphorothioate linkage"
FT      modified_base
FT      16
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      modified_base
FT      17
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      modified_base
FT      18
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      modified_base
FT      19
FT      /*tag= d
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22114 contains a mixed phosphodiester and
XX phosphorothioate backbone and has 3'-O-(2-methoxyethyl) chemistry. It was
XX used in experiments to determine the effects of snake venom
XX phosphodiesterase and liver homogenate on the stability of
XX oligonucleotides. Novel oligonucleotides of the invention have both A-
XX and B-form conformational geometry. The A-form geometry modulates the
XX binding affinity and nuclease resistance of the oligonucleotide. The B-
XX form geometry allows the oligonucleotide to serve as substrate for RNase-
XX H when bound to a target nucleic acid strand. The oligonucleotides can be
XX used to treat psoriasis and other inflammatory skin conditions, skin
XX cancers and viral, bacterial and fungal infections, and in various
XX diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1736 AAAAAAAAAAAAAAAAAA 1754
XX Db 19 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 358
XX AAA88947/C
XX ID AAA88947 standard; DNA; 19 BP.
XX
XX AC AAA88947;
XX
XX DT 05-MAR-2001 (first entry)
XX
XX DE Oligonucleotide ISIS 22110.
XX

```

```

KW      Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW      dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX      diagnosis; ss.
OS      Synthetic.
FH      Key
FH      Location/Qualifiers
FT      modified_base
FT      16
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      modified_base
FT      17
FT      /*tag= b
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      modified_base
FT      18
FT      /*tag= c
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
FT      modified_base
FT      19
FT      /*tag= d
FT      /mod_base= OTHER
FT      /note= "3'-O-(2-methoxyethyl)thymidine"
XX
XX WO200066609-A1.
XX
XX 09-NOV-2000.
XX
XX 03-MAY-2000; 2000WO-US011913.
XX
XX 03-MAY-1999; 99US-00303586.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Manoharan M, Mohan V;
XX
XX WPI; 2000-672833/65.
XX
XX New oligonucleotides containing sequences with A and B geometry, used to
XX treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
XX bacterial infections, bind to single stranded RNA or DNA.
XX
XX Example 54; Page 69; 132pp; English.
XX
XX Oligonucleotide ISIS 22110 contains a phosphodiester backbone and has 3'-
XX O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
XX effects of snake venom phosphodiesterase and liver homogenate on the
XX stability of oligonucleotides. Novel oligonucleotides of the invention
XX have both A- and B-form conformational geometry. The A-form geometry
XX modulates the binding affinity and nuclease resistance of the
XX oligonucleotide. The B-form geometry allows the oligonucleotide to serve
XX as substrate for RNase-H when bound to a target nucleic acid strand. The
XX oligonucleotides can be used to treat psoriasis and other inflammatory
XX skin conditions, skin cancers and viral, bacterial and fungal infections,
XX and in various diagnostic applications
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1736 AAAAAAAAAAAAAAAAAA 1754
XX Db 19 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 359
XX AAA88948/C
XX ID AAA88948 standard; DNA; 19 BP.
XX
XX AC AAA88948;
XX

```

```
DT 05-MAR-2001 (first entry)
XX Oligonucleotide ISIS 22111.
XX Oligonucleotide; nuclease resistance; psoriasis; antipsoriatic;
KW dermatological; cytostatic; virucide; antibacterial; fungicide; therapy;
XX diagnosis; DNA-RNA hybrid; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 16 /*tag= a
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 17 /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT modified_base 18 /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)thymidine"
FT misc_RNA 19 /*tag= e
FT /label= RNA
FT modified_base 19 /*tag= d
FT /mod_base= OTHER
FT /note= "2'-O-(2-methoxyethyl)uridine"
XX WO200066609-A1.
XX 09-NOV-2000.
XX 03-MAY-2000; 2000WO-US011913.
XX 03-MAY-1999; 99US-00303586.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Mohan V;
XX WPI; 2000-672833/65.
XX New oligonucleotides containing sequences with A and B geometry, used to
PT treat and diagnose e.g. psoriasis, skin cancers and viral, fungal and
PT bacterial infections, bind to single stranded RNA or DNA.
XX Example 54; Page 69; 132pp; English.
XX Oligonucleotide ISIS 22111 contains a phosphodiester backbone and has 2'-
CC O-(2-methoxyethyl) chemistry. It was used in experiments to determine the
CC effects of snake venom phosphodiesterase and liver homogenate on the
CC stability of oligonucleotides. Novel oligonucleotides of the invention
CC have both A- and B-form conformational geometry. The A-form geometry
CC modulates the binding affinity and nuclease resistance of the
CC oligonucleotide. The B-form geometry allows the oligonucleotide to serve
CC as substrate for RNase-H when bound to a target nucleic acid strand. The
CC oligonucleotides can be used to treat psoriasis and other inflammatory
CC skin conditions, skin cancers and viral, bacterial and fungal infections,
CC and in various diagnostic applications
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB |||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 361
AAC62454/c
ID AAC62454 standard; DNA; 19 BP.
XX
XX AAC62454;
AC AAC62454;
XX
XX 07-FEB-2001 (first entry)
XX
XX Cleavage of nucleic acids from solid supports assay oligonucleotide #3.

RESULT 360
AAA71630/c
ID AAA71630 standard; DNA; 19 BP.
XX
XX AAA71630;
AC AAA71630;
XX
XX 14-DEC-2000 (first entry)
XX
XX Phosphorothioate 20-mer primer DNA #1.
XX
XX Phosphorothioate; primer; oligomer synthesis; antisense therapy; ss.
XX Synthetic.
XX Key Location/Qualifiers
FH modified_base 1.20 /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorothioate linkage"
XX
XX EP1028124-A2.
XX
XX 16-AUG-2000.
XX
XX 06-SEP-1999; 99EP-00307066.
XX
XX 04-FEB-1999; 99US-0118564P.
XX 09-APR-1999; 99US-00288679.
XX (ISIS-) ISIS PHARM INC.
XX
XX Ravikumar VT, Manoharan M, Capaldi DC, Krotz A, Cole DL;
XX Guzaev A;
XX WPI; 2000-500332/45.
XX
XX Novel method for the production of oligomers with reduced exocyclic
PT adducts comprises treatment with deprotecting and cleaving reagents.
XX Example 2; Page 17; 33pp; English.
XX This invention describes a novel synthetic method (M) comprising: (a)
CC providing a sample comprising a number of oligomers of formula (I); (b)
CC contacting the sample with a deprotecting agent to remove R t groups from
CC the oligomers; and (c) reacting the oligomer with a cleaving reagent. The
CC method is used to produce oligomeric compounds for use in antisense and
CC oligonucleotide therapies. The method enables the synthesis of oligomers
CC with a reduction in the number acrylonitrile groups attached.
CC Acrylonitrile has been demonstrated to be a potent carcinogen in rats.
CC This sequence represents a phosphorothioate 20-mer primer which is used
CC in the method of the invention
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB |||||
19 AAAAAAAAAAAAAAAAAA 1

RESULT 361
AAC62454/c
ID AAC62454 standard; DNA; 19 BP.
XX
XX AAC62454;
AC AAC62454;
XX
XX 07-FEB-2001 (first entry)
XX
XX Cleavage of nucleic acids from solid supports assay oligonucleotide #3.
```

XX Nucleic acid cleavage; solid support; DNA-RNA hybrid;
 KW affinity chromatography; sequencing; mutagenesis; DNA preparation;
 XX nucleic acid purification; ss.

OS Synthetic.

FH Key Location/Qualifiers
 FT misc_RNA 10
 FT /tag= a

XX WO200058329-A1.

XX 05-OCT-2000.

XX 28-MAR-2000; 2000WO-GB001190.

XX 29-MAR-1999; 99GB-00007245.

XX (GOLD/) GOLDSBOROUGH A.

XX WPI; 2000-664908/64.

XX Detaching nucleic acid molecule comprising unconventional nucleotide
 PT incorporated at predetermined site from a solid support involves cleaving
 PT the nucleic acid molecule at the site of unconventional nucleotide.

XX Example 3; Page 34; 47pp; English.

XX The present invention is concerned with the cleavage of nucleic acids
 CC from solid supports. This is carried out by adding a non-conventional
 CC nucleotide into the nucleic acid attached to the support, so that it is
 CC recognised and cleaved by a specific DNA glycosylase and the sequence is
 CC released. This is useful in many molecular biological procedures such as
 CC sequencing, in vitro amplifications, cDNA and template preparation, DNA-
 CC based assays, mutagenesis procedures, nucleic acid purification and
 CC affinity chromatography. The present sequence is an oligonucleotide used
 CC in assays to demonstrate the methods of the invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 362

AAF31458/c

ID AAF31458 standard; DNA; 19 BP.

XX AAF31458;

XX 10-APR-2001 (first entry)

XX Oligonucleotide ISIS 109989.

XX Gene expression; gene therapy; diagnosis; ss.

OS Synthetic.

XX WO200102423-A2.

XX 11-JAN-2001.

XX 07-JUL-2000; 2000WO-US018609.

XX 07-JUL-1999; 99US-00349040.

XX (ISIS-) ISIS PHARM INC.

PA

XX Manoharan M, Cook PD, Prakash TP, Mohan V;
 PI WPI; 2001-138119/14.

XX Guanidium functionalized oligomers prepared from corresponding monomer
 PT units, are hybridizable with a specific RNA or DNA sequence, useful for
 PT diagnostic and therapeutic purposes.

XX Example 26; Page 54; 108pp; English.

XX The present invention relates to nucleotide oligomers comprising monomer
 CC units. Oligomers modulate gene expression when hybridized by a single- or
 CC double-stranded nucleic acid. They are useful for gene therapy,
 CC diagnostic and investigative purposes

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 363

AAF31564/c

ID AAF31564 standard; DNA; 19 BP.

XX AAF31564;

XX 09-APR-2001 (first entry)

XX ISIS sequence 32327.

XX DNA/RNA hybrid; oligomer; C3' methylene hydrogen phosphate; AIDS;
 KW atherosclerosis; ss.

OS Synthetic.

XX WO200102419-A1.

XX 11-JAN-2001.

XX 05-JUL-2000; 2000WO-US040304.

XX 07-JUL-1999; 99US-00349033.

XX (ISIS-) ISIS PHARM INC.

XX Cook PD, Manoharan M, Maier M, An H;

XX WPI; 2001-138117/14.

XX New oligomers for use as research reagent, for treating disease caused by
 PT undesired production of proteins, and for diagnosing and treating AIDS,
 PT atherosclerosis.

XX Example 46; Page 74; 110pp; English.

XX The present invention relates to C3' methylene hydrogen phosphate
 CC oligomers. The oligomers may be used as research reagents, for treating
 CC disease caused by undesired production of proteins and for diagnosing and
 CC treating AIDS and atherosclerosis

XX Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754
 Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 364

AAH46460/c

ID AAH46460 standard; DNA; 19 BP.

AC AAH46460;

XX 14-SEP-2001 (first entry)

XX Oligonucleotide #8.

XX Phosphorothioate; anti-viral therapy; stereochemical pathway; ss.

XX Synthetic.

XX Key

FT modified_base 1..19

FT /tag= a

FT /mod_base= OTHER

FT /note= "All bases are phosphorothioate"

FT modified_base 1

FT /tag= b

FT /mod_base= OTHER

FT /note= "Modified with 2'-O-methoxyethyl"

PN US6242591-B1.

XX 05-JUN-2001.

XX 11-JAN-2000; 2000US-00481486.

XX 15-OCT-1997; 97US-00950779.

XX (ISIS-) ISIS PHARM INC.

XX Cole DL, Ravikumar VT, Cheruvallath ZS;

XX WPI; 2001-407218/43.

XX Preparing sulfurized 2' substituted phosphorothioate oligonucleotides

XX useful in biological research, comprises phosphorylating the 5'-hydroxyl

XX of a nucleic acid having a nucleoside with a 2' modification.

XX Example 12; Col 7; 7pp; English.

XX The present invention relates to a method for preparing phosphorothioate

XX oligonucleotides having at least one nucleoside with a 2' modification.

XX The method comprises phosphorylating the 5'-hydroxyl of a nucleic acid

XX group having at least one nucleoside with a 2' modification in an

XX acetonitrile. The present sequence was used to illustrate the method of

XX the present invention. The method is useful for synthesizing sulphurised

XX 2' substituted phosphorothioate oligonucleotides, which may be used in

XX molecular biological research, in applications such as anti-viral

XX therapy, and for determining the stereochemical pathways of certain

XX enzymes which recognise nucleic acids

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 19; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 2e+02;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 365

AAH25737/c

ID AAH25737 standard; DNA; 19 BP.

XX AAH25737;

XX 14-AUG-2001 (first entry)

XX Human type II RNase H substrate oligonucleotide #4.

XX Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;

XX gene therapy; primer; phosphorothioate backbone; ss.

XX Synthetic.

XX Key

FT modified_base 1..19

FT /tag= a

FT /mod_base= OTHER

FT /note= "optionally phosphorothioate backbone"

FT modified_base 16..19

FT /tag= b

FT /mod_base= OTHER

FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-

FT methoxyethyl)"

PN WO200123613-A1.

XX 05-APR-2001.

XX 29-SEP-2000; 2000WO-US026729.

XX 30-SEP-1999; 99US-00409926.

XX (ISIS-) ISIS PHARM INC.

XX Crooke ST, Lima WF, Wu H, Manoharan M;

XX WPI; 2001-343164/36.

XX Chimeric oligonucleotides that can serve as substrates for human RNase

XX H1, useful for enhancing the effectiveness of antisense gene therapies.

XX Example 54; Page 88; 178pp; English.

XX The present invention provides a number of DNA-RNA oligonucleotides which

XX can act as substrates for human RNase HI (a type II RNase). The sequence

XX consists of two portions, one of which is capable of supporting cleavage

XX of a complementary target RNA and the other of which is incapable of

XX supporting such cleavage. These can be used to enhance the effectiveness

XX of antisense therapies. The present sequence is an RNase H substrate used

XX in the exemplification of the invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 19; DB 1; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 2e+02;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAA 1

RESULT 366

AAH25738/c

ID AAH25738 standard; DNA; 19 BP.

XX AAH25738;

XX 14-AUG-2001 (first entry)

XX Human type II RNase H substrate oligonucleotide #5.

XX Human; RNase H type II; RNase H1 cleavage substrate; antisense therapy;

KW gene therapy; primer; phosphorothioate backbone; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1..19

XX FT *tag= a

XX /mod_base= OTHER

XX /note= "optionally phosphorothioate backbone"

FT modified_base 16..19

FT FT *tag= b

FT /mod_base= OTHER

FT /note= "optionally 3'-O-(2-methoxyethyl) or 2'-O-(2-

FT methoxyethyl)"

FT misc_RNA 19

FT FT *tag= c

XX WO200123613-A1.

XX PN

XX 05-APR-2001.

XX PD

XX 29-SEP-2000; 2000WO-US026729.

XX PF

XX 30-SEP-1999; 99US-00409926.

XX PR

XX (ISIS-) ISIS PHARM INC.

XX PA

XX Crooke ST, Lima WF, Wu H, Manoharan M;

XX PI

XX WPI; 2001-343164/36.

XX DR

XX Chimeric oligonucleotides that can serve as substrates for human RNase

XX H1, useful for enhancing the effectiveness of antisense gene therapies.

XX FT

XX Example 54; Page 88; 178pp; English.

XX PS

XX The present invention provides a number of DNA-RNA oligonucleotides which

XX can act as substrates for human RNase HI (a type II RNase). The sequence

XX consists of two portions, one of which is capable of supporting cleavage

XX of a complementary target RNA and the other of which is incapable of

XX supporting such cleavage. These can be used to enhance the effectiveness

XX of antisense therapies. The present sequence is an RNase H substrate used

XX in the exemplification of the invention

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 367

AAC83664/c

ID AAC83664 standard; DNA; 19 BP.

XX AAC83664;

XX 02-MAR-2001 (first entry)

XX 2'-O-N-[2-(dimethylamino)ethylacetamido]-modified oligo ISIS #32335.

XX 2'-O-acetamido; diagnostic; kinase modulator; nuclease resistance;

XX tumour formation; cancer; protein kinase C expression;

XX cell adhesion molecule expression; multidrug resistance; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 16..19

FT

FT /*tag= a

FT /mod_base= OTHER

XX /note= "2'-O-N-[2-(dimethylamino)ethylacetamido]5MeU"

XX US6147200-A.

XX 14-NOV-2000.

XX 19-AUG-1999; 99US-00378568.

XX 19-AUG-1999; 99US-00378568.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Cook PD, Fraser AS, Prakash TP, Kawasaki NM;

XX WPI; 2001-069824/08.

XX New 2'-O-acetamido modified nucleosides (I) used to produce

XX oligonucleotides which have enhanced nuclease resistance and superior

XX hybridization properties than prior art.

XX Example 12; Col 28; 29pp; English.

XX The present sequence is a modified oligonucleotide. 2'-O-acetamido-

XX modified nucleosides were used to produce oligonucleotides which have

XX enhanced nuclease resistance and superior hybridization properties than

XX prior art. The oligomeric compounds are useful for identification or

XX quantification of ribonucleic acid and deoxyribonucleic acid or for

XX modulating the activity of an ribonucleic acid or deoxyribonucleic acid

XX molecule. They have a modified nucleoside monomer and are specifically

XX hybridizable with a preselected nucleotide sequence of a single-stranded

XX or double-stranded target deoxyribonucleic acid or ribonucleic acid

XX molecule. The oligomers are further useful in a ras-luciferase fusion

XX system using ras-luciferase transactivation. They are useful in abnormal

XX cell proliferation and tumour formation and modulation of expression of

XX protein kinase C and cell adhesion molecules such as ICAM. They are

XX useful in the modulation of proteins related to multidrug resistance and

XX viral genomic nucleic acids such as HOV, herpes viruses, Epstein-Barr

XX virus, cytomegalovirus, papillomavirus, hepatitis C virus and influenza

XX virus

XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 368

AAK98526/c

ID AAK98526 standard; DNA; 19 BP.

XX AAK98526;

XX 16-APR-2002 (first entry)

XX Nucleic acid quantitative analysis related oligonucleotide #1.

XX Target detection; quantitative analysis; probe; medical diagnosis;

XX forensics; bacterial screening; tissue typing; gene expression analysis;

XX genotyping; ss.

XX Synthetic.

XX Key Location/Qualifiers

XX modified_base 1

FT /*tag= a

FT /mod_base= OTHER

```
FT XX /note= "modified by thiol"
PN XX
XX XX
XX XX
PD PD
XX XX
XX 02-JUL-2001; 2001WO-EF007575.
XX PF
XX 01-JUL-2000; 2000DE-01033334.
XX PR
XX (CLON-) CLONDIAG CHIP TECHNOLOGIES GMBH.
XX PA
XX Bickel R, Ehricht R, Ermantraut E, Kaiser T;
PI Schulz T, Wagner G;
XX XX
XX WPI; 2002-154760/20.
DR DR
XX XX
XX Determining targets by interaction with probe array, useful e.g. for
PT diagnosis, based on detecting formation of precipitate at specific probe
PT sites.
XX XX
XX Example 5; Page 47; 92pp; German.
XX XX
XX The present invention relates to a method for the qualitative and
CC quantitative detection of targets in a sample by molecular interaction
CC between the target and probes in an array. The method can be used to
CC detect interactions between nucleic acids, antigens and antibodies or
CC receptor and ligands, particularly in applications such as medical
CC diagnosis, forensic science, bacterial screening, tissue typing for
CC transplantation, monitoring gene expression, and genotyping. The present
CC sequence is a modifying oligonucleotide used in the exemplification of
XX the invention
XX XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 369
ABA91949/c
ID ABA91949 standard; DNA; 19 BP.
XX XX
XX ABA91949;
XX XX
XX 23-MAY-2002 (first entry)
XX DE Methyl thioethyl modified oligonucleotide.
XX XX
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
FH modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 18
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-methyl thioethyl thymidine"
FT modified_base 19
FT /*tag= d
```

```
FT FT /mod_base= OTHER
XX XX /note= "2'-methyl thioethyl thymidine"
PN PN
XX XX
XX US6277982-B1.
XX PD
XX 21-AUG-2001.
XX PF
XX 20-AUG-1999; 99US-00378665.
XX PR
XX 20-AUG-1999; 99US-00378665.
XX XX (ISIS-) ISIS PHARM INC.
XX PA
XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;
PI WPI; 2002-235143/29.
XX DR
XX Alkylation of alcohols, amines, or thiols, useful for preparing
PT nucleosides that are precursors for preparation of oligomeric compounds
PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
XX XX
XX Example 15; Col 35; 45pp; English.
XX XX
XX The present sequence is that of a chimeric oligonucleotide having some 2'
CC -methyl thioethyl modifications. This was compared with oligonucleotides
CC with methoxyethoxy (see ABA91950) and dimethylaminopropyl (see ABA91951)
CC modifications for resistance to snake venom phosphodiesterase. The assay
CC revealed the nuclease resistance of the modified oligomers. The invention
CC provides methods for the alkylation of alcohols, amines, thiols and their
CC derivatives by cyclic sulfate intermediates. In particular, methods for
CC the alkylation of the 2', 3' or 5'-hydroxy position of nucleosides and
CC their analogues with cyclic sulfates to form the 2', 3' or 5'-O-alkyl
CC sulfate modified compounds are disclosed. Displacement of the 2', 3' or
CC 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-modified
CC nucleosides and their analogues. The methods are especially useful for
CC the preparation of 2'-O-alkyl nucleotides, nucleosides and nucleoside
CC surrogates that are precursors for the preparation of oligomeric
CC compounds useful as therapeutics, diagnostics and research reagents
XX XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 370
ABA91951/c
ID ABA91951 standard; DNA; 19 BP.
XX XX
XX ABA91951;
XX XX
XX 23-MAY-2002 (first entry)
XX DE Dimethylaminopropyl modified oligonucleotide.
XX XX
XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
FH modified_base 16
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT modified_base 17
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-dimethylaminopropyl thymidine"
FT modified_base 19
FT /*tag= d
```

FT modified_base 18 /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-dimethylaminopropyl thymidine"
 FT modified_base 19
 FT /*tag= d
 FT /mod_base= OTHER
 FT /note= "2'-dimethylaminopropyl thymidine"
 FT XX

PN US6277982-B1.

XX 21-AUG-2001.

XX 20-AUG-1999; 99US-00378665.

XX 20-AUG-1999; 99US-00378665.

XX (ISIS-) ISIS PHARM INC.

XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;

XX WPI; 2002-235143/29.

XX Alkylation of alcohols, amines, or thiols, useful for preparing
 PT nucleosides that are precursors for preparation of oligomeric compounds
 PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
 XX Example 15; Col 35; 45pp; English.

XX The present sequence is that of a chimeric oligonucleotide having some 2'
 CC -dimethylaminopropyl modifications. This was compared with
 CC oligonucleotides with methyl thioethyl (see ABA91949) and methoxyethoxy
 CC (see ABA91950) modifications for resistance to snake venom
 CC phosphodiesterase. The assay revealed the nuclease resistance of the
 CC modified oligomers. The invention provides methods for the alkylation of
 CC alcohols, amines, thiols and their derivatives by cyclic sulfate
 CC intermediates. In particular, methods for the alkylation of the 2', 3' or
 CC 5'-hydroxy position of nucleosides and their analogues with cyclic
 CC sulfates to form the 2', 3' or 5'-O-alkyl sulfate modified compounds are
 CC disclosed. Displacement of the 2', 3' or 5'-O-sulfate with a nucleophile
 CC provides 2', 3' or 5'-O-modified nucleosides and their analogues. The
 CC methods are especially useful for the preparation of 2'-O-alkyl
 CC nucleotides, nucleosides and nucleoside surrogates that are precursors
 CC for the preparation of oligomeric compounds useful as therapeutics,
 CC diagnostics and research reagents

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 371

ABA91950/C

ID ABA91950 standard; DNA; 19 BP.

XX ABA91950;

XX 23-MAY-2002 (first entry)

XX Methoxyethoxy modified oligonucleotide.

XX 2'-O-alkyl oligonucleotide; nuclease resistance; diagnosis; therapy; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 16

FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 17
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 18
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethoxy thymidine"
 FT modified_base 19
 FT /*tag= d
 FT /mod_base= OTHER
 FT /note= "2'-methoxyethoxy thymidine"
 FT XX

PN US6277982-B1.

XX 21-AUG-2001.

XX 20-AUG-1999; 99US-00378665.

XX 20-AUG-1999; 99US-00378665.

XX (ISIS-) ISIS PHARM INC.

XX Fraser AS, Manoharan M, Cook PD, Jung ME, Kawasaki AM;

XX WPI; 2002-235143/29.

XX Alkylation of alcohols, amines, or thiols, useful for preparing
 PT nucleosides that are precursors for preparation of oligomeric compounds
 PT beneficial as therapeutics, involves use of cyclic sulfate intermediates.
 XX Example 15; Col 35; 45pp; English.

XX The present sequence is that of a chimeric oligonucleotide having some 2'
 CC -methoxyethoxy modifications. This was compared with oligonucleotides
 CC with methyl thioethyl (see ABA91949) and dimethylaminopropyl (see
 CC ABA91951) modifications for resistance to snake venom phosphodiesterase.
 CC The assay revealed the nuclease resistance of the modified oligomers. The
 CC invention provides methods for the alkylation of alcohols, amines, thiols
 CC and their derivatives by cyclic sulfate intermediates. In particular,
 CC methods for the alkylation of the 2', 3' or 5'-hydroxy position of
 CC nucleosides and their analogues with cyclic sulfates to form the 2', 3'
 CC or 5'-O-alkyl sulfate modified compounds are disclosed. Displacement of
 CC the 2', 3' or 5'-O-sulfate with a nucleophile provides 2', 3' or 5'-O-
 CC modified nucleosides and their analogues. The methods are especially
 CC useful for the preparation of 2'-O-alkyl nucleotides, nucleosides and
 CC nucleoside surrogates that are precursors for the preparation of
 CC oligomeric compounds useful as therapeutics, diagnostics and research
 CC reagents

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754

Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 372

ABL51520/C

ID ABL51520 standard; DNA; 19 BP.

XX ABL51520;

XX 01-JUL-2002 (first entry)

XX Tailing reaction related exemplary primer biotin-dT18U SEQ ID NO:1.

XX Tailing reaction; tailed primer; primer; probe; identification;
KW detection; linear amplification scheme; chain extending enzyme;
KW telomerase; ss.
XX
XX Synthetic.

XX Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "biotinylated"
FT 19
FT /tag= b

XX US2002031776-A1.

XX 14-MAR-2002.

XX 26-JUL-2001; 2001US-00917138.

XX 28-MAY-1999; 99US-0136545P.

XX 25-MAY-2000; 2000US-00580358.

XX (TULL/) TULLIS R H.

XX (STRE/) STREIFEL J A.

XX Tullis RH, Streifel JA;

XX WPI; 2002-361176/39.

XX Identifying and detecting nucleic acids, particularly DNA hybridization
PT probes, involves employing chain extending enzymes (e.g. telomerase) to
PT elongate probes to render them readily detectable.

XX Example 1; Page 5; 10pp; English.

XX The present invention describes a method for detecting a nucleic acid
CC probe, which comprises using chain extending enzymes to elongate probes.
CC The method comprises: (a) treating the sample with a chain terminating
CC reagent to prevent polynucleotide chain growth from the nucleic acid in
CC the sample; (b) contacting the sample with the probe containing a
CC terminus capable of elongation by a chain extending enzyme, where the
CC probe hybridises to the nucleic acid in the sample; (c) contacting the
CC sample with a chain extending enzyme and its substrates, which elongates
CC the probe; and (d) detecting the elongated hybridised probe. Also
CC described is a method comprising: (a) treating nucleic acid molecules or
CC modified nucleic acids in a sample with a reagent or reagents that render
CC the nucleic acid chains unextendable by a non-template-dependent enzyme;
CC (b) hybridising the treated molecules with a nucleic acid probe that
CC includes an extendable terminus, under conditions where hybrids form; and
CC (c) treating any hybrids formed with a non-template dependent chain
CC elongating enzyme and its substrates, where any hybridised probe is
CC extended. The method is useful for identifying and detecting nucleic
CC acids, particularly DNA hybridisation probes. The present sequence
CC represents a tailing reaction exemplary primer, which is used in an
CC example from the present invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 1 U; 0 Other;

XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 373

AD42000/c

ID AD42000 standard; DNA; 19 BP.

XX

AC AD42000;

XX 04-NOV-2002 (first entry)

XX Oligonucleotide #3 used to illustrate the method of the invention.

XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.

XX Unidentified.

XX Key Location/Qualifiers
FH modified_base 15.18
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethoxy (MOE) residues"

XX US6403779-B1.

XX 11-JUN-2002.

XX 08-JAN-1999; 99US-00227782.

XX 08-JAN-1999; 99US-00227782.

XX (ISIS-) ISIS PHARM INC.

XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;

XX WPI; 2002-546338/58.

XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.

XX Example 46; Col 31; 24pp; English.

XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention

XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

XX Query Match 1.1%; Score 19; DB 1; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 2e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754

DB 19 AAAAAAAAAAAAAAAAAA 1

RESULT 374

AD42002/c

ID AD42002 standard; DNA; 19 BP.

XX AD42002;

XX 04-NOV-2002 (first entry)

XX Oligonucleotide #5 used to illustrate the method of the invention.

XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.

XX

```

OS Unidentified.
XX Key Location/Qualifiers
FH modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-methoxyethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 33; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 375
AAD42004/C
ID AAD42004 standard; DNA; 19 BP.
XX
XX AAD42004;
AC
XX
XX 04-NOV-2002 (first entry)
DT
XX
XX Oligonucleotide #7 used to illustrate the method of the invention.
DE
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 18
FT /*tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminoxyethyl residue"
XX
XX US6403779-B1.
PN

```

```

XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
XX nucleoside in aprotic solvent, cooling, treating with base, warming,
XX cooling and reacting with ester.
XX
XX Example 46; Col 33; 24pp; English.
XX
XX The present invention relates to a novel method of selective alkylation
XX of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX The method involves dissolving the nucleoside in at least one aprotic
XX solvent, cooling, treating with base, warming, cooling and reacting with
XX a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX nucleotides, nucleosides and nucleoside surrogates used for preparation
XX of oligomeric compounds having improved hybridisation affinity and
XX nuclear resistance, which are useful as therapeutics, diagnostics and
XX research reagents. The present sequence is a modified oligonucleotide
XX used to illustrate the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1
RESULT 376
AAD42010/C
ID AAD42010 standard; DNA; 19 BP.
XX
XX AAD42010;
AC
XX
XX 04-NOV-2002 (first entry)
DT
XX
XX Oligonucleotide #13 used to illustrate the method of the invention.
DE
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH modified_base 16..19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"
XX
XX modified_base 18..19
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX

```

```
PR 08-JAN-1999; 99US-00227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
DR
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
XX for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
XX Example 46; Col 35; 24pp; English.
PS
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 377
AAD42020/c
ID AAD42020 standard; DNA; 19 BP.
XX
XX AAD42020;
XX
XX 04-NOV-2002 (first entry)
XX
XX Oligonucleotide #23 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "2'-O-methyleneiminooxethyl thymidine"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
XX Example 46; Col 35; 24pp; English.
PS
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
XX Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
SQ
Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 19 AAAAAAAAAAAAAAAAAA 1
RESULT 378
AAD42001/c
ID AAD42001 standard; DNA; 19 BP.
XX
XX AAD42001;
XX
XX 04-NOV-2002 (first entry)
XX
XX Oligonucleotide #4 used to illustrate the method of the invention.
XX
XX Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 16..19
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-dimethylaminooxethyl residues"
XX
XX US6403779-B1.
XX
XX 11-JUN-2002.
XX
XX 08-JAN-1999; 99US-00227782.
XX
XX 08-JAN-1999; 99US-00227782.
XX (ISIS-) ISIS PHARM INC.
XX
XX Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX WPI; 2002-546338/58.
XX
XX Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
XX Example 46; Col 31; 24pp; English.
PS
XX The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
```

CC	solvant, cooling, treating with base, warming, cooling and reacting with
CC	a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC	nucleotides, nucleosides and nucleoside surrogates used for preparation
CC	of oligomeric compounds having improved hybridisation affinity and
CC	nuclear resistance, which are useful as therapeutics, diagnostics and
CC	research reagents. The present sequence is a modified oligonucleotide
CC	used to illustrate the method of the invention
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 19;	
Best Local Similarity 100.0%; Pred.No. 2e+02;	
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1736 AAAAAAAAAAAAAAAA 1754 19 AAAAAAAAAAAAAAAA 1
Dd	
RESULT 379	
AAD42011/c	
ID	AAD42011 standard; DNA; 19 BP.
AC	
AAD42011;	
DT	
DT	04-NOV-2002 (first entry)
XX	
XX	Oligonucleotide #14 used to illustrate the method of the invention.
DE	
XX	
KW	Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KX	nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX	
OS	Unidentified.
FH	
Key	Location/Qualifiers
modified_base	16..19
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "2'-dimethylaminoxyethyl thymidine (T-2'DMAOE)"
XX	
PN	US6403779-B1.
XX	
PD	11-JUN-2002.
XX	
PF	08-JAN-1999; 99US-00227782.
XX	
PR	08-JAN-1999; 99US-00227782.
XX	
PA	(ISIS-) ISIS PHARM INC.
PI	
PI	Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
DR	
WI	2002-546338/58.
XX	
PT	Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT	for preparation of 2'-O-alkylated compounds comprises dissolving
PT	nucleoside in aprotic solvent, cooling, treating with base, warming,
PT	cooling and reacting with ester.
XX	
XX	Example 46; Col 37; 24pp; English.
XX	
CC	The present invention relates to a novel method of selective alkylation
CC	of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC	The method involves dissolving the nucleoside in at least one aprotic
CC	solvant, cooling, treating with base, warming, cooling and reacting with
CC	a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC	nucleotides, nucleosides and nucleoside surrogates used for preparation
CC	of oligomeric compounds having improved hybridisation affinity and
CC	nuclear resistance, which are useful as therapeutics, diagnostics and
CC	research reagents. The present sequence is a modified oligonucleotide
CC	used to illustrate the method of the invention
XX	
SQ	Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

```
RESULT 381
AAD42003/c
ID AAD42003 standard; DNA; 19 BP.
XX
AC AAD42003;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #6 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 16..19
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-O-propyl residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 33; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 382
AAD41998/c
ID AAD41998 standard; DNA; 19 BP.
XX
AC AAD41998;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
```

```
DE Oligonucleotide #1 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "5-methyl, 2'-aminoxyethoxy (2'-AOE) residues"
XX
PN US6403779-B1.
XX
PD 11-JUN-2002.
XX
PF 08-JAN-1999; 99US-00227782.
XX
PR 08-JAN-1999; 99US-00227782.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
DR WPI; 2002-546338/58.
XX
PT Alkylating 2' position of 2',3'-dihydroxy sugar moiety of nucleoside used
PT for preparation of 2'-O-alkylated compounds comprises dissolving
PT nucleoside in aprotic solvent, cooling, treating with base, warming,
PT cooling and reacting with ester.
XX
PS Example 46; Col 31; 24pp; English.
XX
CC The present invention relates to a novel method of selective alkylation
CC of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
CC The method involves dissolving the nucleoside in at least one aprotic
CC solvent, cooling, treating with base, warming, cooling and reacting with
CC a reactive ester. The method is useful for the preparation of 2'-O-alkyl
CC nucleotides, nucleosides and nucleoside surrogates used for preparation
CC of oligomeric compounds having improved hybridisation affinity and
CC nuclear resistance, which are useful as therapeutics, diagnostics and
CC research reagents. The present sequence is a modified oligonucleotide
CC used to illustrate the method of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 383
AAD41999/c
ID AAD41999 standard; DNA; 19 BP.
XX
AC AAD41999;
XX
DT 04-NOV-2002 (first entry)
XX
DE Oligonucleotide #2 used to illustrate the method of the invention.
XX
KW Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
KW nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT modified_base 15..18
```



```

FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "5-methyl, 2'-dimethylaminoxyethoxy (2'-DMAOE)
FT      residues"
XX
XX      US6403779-B1.
XX
XX      11-JUN-2002.
XX
XX      08-JAN-1999; 99US-00227782.
XX
XX      08-JAN-1999; 99US-00227782.
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX      WPI; 2002-546338/58.
XX
XX      Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
XX      for preparation of 2'-O-alkylated compounds comprises dissolving
XX      nucleoside in aprotic solvent, cooling, treating with base, warming,
XX      cooling and reacting with ester.
XX
XX      Example 46; Col 31; 24pp; English.
XX
XX      The present invention relates to a novel method of selective alkylation
XX      of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX      The method involves dissolving the nucleoside in at least one aprotic
XX      solvent, cooling, treating with base, warming, cooling and reacting with
XX      a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX      nucleotides, nucleosides and nucleoside surrogates used for preparation
XX      of oligomeric compounds having improved hybridisation affinity and
XX      nuclear resistance, which are useful as therapeutics, diagnostics and
XX      research reagents. The present sequence is a modified oligonucleotide
XX      used to illustrate the method of the invention
XX
XX      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX      Query Match 1.1%; Score 19; DB 1; Length 19;
XX      Best Local Similarity 100.0%; Pred. No. 2e+02;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAA 1
XX
XX      RESULT 384
XX      AAD42009/c
XX      ID AAD42009 standard; DNA; 19 BP.
XX
XX      AAD42009;
XX
XX      04-NOV-2002 (first entry)
XX
XX      Oligonucleotide #12 used to illustrate the method of the invention.
XX
XX      Dihydroxy sugar moiety; 2'-O-alkyl nucleotide; hybridisation affinity;
XX      nuclear resistance; alkylation; therapeutic; diagnostic; ss.
XX
XX      Unidentified.
XX
XX      Key Location/Qualifiers
XX      modified_base 15.18
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "2'-dimethylaminoxyethyl thymidine (T-2'-DMAOE)"
XX
XX      US6403779-B1.
XX
XX      11-JUN-2002.
XX

```

```

PF      08-JAN-1999; 99US-00227782.
XX
XX      08-JAN-1999; 99US-00227782.
XX      (ISIS-) ISIS PHARM INC.
XX
XX      Kawasaki AM, Fraser AS, Manoharan M, Cook PD, Prakash TP;
XX      WPI; 2002-546338/58.
XX
XX      Alkylating 2' position of 2', 3'-dihydroxy sugar moiety of nucleoside used
XX      for preparation of 2'-O-alkylated compounds comprises dissolving
XX      nucleoside in aprotic solvent, cooling, treating with base, warming,
XX      cooling and reacting with ester.
XX
XX      Example 46; Col 35; 24pp; English.
XX
XX      The present invention relates to a novel method of selective alkylation
XX      of the 2' position of 2', 3'-dihydroxy sugar moieties of a nucleoside.
XX      The method involves dissolving the nucleoside in at least one aprotic
XX      solvent, cooling, treating with base, warming, cooling and reacting with
XX      a reactive ester. The method is useful for the preparation of 2'-O-alkyl
XX      nucleotides, nucleosides and nucleoside surrogates used for preparation
XX      of oligomeric compounds having improved hybridisation affinity and
XX      nuclear resistance, which are useful as therapeutics, diagnostics and
XX      research reagents. The present sequence is a modified oligonucleotide
XX      used to illustrate the method of the invention
XX
XX      Sequence 19 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
XX
XX      Query Match 1.1%; Score 19; DB 1; Length 19;
XX      Best Local Similarity 100.0%; Pred. No. 2e+02;
XX      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy      1736 AAAAAAAAAAAAAAAAAA 1754
Db      19 AAAAAAAAAAAAAAAAAA 1
XX
XX      RESULT 385
XX      ABZ58336/c
XX      ID ABZ58336 standard; DNA; 19 BP.
XX
XX      ABZ58336;
XX
XX      28-APR-2003 (first entry)
XX
XX      Oligonucleotide with 2'-O-(2-(methylthio)ethyl)-5-methyluridine.
XX
XX      Oligonucleotide; 2'-O-(2-(methylthio)ethyl)-5-methyluridine; antisense;
XX      DNA-RNA hybrid; ss.
XX
XX      Synthetic.
XX
XX      Key Location/Qualifiers
XX      modified_base 16
XX      /*tag= a
XX      /mod_base= OTHER
XX      /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX      modified_base 17
XX      /*tag= b
XX      /mod_base= OTHER
XX      /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX      modified_base 18
XX      /*tag= c
XX      /mod_base= OTHER
XX      /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX      modified_base 19
XX      /*tag= d
XX      /mod_base= OTHER
XX      /note= "2'-O-(2-methylthio)ethyl)-5-methyluridine"
XX
XX      WO2003004603-A2.
XX

```

XX 16-JAN-2003.
 XX 01-JUL-2002; 2002WO-US020940.
 XX 03-JUL-2001; 2001US-0302683P.
 XX 28-JAN-2002; 2002US-00058740.
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Prakash TP, Manoharan M;
 XX WPI; 2003-239204/23.
 XX
 XX Increasing binding of oligomeric compound to proteins useful in
 XX preparation of antisense therapeutics, involves use of modified
 XX oligomeric compound having oligonucleotide group.
 XX
 XX Example 27; Page 72; 122pp; English.
 XX
 XX The present sequence is an example of an oligonucleotide of the invention
 XX containing 2'-O-(2-(methylthio)ethyl)-5-methyluridine (2'-O-(MTE)-5-
 XX methyluridine) modifications. In examples of the invention, 2'-O-MTE was
 XX incorporated into oligonucleotides and evaluated for antisense properties
 XX in comparison with the known 2'-O-(2-methoxyethyl) (2'-O-MOE)
 XX modification. The 2'-O-MTE modified oligonucleotides exhibited similar
 XX binding affinity to target RNA as their 2'-O-MOE equivalent while binding
 XX to human serum albumin was improved. The modification can be used to
 XX modulate the pharmacokinetics of oligonucleotides, e.g. in antisense
 XX therapy
 XX
 XX Sequence 19 BP; 0 A; 0 C; 0 G; 15 T; 4 U; 0 Other;
 XX
 XX Query Match 1.1%; Score 19; DB 1; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 2e+02;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
 XX |
 XX 19 AAAAAAAAAAAAAAAAAAAAAA 1
 XX
 XX
 XX RESULT 386
 XX AAQ75569/c
 XX ID AAQ75569 standard; DNA; 20 BP.
 XX AC AAQ75569;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 XX and using the aggregate of mRNAs as the template for each reverse
 XX transcription primer; (b) digesting each of the prepared aggregates of
 XX the double-stranded cDNAs with restriction enzyme and; (c)
 XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 20 BP; 0 A; 0 C; 1 G; 19 T; 0 U; 0 Other;
 XX
 XX Query Match 1.1%; Score 19; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1752
 XX |
 XX 19 AAAAAAAAAAAAAAAAAAAAAA 1
 XX
 XX
 XX RESULT 387
 XX AAQ75570/c
 XX ID AAQ75570 standard; DNA; 20 BP.
 XX AC AAQ75570;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.
 XX
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 XX and using the aggregate of mRNAs as the template for each reverse
 XX transcription primer; (b) digesting each of the prepared aggregates of
 XX the double-stranded cDNAs with restriction enzyme and; (c)
 XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX method can be used to analyse gene expression rapidly and easily
 XX
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
 XX
 XX Query Match 1.1%; Score 19; DB 1; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1734 AAAAAAAAAAAAAAAAAAAAAA 1752
 XX |
 XX 19 AAAAAAAAAAAAAAAAAAAAAA 1
 XX
 XX
 XX RESULT 388
 XX AAQ75569/c
 XX ID AAQ75569 standard; DNA; 20 BP.
 XX AC AAQ75569;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 XX aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

```

RESULT 388
AAQ75567/C
ID 1 AAQ75567 standard; DNA; 20 BP.
XX
AC AAQ75567;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ACAAAAAAAAAAAAAAAAAA 1

RESULT 389
AAQ75567/C
ID 1 AAQ75567 standard; cDNA; 20 BP.
XX
AC AAQ75567;
XX
DT 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
DE Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-3.
XX
KW Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
OS Synthetic.
XX
PN EP676470-A1.
XX
PD 11-OCT-1995.
XX

RESULT 390
AAV07752/C
ID 1 AAV07752 standard; DNA; 20 BP.
XX
AC AAV07752;
XX
DT 07-DEC-1998 (first entry)
XX
DE Phosphorothioate oligonucleotide.
XX
KW phosphorothioate; sulphurisation; heterocycle; automated synthesis;
KW antisense; EDITH; Beaucage reagent; ss.
XX
OS Synthetic.
XX
KH Key Location/Qualifiers
FT misc_feature 1..20 a
FT /tag= a
FT /note= "phosphorothioate internucleotide linkages"
XX
PN WO9741130-A2.
XX
PD 06-NOV-1997.
XX
PF 29-APR-1997; 97WO-US007118.

```

04-OCT-1990; 95EP-00105391.

16-OCT-1989; 89US-00422383.

11-JUN-1990; 90US-00537198.

24-AUG-1990; 90US-00573616.

28-SEP-1990; 90WO-US005548.

01-OCT-1990; 90US-00589701.

(AMGE-) AMGEN INC.

Zeebo KM, Suggs SV, Bosselman RA, Martin PH;

WPI; 1995-346090/45.

New stem cell factor polypeptide(s) - for stimulating the growth of primitive progenitor cells, esp. for treating disorders involving blood cells.

Example 3; Fig 12C; 127pp; English.

AAT04915-T04922 are oligonucleotide primers and probes used for the amplification and sequencing of mammalian stem cell factor (SCF). Non-naturally occurring SCF and C-terminally truncated polypeptides, having amino acid sequences sufficiently duplicative of naturally occurring SCF, stimulate growth of primitive progenitors such as haematopoietic progenitor cells, neural stem cells and primordial germ stem cells. The peptides can be used in a composition for treating leucopenia, anaemia or thrombocytopenia, for enhancing engraftment of bone marrow during transplantation or for bone marrow recovery after chemotherapy or radiation-induced bone marrow aplasia or myelosuppression. They can also be used for treating neoplasia, nerve damage, infertility, intestinal damage or myeloproliferative disorders. Antibodies may be raised against the peptides for use in detection or neutralisation of SCF in serum. SCF may be useful for the treatment of AIDS and severe combined immunodeficiency (SCID) states alone or in combination with other factors such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)

Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 390

AAV07752/C

ID 1 AAV07752 standard; DNA; 20 BP.

XX

AC AAV07752;

XX

DT 07-DEC-1998 (first entry)

XX

DE Phosphorothioate oligonucleotide.

XX

KW phosphorothioate; sulphurisation; heterocycle; automated synthesis;

KW antisense; EDITH; Beaucage reagent; ss.

XX

OS Synthetic.

XX

KH Key Location/Qualifiers

FT misc_feature 1..20 a

FT /tag= a

FT /note= "phosphorothioate internucleotide linkages"

XX

PN WO9741130-A2.

XX

PD 06-NOV-1997.

XX

PF 29-APR-1997; 97WO-US007118.

```
XX 30-APR-1996; 96US-00641920.
XX (MINU ) UNIV MINNESOTA.
XX (LOU ) UNIV LOUISIANA STATE & AGRIC.
XX
XX Barany G, Musier-Forsyth K, Xu Q, Chen L, Hammer RP;
XX WPI; 1997-549671/50.
XX
XX Sulphurisation of phosphorus-containing compounds, e.g.
XX oligo:nucleotides) - by contacting the compound with a di:sulphide-
XX containing five-membered heterocycle.
XX
XX Example 7; Page 30; 51pp; English.
XX
XX The present invention provides a method for sulphurising phosphorus-
XX containing compounds. It comprises contacting the phosphorus-containing
XX compound which a 1,2,4-dithiazolidine-2,5-dione compound or a 3-
XX substituted-1,2,4-dithiazolin-5-one compound. The method is especially
XX useful for incorporation of phosphorothioate linkages into biologically
XX important molecules such as DNA, RNA and phosphopeptides. Molecules
XX containing such linkages are useful e.g. as antisense compounds for
XX inhibiting gene expression, as reagents for studying DNA-protein or RNA-
XX protein interactions, or as catalytic RNA. The present sequence
XX represents an oligonucleotide with phosphorothioate linkages prepared by
XX the method of the invention
XX
XX Sequence 20 BP; 1 A; 0 C; 0 G; 0 T; 19 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAAAAAA 1754
XX Db 19 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 391
XX AAAL3752/c
XX ID AAAL3752 standard; DNA; 20 BP.
XX AC AAAL3752;
XX
XX DT 27-JUL-2000 (first entry)
XX
XX DE Stem cell factor universal oligonucleotide 220-3.
XX
XX KW Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX KW primitive progenitor cell; haematopoietic disorder; syngeneic;
XX KW allogeneic; autologous bone marrow transplant; gene therapy;
XX KW transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX KW cancer; ss.
XX
XX OS Synthetic.
XX
XX PN EP92579-A1.
XX
XX PD 12-APR-2000.
XX
XX PF 04-OCT-1990; 99EP-00122861.
XX
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90WO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 04-OCT-1990; 90EP-00310899.
XX
XX (AMGE-) AMGEN INC.
XX
XX Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
```

```
XX WPI; 2000-259135/23.
XX
XX Production of hematopoietic cells suitable for administration to a
XX subject using progenitor cells and expanding the cells using stem cell
XX factor.
XX
XX Example 3; Fig 12C; 123pp; English.
XX
XX A method has been developed of making haematopoietic cells suitable for
XX administration to a subject. The method comprises: (a) obtaining
XX haematopoietic progenitor cells from a donor; and (b) expanding the cells
XX by adding to the cells a haematopoietically effective dose of a
XX polypeptide product having at least part of the primary structural
XX confirmation and one or more of the biological properties of naturally
XX occurring stem cell factor (SCF). The method is useful for stimulating
XX primitive progenitor cells including early haematopoietic progenitor
XX cells which are capable of maturing to erythroid, megakaryocyte,
XX granulocyte, lymphocyte and macrophage cells. SCF results in absolute
XX increases in haematopoietic cells of both myeloid and lymphoid lineages.
XX SCF is useful for treating haematopoietic disorders. The method is useful
XX for expanding early haematopoietic progenitors in syngeneic, allogeneic
XX or autologous bone marrow transplant. SCF is useful for enhancing the
XX efficiency of gene therapy based on transfecting haematopoietic stem
XX cells. SCF is also useful for combating the myelosuppressive effects of
XX anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
XX after acute blood loss and as a boost to the immune system for fighting
XX neoplasia (cancer). The present sequence represents a universal
XX oligonucleotide which is used in an example from the present invention
XX
XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 2.1e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1735 CAAAAAAAAAAAAAAAAA 1753
XX Db 19 CAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 392
XX AAH41331/c
XX ID AAH41331 standard; DNA; 20 BP.
XX AC AAH41331;
XX
XX DT 21-AUG-2001 (first entry)
XX
XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:32.
XX
XX KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX
XX OS Synthetic.
XX
XX PN US6207454-B1.
XX
XX PD 27-MAR-2001.
XX
XX PF 31-DEC-1998; 98US-00224681.
XX
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.
XX PR 21-DEC-1993; 93US-00172329.
XX PR 24-MAY-1995; 95US-00449653.
XX PR 12-JAN-1998; 98US-00005893.
XX
XX (AMGE-) AMGEN INC.
XX
```

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-366062/38.
 XX
 XX Enhancing efficiency of transfer of polynucleotide into a target
 PT mammalian cell in vitro, involves exposing cell that expresses a stem
 PT cell factor receptor to stem cell factor, and introducing polynucleotide
 PT into cell in vitro.
 XX
 XX Example 3; Fig 12C; 210pp; English.
 XX
 CC The present invention describes a method for enhancing (E) the efficiency
 CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
 CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
 CC receptor to a biologically active SCF, its analogue or fragment, which
 CC induces cell proliferation, and introducing (I) to (II) in vitro.
 CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
 CC The method is useful for enhancing the efficiency of the transfer of a
 CC polynucleotide into a target mammalian cell in vitro. The method is
 CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
 CC AAB98390 represent sequences used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAA AAAAAAAAAA 1753
 Db 19 CAAAAA AAAAAAAAAA 1

RESULT 393
 AAS04111/C
 ID AAS04111 standard; DNA; 20 BP.
 XX
 AC AAS04111;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
 XX
 KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN US6207417-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 07-JUN-1995; 95US-00482918.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 21-DEC-1993; 93US-00172329.
 XX
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-298941/31.
 DR
 XX Novel nucleic acids encoding stem cell factor useful for treating

PT disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
 PT disease, Kala azar, anemia and septicemia.
 XX
 PS Example 3; Fig 12C; 209pp; English.
 XX
 CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal
 CC oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
 CC polynucleotides encoding them. SCF stimulate primitive progenitor cells
 CC including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
 CC (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAA AAAAAAAAAA 1753
 Db 19 CAAAAA AAAAAAAAAA 1

RESULT 394
 AAF89091/C
 ID AAF89091 standard; DNA; 20 BP.
 XX
 AC AAF89091;
 XX
 DT 13-JUL-2001 (first entry)
 XX
 DE Mammalian stem cell factor PCR primer SEQ ID NO: 32.
 XX
 KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
 KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
 KW neurological damage; intestinal damage; infertility; AIDS; SCID;
 KW severe combined immunodeficiency; PCR primer; ss.
 XX
 OS Mammalia.
 XX
 PN US6207802-B1.
 XX
 PD 27-MAR-2001.
 XX
 PF 09-NOV-1994; 94US-00336728.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 25-NOV-1992; 92US-00982255.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 PI WPI; 2001-353108/37.
 DR
 XX Novel isolated non-human mammalian stem cell factor polypeptide
 PT stimulating growth of early hematopoietic progenitor cells, useful for
 PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
 PT sarcoidosis.
 XX

PS Example 3; Fig 12C; 209pp; English.

CC The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early haematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention

XX Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753

Db 19 CAAAAAAAAAAAAAAAAA 1

RESULT 395

AAS05714

ID AAS05714 standard; DNA; 20 BP.

XX AAS05714;

XX AAS05714;

DT 07-SEP-2001 (first entry)

DE Aminopurine substituted region of an RP-TFO.

XX reverse phase triplex forming oligonucleotide; RP-TFO;

KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;

KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.

XX Synthetic.

OS Synthetic.

FH Key Location/Qualifiers

FT modified_base

FT /*tag= a

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= b

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= c

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT Modified_base

FT /*tag= d

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= f

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= g

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= g

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= h

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= h

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= i

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= j

FT /label= OTHER

FT /note= "Other= Hypoxanthine or Inosine"

FT modified_base

FT /*tag= k

FT /label= OTHER

FT /note= "A is aminopurine substituted"

FT modified_base

FT /*tag= l

FT /label= OTHER

FT /note= "A is aminopurine substituted"

PN WO200132929-A1.

XX 10-MAY-2001.

PD 03-NOV-2000; 2000WO-US030534.

XX 03-NOV-1999; 99US-0163356P.

PR 03-NOV-1999; 99US-0163416P.

PR 21-DEC-1999; 99US-0171348P.

PR 07-JUL-2000; 2000US-0216579P.

XX (CYGE-) CYGENE INC.

PA (OSTE/) OSTE C C.

XX Oste CC, Ramborg ER;

PI WPI; 2001-343488/36.

XX Analyzing target nucleic acid sequences, useful for population genetics,

PT drug development and diagnosing cancer, comprises hybridizing triple

PT forming oligonucleotide and probe to target sequence.

XX Example 2; Page 66; 141pp; English.

XX The sequence is a second reverse phase triplex forming oligonucleotide,

CC RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the

CC method of the invention. The invention relates to analysing target

CC nucleic acid sequences comprising restricting isolated DNA, hybridising

CC at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',

CC exonuclease to form a protected nucleic acid sequence (PNAS) tail

CC structure, hybridising the captured structure with a single nucleotide

CC polymorphisms (SNP) identification probe and determining the SNP score.

CC The methods can be used for analysing target nucleic acid sequences,

CC especially genomic DNA sequences, to determine if they contain SNPs or

CC short tandem repeats (STRs). The methods can be used to detect SNPs for

CC use in population genetics, drug development, forensics, cancer, genetic

CC disease research, genomic analysis, diagnostics and therapeutics in

CC humans, plants and animals

XX Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

SQ Query Match 1.1%; Score 19; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 2.1e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755

Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 396

AAS05715/c

ID AAS05715 standard; DNA; 20 BP.

XX AAS05715;

AC AAS05715;

XX 07-SEP-2001 (first entry)

```
XX DE 8-aminopurine substituted region of an RP-TFO.
XX KW reverse phase triplex forming oligonucleotide; RP-TFO;
XX KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
XX KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 17
XX FT /*tag= a
XX FT /label= OTHER
XX FT /note= "Other= Hypoxanthine or Inosine"
XX PN WO200132929-A1.
XX PD 10-MAY-2001.
XX PF 03-NOV-2000; 2000WO-US030534.
XX PR 03-NOV-1999; 99US-0163356P.
XX PR 03-NOV-1999; 99US-0163416P.
XX PR 21-DEC-1999; 99US-0171348P.
XX PR 07-JUL-2000; 2000US-0216579P.
XX FA (CYGE-) CYGENE INC.
XX PA (OSTE/) OSTE C C.
XX PI Oste CC, Ramberg ER;
XX DR WPI; 2001-343488/36.
XX PS Analyzing target nucleic acid sequences, useful for population genetics,
XX PT drug development and diagnosing cancer, comprises hybridizing triple
XX PT forming oligonucleotide and probe to target sequence.
XX Example 2; Page 66; 141pp; English.
XX The sequence is a second reverse phase triplex forming oligonucleotide,
XX RP-TFO (3' to the SNP) used to analyse Factor V Leiden SNP using the
XX method of the invention. The invention relates to analysing target
XX nucleic acid sequences comprising restricting isolated DNA, hybridising
XX at least one triplex forming oligonucleotide (TFO), adding a 3' to 5',
XX exonuclease to form a protected nucleic acid sequence (PNAS) tail
XX structure, hybridising the captured structure with a single nucleotide
XX polymorphisms (SNP) identification probe and determining the SNP score.
XX The methods can be used for analysing target nucleic acid sequences,
XX especially genomic DNA sequences, to determine if they contain SNPs or
XX short tandem repeats (STRs). The methods can be used to detect SNPs for
XX use in population genetics, drug development, forensics, cancer, genetic
XX disease research, genomic analysis, diagnostics and therapeutics in
XX humans, plants and animals
XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 19 T; 0 U; 1 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAA 1
RESULT 397
AAH23889/c
ID AAH23889 standard; DNA; 20 BP.
XX AC AAH23889;
XX DT 07-AUG-2001 (first entry)
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX FH US6204363-B1.
XX FT 20-MAR-2001.
XX PF 25-NOV-1992; 92US-00982255.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 10-APR-1991; 91US-00684535.
XX FA (AMGE-) AMGEN INC.
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX DR WPI; 2001-256683/26.
XX PS New stem cell factor polypeptides and their analogs which stimulate
XX PT growth of early hematopoietic progenitors useful for treating aplastic
XX PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's
XX PT disease.
XX Example 3; Fig 12C; 166pp; English.
XX The present sequence for universal PCR primer 220-3 is 1 of 8 universal
XX oligonucleotides (AAH23888-AAH23895) used in the isolation of the human
XX SCF (stem cell factor) cDNA sequence. The present invention relates to
XX novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the
XX polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX including early haematopoietic progenitor cells. The invention also
XX describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides
XX (AAH23893-AAH23897) used in the isolation of human and rat SCF sequences.
XX The polynucleotide encoding SCF is useful for producing SCF and useful in
XX gene therapy. It is useful for treating disorders involving blood cells
XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
XX B12 and folic acid deficiency, pyridoxine deficiency, and
XX hypopigmentation disorders such as piebaldism and vitiligo
XX SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CAAAAAAAAAAAAAAAAA 1
RESULT 398
AAS04212/c
ID AAS04212 standard; DNA; 20 BP.
XX AC AAS04212;
XX DT 29-AUG-2001 (first entry)
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-3.
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
```

KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.
 XX Homo sapiens.
 XX
 PN US6218148-B1.
 XX
 PD 17-APR-2001.
 XX
 PF 21-DEC-1993; 93US-00172329.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 25-NOV-1992; 92US-00982255.
 XX
 XX (AMGE-) AMGEN INC.
 PA
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-281051/29.
 DR
 XX
 XX Isolated DNA sequence, encoding polypeptide product useful for
 PT stimulating growth of early hematopoietic progenitor cells.
 PT
 XX
 PS Example 3; Fig 12C; 167pp; English.
 XX
 CC The present sequence for universal PCR primer 220-3 is 1 of 8 universal
 CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early hematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1735 CAAAAAAAAAAAAAAAAA 1753
 DB 19 CAAAAAAAAAAAAAAAAA 1
 RESULT 399
 AAS10447/c
 ID AAS10447 standard; DNA; 20 BP.
 XX
 XX AAS10447;
 AC
 DT 24-OCT-2001 (first entry)
 XX
 DE Human stem cell factor (SCF) cDNA universal PCR primer 220-3.
 XX
 KW Human; stem cell factor; SCF; hematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX

PN US6248319-B1.
 XX
 PD 19-JUN-2001.
 XX
 PF 24-MAY-1995; 95US-00449653.
 XX
 PR 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00884535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 XX
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 XX WPI; 2001-407312/43.
 DR
 XX
 XX Increasing the number of early hematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell factor.
 XX
 PS Example 3; Fig 12C; 210pp; English.
 XX
 CC The present sequence for universal PCR primer 220-3 is 1 of 19 PCR
 CC primers (AAS10435-AAS10453) used to amplify various portions of the human
 CC SCF cDNA sequence. The sequence is described in an invention relating to
 CC novel stem cell factors, the polynucleotides encoding them and methods
 CC for producing the stem cell factors. The methods involve increasing the
 CC number of early hematopoietic progenitor cells in human peripheral blood
 CC by administering a hematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood disorders,
 CC including myelofibrosis, myelocytosis, osteopetrosis, metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1735 CAAAAAAAAAAAAAAAAA 1753
 DB 19 CAAAAAAAAAAAAAAAAA 1
 RESULT 400
 AAD35464/c
 ID AAD35464 standard; DNA; 20 BP.
 XX
 XX AAD35464;
 AC
 DT 25-JUL-2002 (first entry)
 XX
 DE Rat SCF 5' cDNA amplifying PCR primer, 220-3.
 XX
 KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
 KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
 KW infertility; neoplasia; myelofibrosis; myelocytosis; osteopetrosis;
 KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
 KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
 KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
 KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
 KW disseminated fungus disease; Fulminating septicemia; piebaldism; AIDS;
 KW acquired immune deficiency syndrome; malaria; military tuberculosis;

KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
 KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
 KW primer; ss.
 XX
 OS Rattus sp.
 XX
 XX US2002018763-A1.
 PN
 XX PD 14-FEB-2002.
 XX
 PF 12-JAN-1998; 98US-00005243.
 XX
 XX 24-MAY-1995; 95US-00449653.
 XX
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSLMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
 FI WPI; 2002-350789/38.
 DR
 XX Novel non-naturally-occurring stem cell factor polypeptide, useful for
 PT treating leucopenia, thrombocytopenia, anemia and for enhancing
 PT engraftment of bone marrow during transplantation in a mammal.
 XX
 XX Example 3; Fig 12C; 217pp; English.
 PS
 XX The present invention relates to novel non-naturally-occurring stem cell
 CC factor (SCF) polypeptides having an amino acid sequence sufficiently
 CC duplicative of that of naturally-occurring SCF to allow possession of
 CC haematopoietic biological activity of naturally occurring SCF. Sequences
 CC of the invention are useful for treating leucopenia, thrombocytopenia,
 CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
 CC engraftment of bone marrow during transplantation in mammals and chemical
 CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
 CC are also useful for treating acquired immune deficiency in a human, nerve
 CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
 CC damage in a mammal. SCF sequences are useful for preparing biologically
 CC active polymer polypeptide adduct, for enhancing transfection of early
 CC haematopoietic progenitor cells with a gene, and transfer of a gene into
 CC a mammal. They are useful for treating myelofibrosis, myeloclerosis,
 CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, Fulminating septicemia, pyridoxine deficiency, vitamin B12
 CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is a PCR primer which is used for
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
 CC exemplification of the invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
 Db 19 CAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 401
 ABS73848/C
 ID ABS73848 standard; DNA; 20 BP.
 XX
 AC ABS73848;
 XX
 DT 05-DEC-2002 (first entry)

XX SCF universal oligonucleotide 220-3.
 DE Stem cell factor; SCF; blood-forming system; blood cell disorder;
 XX haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculosis; cytostatic;
 KW antianaemic; antifungal; antimalarial; dermatological; ss.
 XX
 OS Synthetic.
 XX
 XX EP1241258-A2.
 PN
 XX 18-SEP-2002.
 PD
 XX 04-OCT-1990; 2002EP-00008587.
 PF
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 28-SEP-1990; 90WO-US005548.
 PR 01-OCT-1990; 90US-00589701.
 PR 04-OCT-1990; 90EP-00310899.
 PR 04-OCT-1990; 95EP-00105391.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;
 FI WPI; 2002-684093/74.
 DR
 XX Production of a human stem cell factor (SCF) polypeptide for treating
 PT disorders involving blood cells, such as leukemia, comprises culturing
 PT mammalian cells comprising non-human SCF promoter DNA linked to DNA
 PT encoding the human SCF.
 XX
 XX Example 3; Fig 12C; 120pp; English.
 PS
 XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic) system in
 CC mammals, particularly humans. The method of the invention is useful for
 CC the production of human SCF. The stem cell factors are useful to treat
 CC disorders involving blood cells e.g. metastatic carcinoma, acute
 CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
 CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus
 CC disease, malaria, and vitiligo. The present sequence representing a
 CC universal oligonucleotide for SCF DNA is used in the examples of the
 CC present invention
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
 Db 19 CAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 402
 ABZ88880
 ID ABZ88880 standard; DNA; 20 BP.
 XX
 AC ABZ88880;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4122; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 2 AAAAAAAAAAAAAAAAAA 20

RESULT 403
ABZ89179
ID ABZ89179 standard; DNA; 20 BP.
XX
AC ABZ89179;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4421; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 2 AAAAAAAAAAAAAAAAAA 20

RESULT 404
ABZ99050/c
ID ABZ99050 standard; DNA; 20 BP.
XX
AC ABZ99050;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human PDE4C oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 14299; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1754
|||||
Db 19 AAAAAAAAAAAAAAAAAA 1

RESULT 405
ABZ89678
ID ABZ89678 standard; DNA; 20 BP.
XX
AC ABZ89678;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4920; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 1.1%; Score 19; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
|||||
Db 1 AAAAAAAAAAAAAAAAAA 20

RESULT 406
ABZ87681/C
ID ABZ87681 standard; DNA; 20 BP.
XX
AC ABZ87681;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 2923; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1754
 DB 19 AAAAAAAAAAAAAAAAAA 1
 RESULT 407
 ABZ89677
 ID ABZ89677 standard; DNA; 20 BP.
 XX
 AC ABZ89677;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4919; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 19 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1755
 DB 1 AAAAAAAAAAAAAAAAAA 20
 RESULT 408
 ADE52460/C
 ID ADE52460 standard; DNA; 20 BP.
 XX
 AC ADE52460;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Stem cell factor (SCF) related DNA #31.
 XX
 KW Stem cell factor; SCF; haematopoietic activity; infertility;

KW intestinal damage; myeloproliferative disorder; leucopenia;
 KW thrombocytopenia; anaemia; bone marrow transplant; immune deficiency;
 KW neoplasia; nerve damage; osteoporosis; metastatic carcinoma; leukaemia;
 KW military tuberculosis; haematopoietic progenitor cell; ss.
 XX
 OS Synthetic.
 XX
 PN US2002031491-A1.
 XX
 PD 14-MAR-2002.
 XX
 XX
 PF 31-DEC-1998; 98US-00224683.
 XX
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 PR 24-MAY-1995; 95US-00449653.
 PR 12-JAN-1998; 98US-00005893.
 XX
 PA (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.
 XX
 PI Zsebo KM, Bosseelman RA, Suggs SV, Martin FH;
 XX
 DR WPI; 2003-851459/79.
 XX
 XX New non-natural stem cell factor, useful for treating e.g. leucopenia or
 PT immune deficiency, also related nucleic acid and antibodies.
 PT
 XX Disclosure; SEQ ID NO 32; 217pp; English.
 PS
 XX The invention relates to stem cell factor (SCF) polypeptides with
 CC haematopoietic activity and the polynucleotides encoding them. The
 CC polypeptides are used for treating infertility, intestinal damage,
 CC myeloproliferative disorders, leucopenia, thrombocytopenia or anaemia.
 CC for improving engraftment of bone marrow transplants, for enhancing bone
 CC marrow recovery after radiotherapy or chemotherapy and in treatment of
 CC immune deficiency, neoplasia, nerve damage, osteoporosis, metastatic
 CC carcinoma, leukaemia and military tuberculosis. The SCF polypeptides are
 CC also used to expand haematopoietic progenitor cells for transplantation
 CC and to prepare such cells for transfection with a gene. The SCF
 CC polynucleotides can be used for recombinant expression of the
 CC polypeptides and also as probes for mapping of the SCF gene, for
 CC identifying SCF-related diseases and as a marker for neighbouring genes.
 CC Antibodies raised against the polypeptides are useful in diagnosis and to
 CC remove SCF from blood. This sequence represents SCF related DNA of the
 CC invention.
 XX
 SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.1e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA...AAAAA 1753
 DB 19 CAAAAA...AAAAA 1
 RESULT 409
 AAQ75651/c
 ID AAQ75651 standard; DNA; 21 BP.
 XX
 AC AAQ75651;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 XX 16-APR-1993; 93JP-00112515.
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 AC...AAAAA 1752
 DB 19 AC...AAAAA 1
 RESULT 410
 AAQ75639/c
 ID AAQ75639 standard; DNA; 21 BP.
 XX
 AC AAQ75639;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 XX 16-APR-1993; 93JP-00112515.
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT

DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 XX 16-APR-1993; 93JP-00112515.
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT
 XX Disclosure; Page 6; 11pp; Japanese.
 PS
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 AC...AAAAA 1752
 DB 19 AC...AAAAA 1
 RESULT 410
 AAQ75639/c
 ID AAQ75639 standard; DNA; 21 BP.
 XX
 AC AAQ75639;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 XX Reverse transcription primer used in cDNA analysis technique.
 DE
 XX Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 OS
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 XX 16-APR-1993; 93JP-00112515.
 PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 PT

```
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAAAAAA 1752
DB 19 ACAAAAAAAAAAAAAAAAAA 1
RESULT 411
AAQ75650/c
ID AAQ75650 standard; DNA; 21 BP.
XX AC AAQ75650;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAAAAAA 1752
DB 19 ACAAAAAAAAAAAAAAAAAA 1
RESULT 413
AAQ75649/c
ID AAQ75649 standard; DNA; 21 BP.
XX AC AAQ75649;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAAAAAA 1752
DB 19 ACAAAAAAAAAAAAAAAAAA 1
```

PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 1 G; 20 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ACAAAAAAAAAAAAAAAAAA 1
RESULT 414
AAQ75653/c
ID AAQ75653 standard; DNA; 21 BP.
XX
AC AAQ75653;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PD
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

XX SQ Sequence 21 BP; 0 A; 1 C; 1 G; 19 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ACAAAAAAAAAAAAAAAAAA 1
RESULT 415
AAQ75654/c
ID AAQ75654 standard; DNA; 21 BP.
XX
AC AAQ75654;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
PN
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.1%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ACAAAAAAAAAAAAAAAAAA 1
RESULT 416
ABA93238
ID ABA93238 standard; DNA; 22 BP.
XX
AC ABA93238;
XX
XX 18-APR-2002 (first entry)
DT PolyA adaptor oligonucleotide SEQ ID NO:1.
XX
DE

XX KW Detection; comparative detection; adaptor; ss.
 XX OS Synthetic.
 XX PN JP2001333800-A.
 XX PD 04-DEC-2001.
 XX PF 30-MAY-2000; 2000JP-00160324.
 XX PR 30-MAY-2000; 2000JP-00160324.
 XX PA (UNIT-) UNITECH CO LTD.
 XX DR WPI; 2002-135950/18.
 XX PT Comparative detection of the amounts of RNA and DNA.
 XX PS Disclosure; Page 9; 9pp; Japanese.
 XX CC The present invention describes a method for the comparative detection of the amount of an RNA. The method comprises: (a) cDNAs obtained by transcribing respectively from at least two tissue RNAs are respectively fragmented by using a same restriction enzyme; (b) each different adaptor and a common adaptor are added to each of the cDNA fragments derived from the same or different tissues by the step (a); (c) the resultant adaptor-added cDNAs are mixed together; (d) an adaptor primer having the common sequence to said different adaptor and a gene-specific adaptor are used to amplify said adaptor-added cDNAs containing no region derived from polyadenylic acid of the mRNA before the addition of the adaptor among the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the cDNA amounts are measured between the tissues; (f) the RNA is detected from the measured result; (g) each different adaptor and a common adaptor are added to each of the genomic DNA fragments derived from a same or different individuals; (h) the resultant adaptor-added genomic DNAs are mixed together; (i) the adaptor-added genomic DNAs are amplified by using an adaptor primer having the common sequence to the different adaptor and a sequence-specific adaptor; and (j) the ratios of the amplified amounts of the genomic DNAs are measured between the individuals. The method is used for the detection of the amounts of RNA and DNA. The present sequence represents an oligonucleotide which is used in the exemplification of the present invention

XX SQ Sequence 22 BP; 19 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CAAAAA AAAAAAAAAA 1753
 DB 4 CAAAAA AAAAAAAAAA 22
 |||||

RESULT 417
 AAQ75028
 ID AAQ75028 standard; DNA; 23 BP.
 XX AC AAQ75028;
 XX DT 25-MAR-2003 (revised)
 DT 03-AUG-1995 (first entry)
 XX DE LCR oligo 2.
 XX KW Synthetic oligo; solid phase immunoassay; ss.
 XX OS Synthetic.
 XX PN WO9426932-A1.
 XX PD 24-NOV-1994.

XX PF 13-MAY-1994; 94WO-US005407.
 XX PR 13-MAY-1993; 93US-00061694.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fields HA, Khudyakov YE;
 XX DR WPI; 1995-006819/01.
 XX PT Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection.
 XX PS Example; Page 13; 34pp; English.
 XX CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides. They are used in a method for detecting an antigen in a subject. The method involves binding the antigen to a solid support and then reacting it with an immunoreactive ligand (L) bound to an oligo; removing any unreacted L, and then detecting the presence of the oligo. A similar method can be used to detect Abs, in which case the ligand is an oligo-labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab to be detected at very low levels. An exemplary oligo is AAQ75024 which can be covalently attached by the 5'- terminus to the N- or C-terminal of a synthetic peptide. For LCR using oligo AAQ75024, oligos 1-4 (see AAQ75027-Q75030) can be used. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 23 BP; 19 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 1.1%; Score 19; DB 1; Length 23;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CAAAAA AAAAAAAAAA 1753
 DB 5 CAAAAA AAAAAAAAAA 23
 |||||

RESULT 418
 AAQ75029/c
 ID AAQ75029 standard; RNA; 23 BP.
 XX AC AAQ75029;
 XX DT 25-MAR-2003 (revised)
 DT 03-AUG-1995 (first entry)
 XX DE LCR oligo 3.
 XX KW Synthetic oligo; solid phase immunoassay; ss.
 XX OS Synthetic.
 XX PN WO9426932-A1.
 XX PD 24-NOV-1994.
 XX PF 13-MAY-1994; 94WO-US005407.
 XX PR 13-MAY-1993; 93US-00061694.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Fields HA, Khudyakov YE;
 XX DR WPI; 1995-006819/01.
 XX PT Solid phase immunoassay using oligo:nucleotide as label - also new conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for diagnosing hepatitis C or E virus infection.


```

XX PS Example; Page 13; 34pp; English.
XX CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
XX CC They are used in a method for detecting an antigen in a subject. The
XX CC method involves binding the antigen to a solid support and then reacting
XX CC it with an immunoreactive ligand (L) bound to an oligo; removing any
XX CC unreacted L, and then detecting the presence of the oligo. A similar
XX CC method can be used to detect Abs, in which case the ligand is an oligo-
XX CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab
XX CC to be detected at very low levels. An exemplary oligo is AAQ75024 which
XX CC can be covalently attached by the 5'-terminus to the N- or C-terminal of
XX CC a synthetic peptide. For LCR using oligo AAZ75024, oligos 1-4 (see
XX CC field.)
XX SQ Sequence 23 BP; 0 A; 0 C; 4 G; 1 T; 18 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 23;
XX Best Local Similarity 100.0%; Pred. No. 2.4e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
XX Db 19 CAAAAAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 419
XX AAH43079/C
XX ID AAH43079 standard; DNA; 24 BP.
XX AC AAH43079;
XX DT 15-OCT-2001 (first entry)
XX DE Nucleotide sequence of a synthetic oligonucleotide.
XX KW Nucleic acid immobilisation; ss.
XX OS Synthetic.
XX PN WO200155365-A1.
XX PD 02-AUG-2001.
XX PF 24-JAN-2001; 2001WO-JP000443.
XX PR 27-JAN-2000; 2000JP-00019301.
XX PA (TOJO) TOYO KOHAN CO LTD.
XX PI Tanga M, Okamura H, Takagi K, Takahashi K;
XX DR WPI; 2001-488794/53.
XX PT Support for immobilizing nucleotides.
XX PS Example 1; Page 8; 18pp; Japanese.
XX CC The specification describes a support for immobilizing nucleotides which
XX CC contributes to the efficient clarification of DNA without damaging the
XX CC terminal parts of the DNA. The support is a chemically treated modified
XX CC substrate on which oligonucleotides with restriction enzyme cleavage
XX CC sites are immobilised. The support is useful for immobilizing nucleic
XX CC acids such as DNA. The present sequence represents a synthetic
XX CC oligonucleotide used in the course of the invention
XX SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
XX Db 24 CAAAAAAAAAAAAAAAAAAAAA 6
XX
XX RESULT 420
XX ABQ79878/C
XX ID ABQ79878 standard; DNA; 24 BP.
XX AC ABQ79878;
XX DT 23-DEC-2002 (first entry)
XX DE Nucleotide sequence of a PCR primer #8.
XX KW Polymerase chain reaction; thermal cycle; immobilisation;
XX genetic engineering; PCR; primer; ss.
XX OS Synthetic.
XX PN JP2002191369-A.
XX PD 09-JUL-2002.
XX PF 27-DEC-2000; 2000JP-00399573.
XX PR 27-DEC-2000; 2000JP-00399573.
XX PA (TOJO) TOYO KOHAN CO LTD.
XX PA (TAKA) TAKAHASHI K.
XX DR WPI; 2002-630904/68.
XX KW Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
XX PT a substrate on which a DNA is immobilized used in medical, biochemical,
XX PT molecular biological and gene engineering fields.
XX PS Example; Page 10; 13pp; Japanese.
XX CC The invention relates to performing a thermal cycle of PCR by using a
XX CC substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
XX CC method is useful in the medical, biochemical, molecular biological and
XX CC genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
XX CC used in the method of the invention
XX SQ Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.1%; Score 19; DB 1; Length 24;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
XX Db 24 CAAAAAAAAAAAAAAAAAAAAA 6
XX
XX RESULT 421
XX ADC75073/C
XX ID ADC75073 standard; DNA; 24 BP.
XX AC ADC75073;
XX DT 01-JAN-2004 (first entry)
XX DE Biosensor related oligonucleotide of the invention SEQ ID NO:1.
XX KW ss; biosensor; hybridisation.
XX OS Synthetic.
XX PN JP2003172737-A.
XX PD 20-JUN-2003.

```

XX PF 07-DEC-2001; 2001JP-00374764.
XX PR 07-DEC-2001; 2001JP-00374764.
XX PA (TOJO) TOYO KOHAN CO LTD.
XX DR WPI; 2003-819164/77.
XX PT Solid support body comprising crystal resonator on which a surface
PT treatment layer is formed, and a substrate whose surface treatment layer
PT is chemically modified, useful as biosensor.
XX PS Disclosure; SEQ ID NO 1; 7pp; Japanese.
XX CC The invention relates to a novel solid support body comprising a crystal
CC resonator on which a surface treatment layer is formed. The biosensor is
CC useful for analysing biological samples e.g., gene, a protein, and a
CC peptide, and for analysing bioactive substances. Preferably, the
CC biosensor is useful for analysing base sequences by carrying out
CC hybridisation. The present sequence is used in the exemplification of the
CC invention.
XX Sequence 24 BP; 3 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 19; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1735 CAAAAA...AAAAA 1753
DB 24 CAAAAA...AAAAA 6
RESULT 422
AA162055
ID AA162055 standard; DNA; 25 BP.
XX AC AA162055;
XX DT 16-OCT-2001 (first entry)
XX DE Soybean 318013 region A3 DNA reverse primer; SEQ ID NO: 686.
XX KW Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;
KW SCN resistance; rhg1; Rhg4; SCN resistant allele; plant breeding;
KW 240017 region G3; 318013 region A3; 515002 region G2; PCR primer; ss.
XX OS Glycine max.
XX PN WO200151627-A2.
XX PD 19-JUL-2001.
XX PF 05-JAN-2001; 2001WO-US000552.
XX PR 07-JAN-2000; 2000US-0174880P.
XX PA (MONS) MONSANTO CO.
XX PI Hauge BM, Wang ML, Parsons JD, Parnell LD;
XX WPI; 2001-425872/45.
XX PT New purified nucleic acid for producing a soybean plant having soybean
PT cyst nematode resistance and for use in plant breeding programs.
XX PS Claim 25; Page 1196; 1353pp; English.
XX CC The invention relates to nucleic acid molecules from regions of the
CC soybean genome which are associated with soybean cyst nematode (SCN)
CC resistance. The nucleic acids are used to transform plants, and can
CC produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.

CC The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC of soybean plants and for introgressing SCN resistance or partial SCN
CC resistance into soybean plants. They can also be used in plant breeding
CC programmes. The invention also relates to proteins encoded by such
CC nucleic acid molecules, as well as antibodies capable of recognising
CC these proteins. The present sequence is a primer used to amplify a region
CC of the soybean genome
XX Sequence 25 BP; 12 A; 1 C; 12 G; 0 T; 0 U; 0 Other;
SQ Query Match 1.1%; Score 19; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 860 CAGGAAGAGGAGGAGG 878
DB 1 CAGGAAGAGGAGGAGG 19
RESULT 423
ABQ73254/c
ID ABQ73254 standard; DNA; 24 BP.
XX AC ABQ73254;
XX DT 30-SEP-2002 (first entry)
XX DE Human macro protein 17.49 PCR primer 1 SEQ ID NO:3.
XX KW Human; macro protein 17.40; nerve system disorder disease;
KW protein metabolic disorder relative disease; PCR primer; ss.
XX OS Homo sapiens.
XX PN CN1339462-A.
XX PD 13-MAR-2002.
XX PF 21-AUG-2000; 2000CN-00119647.
XX PR 21-AUG-2000; 2000CN-00119647.
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX PI Mao Y, Xie Y;
XX WPI; 2002-455361/49.
XX PT New polypeptide-human macro protein 17.49 and polynucleotide for encoding
XX such polypeptide.
XX PS Example 2; Page 18; 32pp; Chinese.
XX CC The present invention describes human macro protein 17.49 (I). Also
CC described is a process for producing (I) using DNA recombination
CC technology. (I) and the polynucleotide encoding it can be used for
CC treating various diseases, such as nerve system disorder disease and
CC protein metabolic disorder relative disease. The present sequence
CC represents a PCR primer for (I), which is used in an example from the
CC present invention
XX Sequence 24 BP; 2 A; 0 C; 4 G; 17 T; 0 U; 1 Other;
SQ Query Match 1.1%; Score 18.8; DB 1; Length 24;
Best Local Similarity 87.0%; Pred. No. 2.6e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX 1731 TTTCACAAAAA...AAAAA 1753
DB 24 TCTCCAAAAA...AAAAA 2
RESULT 424

AAC96256/c
 ID AAC96256 standard; DNA; 25 BP.
 XX
 AC AAC96256;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE HLA DPA1 gene PCR primer #13.
 XX
 KW DNA sequence analysis; sequencing; protein structure;
 KW gene typing; organ donation; bacteria identification; 16s rRNA; HLA;
 KW human leukocyte antigen; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO200065088-A2.
 XX
 PD 02-NOV-2000.
 XX
 PF 20-APR-2000; 2000WO-EP003636.
 XX
 PR 26-APR-1999; 99EP-00303215.
 XX
 PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 XX
 FI Ulfendahl P, Wong K;
 XX
 DR WPI; 2000-679677/66.
 XX
 PT Identifying extendible primers for use in identification, or
 PT classifying of a nucleic acid of an organism, allele or gene such as
 PT class 1/2 HLA comprises identifying all possible nucleotide sequences of
 PT specific length.
 XX
 PS Claim 14; Page 48; 66pp; English.
 XX
 CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC receiver, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16s rRNA genes in
 CC particular
 XX
 SQ Sequence 25 BP; 3 A; 2 C; 3 G; 17 T; 0 U; 0 Other;
 Query Match 1.1%; Score 18.8; DB 1; Length 25;
 Best Local Similarity 90.9%; Pred. No. 2.7e+02;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1731 TTTACAAAAA 1752
 Db 22 TGTACACAAAAA 1
 RESULT 425
 AAC975584/c
 ID AAC975584 standard; DNA; 20 BP.
 XX
 AC AAC975584;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 Qy 1731 TTTACAAAAA 1752
 Db 22 TGTACACAAAAA 1
 RESULT 426
 AAC975585/c
 ID AAC975585 standard; DNA; 20 BP.
 XX
 AC AAC975585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 Qy 1731 TTTACAAAAA 1752
 Db 22 TGTACACAAAAA 1
 RESULT 425
 AAC975584/c
 ID AAC975584 standard; DNA; 20 BP.
 XX
 AC AAC975584;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1733 TACAAAAA 1752
 Db 20 TATAAAAA 1
 RESULT 426
 AAC975585/c
 ID AAC975585 standard; DNA; 20 BP.
 XX
 AC AAC975585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 Qy 1733 TACAAAAA 1752
 Db 20 TATAAAAA 1
 RESULT 426
 AAC975585/c
 ID AAC975585 standard; DNA; 20 BP.
 XX
 AC AAC975585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 Qy 1733 TACAAAAA 1752
 Db 20 TATAAAAA 1
 RESULT 426
 AAC975585/c
 ID AAC975585 standard; DNA; 20 BP.
 XX
 AC AAC975585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 Qy 1733 TACAAAAA 1752
 Db 20 TATAAAAA 1
 RESULT 426
 AAC975585/c
 ID AAC975585 standard; DNA; 20 BP.
 XX
 AC AAC975585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 Qy 1733 TACAAAAA 1752
 Db 20 TATAAAAA 1
 RESULT 426
 AAC975585/c
 ID AAC975585 standard; DNA; 20 BP.
 XX
 AC AAC975585;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 FN JP06303997-A.
 XX
 PD 01-NOV-1994.

CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
 |||
 Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 427
 AAQ75572/c
 ID AAQ75572 standard; DNA; 20 BP.

XX AC AAQ75572;

XX DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 and using the aggregate of mRNAs as the template for each reverse
 transcription primer; (b) digesting each of the prepared aggregates of
 the double-stranded cDNAs with restriction enzyme and; (c)
 electrophoresing the digested aggregate of cDNAs in separate lanes. The
 method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAAAAAA 1752
 |||
 Db 20 TCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 428
 AAQ75560/c
 ID AAQ75560 standard; DNA; 20 BP.

XX AC AAQ75560;

XX DT 04-AUG-1995 (first entry)

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 and using the aggregate of mRNAs as the template for each reverse
 transcription primer; (b) digesting each of the prepared aggregates of
 the double-stranded cDNAs with restriction enzyme and; (c)
 electrophoresing the digested aggregate of cDNAs in separate lanes. The
 method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAAAAAA 1752
 |||
 Db 20 TCAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 429

AAQ75577/c
 ID AAQ75577 standard; DNA; 20 BP.

XX AC AAQ75577;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 by digestion with restriction enzymes.

```
XX PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          1.0%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 2.5e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    Qy 1734 ACAAAAAAAAAAAAAAAAAA 1753
    Db 20 ACTAAAAAAAAAAAAAAAAA 1
    |||||||
    |||||||

RESULT 430
AAQ75593/c
ID AAQ75593 standard; DNA; 20 BP.
XX
AC AAQ75593;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          1.0%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 2.5e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    Qy 1734 ACAAAAAAAAAAAAAAAAAA 1753
    Db 20 ACGAAAAAAAAAAAAAAAAA 1
    |||||||
    |||||||

RESULT 431
AAQ75561/c
ID AAQ75561 standard; DNA; 20 BP.
XX
AC AAQ75561;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
    Query Match          1.0%; Score 18.4; DB 1; Length 20;
    Best Local Similarity 95.0%; Pred. No. 2.5e+02;
    Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    Qy 1734 ACAAAAAAAAAAAAAAAAAA 1753
    Db 20 ACCAAAAAAAAAAAAAAAAA 1
    |||||||
    |||||||

RESULT 432
AAQ75601/c
ID AAQ75601 standard; DNA; 20 BP.
XX
AC AAQ75601;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
```

```
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAA 1
RESULT 433
AAQ75564/c
ID AAQ75564 standard; DNA; 20 BP.
XX
AC AAQ75564;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAAAAAA 1755
DB 20 AAAAAAAAAAAAAAAAAA 1
RESULT 433
AAQ75564/c
ID AAQ75564 standard; DNA; 20 BP.
XX
AC AAQ75564;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1733 TACAAAAAAAAAAAAAAAAA 1752
DB 20 TAGAAAAAAAAAAAAAAAAA 1
RESULT 435
AAQ75583/c
ID AAQ75583 standard; DNA; 20 BP.
XX
AC AAQ75583;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
SQ Sequence 20 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1733 TACAAAAAAAAAAAAAAAAA 1752
DB 20 TAGAAAAAAAAAAAAAAAAA 1
RESULT 435
AAQ75583/c
ID AAQ75583 standard; DNA; 20 BP.
XX
AC AAQ75583;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
```



```

RESULT 438
AAT04916/c
ID AAT04916 standard; cDNA; 20 BP.
XX
XX
AC AAT04916;
XX
XX 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-7.
DE
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
XX Synthetic.
OS
XX EP676470-A1.
PN
XX 11-OCT-1995.
PD
XX 04-OCT-1990; 95EP-00105391.
PF
XX 16-OCT-1989; 89US-00422383.
PR
XX 11-JUN-1990; 90US-00537198.
PR
XX 24-AUG-1990; 90US-00573616.
PR
XX 28-SEP-1990; 90WO-US005548.
PR
XX 01-OCT-1990; 90US-00589701.
XX
XX (AMGE-) AMGEN INC.
PA
XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
PI
XX WPI; 1995-346090/45.
XX
XX New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving blood
PT cells.
XX
XX Example 3; Fig 12C; 127pp; English.
PS
XX AAT04915-T04922 are oligonucleotide primers and probes used for the
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC naturally occurring SCF and C-terminally truncated polypeptides, having
CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
CC stimulate growth of primitive progenitors such as haematopoietic
CC progenitor cells, neural stem cells and primordial germ stem cells. The
CC peptides can be used in a composition for treating leucopenia, anaemia or
CC thrombocytopenia, for enhancing engraftment of bone marrow during
CC transplantation or for bone marrow recovery after chemotherapy or
CC radiation-induced bone marrow aplasia or myelosuppression. They can also
CC be used for treating neoplasia, nerve damage, infertility, intestinal
CC damage or myeloproliferative disorders. Antibodies may be raised against
CC the peptides for use in detection or neutralisation of SCF in serum. SCF
CC may be useful for the treatment of AIDS and severe combined
CC immunodeficiency (SCID) states alone or in combination with other factors
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 439
AAT04918/c
ID AAT04918 standard; cDNA; 20 BP.
XX
XX
AC AAT04918;
XX
XX 25-MAR-2003 (revised)
DT 15-MAY-1996 (first entry)
XX
XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 220-11.
DE
XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;
KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;
KW transplant; neoplasia; myelosuppression; bone marrow; ss.
XX
XX Synthetic.
OS
XX EP676470-A1.
PN
XX 11-OCT-1995.
PD
XX 04-OCT-1990; 95EP-00105391.
PF
XX 16-OCT-1989; 89US-00422383.
PR
XX 11-JUN-1990; 90US-00537198.
PR
XX 24-AUG-1990; 90US-00573616.
PR
XX 28-SEP-1990; 90WO-US005548.
PR
XX 01-OCT-1990; 90US-00589701.
XX
XX (AMGE-) AMGEN INC.
PA
XX Zeebo KM, Suggs SV, Bosselman RA, Martin FH;
PI
XX WPI; 1995-346090/45.
XX
XX New stem cell factor polypeptide(s) - for stimulating the growth of
PT primitive progenitor cells, esp. for treating disorders involving blood
PT cells.
XX
XX Example 3; Fig 12C; 127pp; English.
PS
XX AAT04915-T04922 are oligonucleotide primers and probes used for the
CC amplification and sequencing of mammalian stem cell factor (SCF). Non-
CC naturally occurring SCF and C-terminally truncated polypeptides, having
CC amino acid sequences sufficiently duplicative of naturally occurring SCF,
CC stimulate growth of primitive progenitors such as haematopoietic
CC progenitor cells, neural stem cells and primordial germ stem cells. The
CC peptides can be used in a composition for treating leucopenia, anaemia or
CC thrombocytopenia, for enhancing engraftment of bone marrow during
CC transplantation or for bone marrow recovery after chemotherapy or
CC radiation-induced bone marrow aplasia or myelosuppression. They can also
CC be used for treating neoplasia, nerve damage, infertility, intestinal
CC damage or myeloproliferative disorders. Antibodies may be raised against
CC the peptides for use in detection or neutralisation of SCF in serum. SCF
CC may be useful for the treatment of AIDS and severe combined
CC immunodeficiency (SCID) states alone or in combination with other factors
CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 440
AAAL3753/c
ID AAAL3753 standard; DNA; 20 BP.
XX
XX AAAL3753;
XX
XX 27-JUL-2000 (first entry)
DT

```



```

XX DE Stem cell factor universal oligonucleotide 220-7.
XX DE
XX DE Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX DE primitive progenitor cell; haematopoietic disorder; syngeneic;
XX DE allogeneic; autologous bone marrow transplant; gene therapy;
XX DE transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX DE cancer; ss.
XX OS Synthetic.
XX OS EP992579-A1.
XX PN 12-APR-2000.
XX PD
XX PF 04-OCT-1990; 99EP-00122861.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90WO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 04-OCT-1990; 90EP-00310899.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX PI WPI; 2000-259135/23.
XX DR
XX PT Production of hematopoietic cells suitable for administration to a
XX PT subject using progenitor cells and expanding the cells using stem cell
XX PT factor.
XX PS Example 3; Fig 12C; 123pp; English.
XX PS
XX CC A method has been developed of making haematopoietic cells suitable for
XX CC administration to a subject. The method comprises: (a) obtaining
XX CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
XX CC by adding to the cells a haematopoietically effective dose of a
XX CC polypeptide product having at least part of the primary structural
XX CC confirmation and one or more of the biological properties of naturally
XX CC occurring stem cell factor (SCF). The method is useful for stimulating
XX CC primitive progenitor cells including early haematopoietic progenitor
XX CC cells which are capable of maturing to erythroid, megakaryocyte,
XX CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
XX CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
XX CC SCF is useful for treating haematopoietic disorders. The method is useful
XX CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
XX CC or autologous bone marrow transplant. SCF is useful for enhancing the
XX CC efficiency of gene therapy based on transfecting haematopoietic stem
XX CC cells. SCF is also useful for combating the myelosuppressive effects of
XX CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
XX CC after acute blood loss and as a boost to the immune system for fighting
XX CC neoplasia (cancer). The present sequence represents a universal
XX CC oligonucleotide which is used in an example from the present invention
XX CC
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX SQ
XX SQ Query Match 1.0%; Score 18.4; DB 1; Length 20;
XX SQ Best Local Similarity 95.0%; Pred. No. 2.5e+02;
XX SQ Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX SQ
Oy 1735 CAAAAA..... 1754
Db |..... 1
Db 20 CTA..... 1
RESULT 441
AAAI3754/c
ID AAA13754 standard; DNA; 20 BP.
XX AC
XX AC AAA13754;

```

```

XX DT 27-JUL-2000 (first entry)
XX DE Stem cell factor universal oligonucleotide 220-11.
XX DE
XX DE Stem cell factor; SCF; haematopoietic progenitor cell; blood forming;
XX DE primitive progenitor cell; haematopoietic disorder; syngeneic;
XX DE allogeneic; autologous bone marrow transplant; gene therapy;
XX DE transfection; haematopoietic stem cell; acute blood loss; neoplasia;
XX DE cancer; ss.
XX OS Synthetic.
XX OS EP992579-A1.
XX PN 12-APR-2000.
XX PD
XX PF 04-OCT-1990; 99EP-00122861.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 28-SEP-1990; 90WO-US005548.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 04-OCT-1990; 90EP-00310899.
XX PA (AMGE-) AMGEN INC.
XX PI Zsebo KM, Suggs SV, Bosselmann RA, Martin FH;
XX PI WPI; 2000-259135/23.
XX DR
XX PT Production of hematopoietic cells suitable for administration to a
XX PT subject using progenitor cells and expanding the cells using stem cell
XX PT factor.
XX PS Example 3; Fig 12C; 123pp; English.
XX PS
XX CC A method has been developed of making haematopoietic cells suitable for
XX CC administration to a subject. The method comprises: (a) obtaining
XX CC haematopoietic progenitor cells from a donor; and (b) expanding the cells
XX CC by adding to the cells a haematopoietically effective dose of a
XX CC polypeptide product having at least part of the primary structural
XX CC confirmation and one or more of the biological properties of naturally
XX CC occurring stem cell factor (SCF). The method is useful for stimulating
XX CC primitive progenitor cells including early haematopoietic progenitor
XX CC cells which are capable of maturing to erythroid, megakaryocyte,
XX CC granulocyte, lymphocyte and macrophage cells. SCF results in absolute
XX CC increases in haematopoietic cells of both myeloid and lymphoid lineages.
XX CC SCF is useful for treating haematopoietic disorders. The method is useful
XX CC for expanding early haematopoietic progenitors in syngeneic, allogeneic
XX CC or autologous bone marrow transplant. SCF is useful for enhancing the
XX CC efficiency of gene therapy based on transfecting haematopoietic stem
XX CC cells. SCF is also useful for combating the myelosuppressive effects of
XX CC anti-HIV drugs such as AZT and for enhancing haematopoietic recovery
XX CC after acute blood loss and as a boost to the immune system for fighting
XX CC neoplasia (cancer). The present sequence represents a universal
XX CC oligonucleotide which is used in an example from the present invention
XX CC
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX SQ
XX SQ Query Match 1.0%; Score 18.4; DB 1; Length 20;
XX SQ Best Local Similarity 95.0%; Pred. No. 2.5e+02;
XX SQ Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX SQ
Oy 1735 CAAAAA..... 1754
Db |..... 1
Db 20 CGAAAAA..... 1
RESULT 442
AAH41332/c
ID AAH41332 standard; DNA; 20 BP.

```

```

XX AAH41332;
XX
XX DT 21-AUG-2001 (first entry)
XX
XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:33.
XX
XX KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
XX KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX
XX OS Synthetic.
XX
XX PN US6207454-B1.
XX
XX PD 27-MAR-2001.
XX
XX PF 31-DEC-1998; 98US-00224681.
XX
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.
XX PR 21-DEC-1993; 93US-00172329.
XX PR 24-MAY-1995; 95US-00449653.
XX PR 12-JAN-1998; 98US-00005893.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX DR WPI; 2001-366062/38.
XX
XX PT Enhancing efficiency of transfer of polynucleotide into a target
XX PT mammalian cell in vitro, involves exposing cell that expresses a stem
XX PT cell factor receptor to stem cell factor, and introducing polynucleotide
XX PT into cell in vitro.
XX
XX PS Example 3; Fig 12C; 210pp; English.
XX
XX CC The present invention describes a method for enhancing (E) the efficiency
XX CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
XX CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
XX CC receptor to a biologically active SCF, its analogue or fragment, which
XX CC induces cell proliferation, and introducing (I) to (II) in vitro.
XX CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
XX CC The method is useful for enhancing the efficiency of the transfer of a
XX CC polynucleotide into a target mammalian cell in vitro. The method is
XX CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
XX CC AAB98390 represent sequences used in the exemplification of the present
XX CC invention
XX
XX SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 2.5e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CTAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 443
ID AAH41333 standard; DNA; 20 BP.
XX
XX AC AAH41333;
XX
XX DT 21-AUG-2001 (first entry)
XX
XX DE Universal stem cell factor (SCF) related oligonucleotide SEQ ID NO:34.
XX

```

```

KW Stem cell factor; SCF; stem cell factor receptor; blood cell disorder;
KW gene therapy; PCR primer; mutagenesis; probe; ss.
XX
XX OS Synthetic.
XX
XX PN US6207454-B1.
XX
XX PD 27-MAR-2001.
XX
XX PF 31-DEC-1998; 98US-00224681.
XX
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.
XX PR 21-DEC-1993; 93US-00172329.
XX PR 24-MAY-1995; 95US-00449653.
XX PR 12-JAN-1998; 98US-00005893.
XX
XX PA (AMGE-) AMGEN INC.
XX
XX PI Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX
XX DR WPI; 2001-366062/38.
XX
XX PT Enhancing efficiency of transfer of polynucleotide into a target
XX PT mammalian cell in vitro, involves exposing cell that expresses a stem
XX PT cell factor receptor to stem cell factor, and introducing polynucleotide
XX PT into cell in vitro.
XX
XX PS Example 3; Fig 12C; 210pp; English.
XX
XX CC The present invention describes a method for enhancing (E) the efficiency
XX CC of transfer of a polynucleotide (I) into a target mammalian cell (II) in
XX CC vitro, comprising exposing (II) that expresses a stem cell factor (SCF)
XX CC receptor to a biologically active SCF, its analogue or fragment, which
XX CC induces cell proliferation, and introducing (I) to (II) in vitro.
XX CC Exposure of SCF to (II) results in increased uptake of (I) into the cell.
XX CC The method is useful for enhancing the efficiency of the transfer of a
XX CC polynucleotide into a target mammalian cell in vitro. The method is
XX CC useful in gene therapy techniques. AAH41301 to AAH41364 and AAB98351 to
XX CC AAB98390 represent sequences used in the exemplification of the present
XX CC invention
XX
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18.4; DB 1; Length 20;
XX Best Local Similarity 95.0%; Pred. No. 2.5e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
DB 20 CGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 444
ID AAS04112/c
XX
XX AC AAS04112;
XX
XX DT 29-AUG-2001 (first entry)
XX
XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.
XX
XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX KW anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX KW PCR primer; ss.
XX
XX OS Homo sapiens.
XX

```

```

PN US6207417-B1.
XX
FD 27-MAR-2001.
XX
XX PF 07-JUN-1995; 95US-00482918.
XX
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 21-DEC-1993; 93US-00172329.
XX
XX (ZSEB/) ZSEBO K M.
XX (BOSS/) BOSSELMAN R A.
XX (SUGG/) SUGGS S V.
XX (MART/) MARTIN F H.
XX
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-298941/31.
XX
XX Novel nucleic acids encoding stem cell factor useful for treating
XX disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
XX disease, Kala azar, anemia and septicemia.
XX
XX Example 3; Fig 12C; 209pp; English.
XX
XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
XX oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
XX SCF (stem cell factor) cDNA sequence. The present invention relates to
XX novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
XX polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX including early haematopoietic progenitor cells. The invention also
XX describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
XX (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
XX The polynucleotide encoding SCF is useful for producing SCF and useful in
XX gene therapy. It is useful for treating disorders involving blood cells
XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
XX and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
XX disorders such as piebaldism and vitiligo
XX
XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA... 1754
Db 20 CTA... 1

RESULT 445
AAS04113/c
ID AAS04113 standard; DNA; 20 BP.
XX
XX AC AAS04113;
XX
XX 29-AUG-2001 (first entry)
XX
XX Human SCF (stem cell factor) cDNA universal PCR primer 220-11.
XX
XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
XX blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
XX anaemia; Kala azar; septicemia; malaria; hypopigmentation disorder;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX US6207417-B1.

```

```

XX
FD 27-MAR-2001.
XX
XX PF 07-JUN-1995; 95US-00482918.
XX
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 21-DEC-1993; 93US-00172329.
XX
XX (ZSEB/) ZSEBO K M.
XX (BOSS/) BOSSELMAN R A.
XX (SUGG/) SUGGS S V.
XX (MART/) MARTIN F H.
XX
XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-298941/31.
XX
XX Novel nucleic acids encoding stem cell factor useful for treating
XX disorders involving blood cells, e.g. leukemia, splenomegaly, Hodgkin's
XX disease, Kala azar, anemia and septicemia.
XX
XX Example 3; Fig 12C; 209pp; English.
XX
XX The present sequence for universal PCR primer 220-11 is 1 of 8 universal
XX oligonucleotides (AAS04110-AAS04117) used in the isolation of the human
XX SCF (stem cell factor) cDNA sequence. The present invention relates to
XX novel stem cell factors (AAU02453-AAU02458, AAU02460, AAU02461) and the
XX polynucleotides encoding them. SCF stimulate primitive progenitor cells
XX including early haematopoietic progenitor cells. The invention also
XX describes SCF peptides (AAU02462-AAU02481) and the oligonucleotides
XX (AAS04081-AAS04117) used in the isolation of human and rat SCF sequences.
XX The polynucleotide encoding SCF is useful for producing SCF and useful in
XX gene therapy. It is useful for treating disorders involving blood cells
XX such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
XX myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
XX congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
XX disseminated fungus disease, Fulminating septicemia, malaria, vitamin B12
XX and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
XX disorders such as piebaldism and vitiligo
XX
XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA... 1754
Db 20 CGAAAA... 1

RESULT 446
AAF89092/c
ID AAF89092 standard; DNA; 20 BP.
XX
XX AC AAF89092;
XX
XX 13-JUL-2001 (first entry)
XX
XX Mammalian stem cell factor PCR primer SEQ ID NO: 33.
XX
XX Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
XX gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
XX neurological damage; intestinal damage; infertility; AIDS; SCID;
XX severe combined immunodeficiency; PCR primer; ss.
XX
XX Mammalia.
XX
XX US6207802-B1.

```

```

PD XX 27-MAR-2001.
PF XX 09-NOV-1994; 94US-00336728.
PR XX 16-OCT-1989; 89US-00422383.
PR 11-JUN-1990; 90US-00537198.
PR 24-AUG-1990; 90US-00573616.
PR 01-OCT-1990; 90US-00589701.
PR 25-NOV-1992; 92US-00982255.
XX XX (AMGE-) AMGEN INC.
PA XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI XX WPI; 2001-353108/37.
DR XX
XX 16-OCT-1989; 89US-00422383.
XX 11-JUN-1990; 90US-00537198.
XX 24-AUG-1990; 90US-00573616.
XX 01-OCT-1990; 90US-00589701.
XX 25-NOV-1992; 92US-00982255.
XX XX (AMGE-) AMGEN INC.
PA XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
PI XX WPI; 2001-353108/37.
DR XX
XX Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early hematopoietic progenitor cells, useful for
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis.
XX XX
PS Example 3; Fig 12C; 209pp; English.
XX The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early hematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention
XX XX
SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1754
DB 20 CTA...AAAAA 1

RESULT 447
AAF89093/c
ID AAF89093 standard; DNA; 20 BP.
XX AC AAF89093;
XX DT 13-JUL-2001 (first entry)
XX DE Mammalian stem cell factor PCR primer SEQ ID NO: 34.
XX KW Human; rat; mammal; stem cell factor; SCF; cell growth stimulation;
KW gene therapy; haematopoietic disorder; aplastic anaemia; leukaemia;
KW neurological damage; intestinal damage; infertility; AIDS; SCID;
KW severe combined immunodeficiency; PCR primer; ss.
XX OS Mammalia.
XX PN US6207802-B1.
XX PD 27-MAR-2001.
XX PF 09-NOV-1994; 94US-00336728.
XX PR 16-OCT-1989; 89US-00422383.
XX PR 11-JUN-1990; 90US-00537198.
XX PR 24-AUG-1990; 90US-00573616.
XX PR 01-OCT-1990; 90US-00589701.
XX PR 25-NOV-1992; 92US-00982255.

```

```

PA (AMGE-) AMGEN INC.
XX Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2001-353108/37.
XX Novel isolated non-human mammalian stem cell factor polypeptide
PT stimulating growth of early hematopoietic progenitor cells, useful for
PT treating aplastic anemia, lymphoma, Letterer-Siwe disease, Kala azar,
PT sarcoidosis.
XX XX
PS Example 3; Fig 12C; 209pp; English.
XX The present invention provides the protein and coding sequences of
CC mammalian stem cell factors (SCFs). These are capable of stimulating the
CC growth of early hematopoietic progenitor cells, neural stem cells and
CC primordial germ stem cells. The sequences are useful in the treatment of
CC leukaemias, haematopoietic disorders, aplastic anaemia, paroxysmal
CC nocturnal haemoglobinuria, malaria, pigmentation disorders, neurological
CC and intestinal damage, infertility, AIDS and severe combined
CC immunodeficiency (SCID). The present sequence is primer used to amplify
CC an SCF in the exemplification of the invention
XX XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1754
DB 20 CGAAAAA...AAAAA 1

RESULT 448
AAF8959/c
ID AAF8959 standard; DNA; 20 BP.
XX AC AAF8959;
XX DT 06-AUG-2001 (first entry)
XX DE BAP28 gene fragment amplifying primer BAP28polyTcourt.
XX KW BAP28; prostate; tumour; cancer; diagnostic; genetic analysis; PCTA-1;
KW PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200100669-A2.
XX PD 04-JAN-2001.
XX PF 23-JUN-2000; 2000WO-IB001183.
XX PR 25-JUN-1999; 99US-0141323p.
XX PR 18-JAN-2000; 2000US-0176880p.
XX PA (GEST ) GENSET.
XX PI Barry C, Bougueleret L, Chumakov I, Cohen-Akenine A;
XX WPI; 2001-367032/38.
XX New BAP28 polynucleotides and polypeptides overexpressed in prostate
PT cancer cells for diagnosing prostate tumors, e.g. by hybridization or
PT polymerase chain reaction assays.
XX Example; Page 347; 349pp; English.
XX The invention is directed to BAP28 polypeptides, BAP28 polynucleotide
CC sequences and regulatory region located at the 3' and 5' ends of the
CC BAP28 coding region. The BAP28 polypeptides can be expressed by standard

```

CC recombinant methodology. BAP28 polynucleotides and polypeptides have been
 CC found to be over expressed in prostate tumour cells, therefore levels of
 CC BAP28 expression and/or activity may be assayed (e.g. by polymerase chain
 CC reaction (PCR)) to diagnose patient suffering from or susceptible to
 CC prostate cancer. Antibodies specific for the BAP28 polypeptides are
 CC useful as diagnostic reagents. Biallelic markers of the BAP28 gene are
 CC useful in genetic analysis. Sequences AAF8934-963 represent primers for
 CC the BAP28 gene and PC7A-1 gene (the coding strand of PC7A-1 gene is on
 CC the opposite of the coding strand of BAP28)

SQ Sequence 20 BP; 2 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1731 TTTACAAAAA 1750

Db 20 TATACAAAAA 1

RESULT 449

AAH23891/C

ID AAH23891 standard; DNA; 20 BP.

XX AC AAH23891;

XX DT 07-AUG-2001 (first entry)

XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.

XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

XX KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;

XX KW PCR primer; ss.

XX OS Homo sapiens.

XX PN US6204363-B1.

XX PD 20-MAR-2001.

XX PF 25-NOV-1992; 92US-00982255.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 10-APR-1991; 91US-00684535.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX DR WPI; 2001-256683/26.

XX PT New stem cell factor polypeptides and their analogs which stimulate

XX PT growth of early hematopoietic progenitors, useful for treating aplastic

XX PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's

XX PT disease.

XX PS Example 3; Fig 12C; 166pp; English.

XX CC The present sequence for universal PCR primer 220-11 is 1 of 8 universal

XX CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human

XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to

XX CC novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the

XX CC polynucleotides encoding them. SCF stimulate primitive progenitor cells

XX CC including early haematopoietic progenitor cells. The invention also

XX CC describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides

XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.

XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in

XX CC gene therapy. It is useful for treating disorders involving blood cells

CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicemia, malaria, vitamin
 CC B12 and folic acid deficiency, pyridoxine deficiency, and
 CC hypopigmentation disorders such as piebaldism and vitiligo

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1735 CAAAAA 1754

Db 20 CGAAAAA 1

RESULT 450

AAH23890/C

ID AAH23890 standard; DNA; 20 BP.

XX AC AAH23890;

XX DT 07-AUG-2001 (first entry)

XX DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.

XX KW Human; stem cell factor; SCF; early haematopoietic progenitor cell;

XX KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;

XX KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;

XX KW PCR primer; ss.

XX OS Homo sapiens.

XX PN US6204363-B1.

XX PD 20-MAR-2001.

XX PF 25-NOV-1992; 92US-00982255.

XX PR 16-OCT-1989; 89US-00422383.

XX PR 11-JUN-1990; 90US-00537198.

XX PR 24-AUG-1990; 90US-00573616.

XX PR 01-OCT-1990; 90US-00589701.

XX PR 10-APR-1991; 91US-00684535.

XX PA (AMGE-) AMGEN INC.

XX PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX DR WPI; 2001-256683/26.

XX PT New stem cell factor polypeptides and their analogs which stimulate

XX PT growth of early hematopoietic progenitors, useful for treating aplastic

XX PT anemia, carcinoma, multiple myeloma, vitiligo, kala azar, Hodgkin's

XX PT disease.

XX PS Example 3; Fig 12C; 166pp; English.

XX CC The present sequence for universal PCR primer 220-7 is 1 of 8 universal

XX CC oligonucleotides (AAH23888-AAH23895) used in the isolation of the human

XX CC SCF (stem cell factor) cDNA sequence. The present invention relates to

XX CC novel stem cell factors (AAB73561-AAB73568, AAB73571-AAB73576) and the

XX CC polynucleotides encoding them. SCF stimulate primitive progenitor cells

XX CC including early haematopoietic progenitor cells. The invention also

XX CC describes SCF peptides (AAB73578-AAB73597) and the oligonucleotides

XX CC (AAH23859-AAH23887) used in the isolation of human and rat SCF sequences.

XX CC The polynucleotide encoding SCF is useful for producing SCF and useful in

XX CC gene therapy. It is useful for treating disorders involving blood cells

XX CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple

XX CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,

XX CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,

CC disseminated fungus disease, Fulminating septicaemia, malaria, vitamin
 CC B12 and folic acid deficiency, pyridoxine deficiency, and
 CC hypopigmentation disorders such as piebaldism and vitiligo
 SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
 Db 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 451
 AAS04213/C
 ID AAS04213 standard; DNA; 20 BP.

XX AAS04213;

DT 29-AUG-2001 (first entry)

DE Human SCF (stem cell factor) cDNA universal PCR primer 220-7.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.

XX Homo sapiens.

PN US6218148-B1.

PD 17-APR-2001.

PF 21-DEC-1993; 93US-00172329.

XX 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-281051/29.

XX Isolated DNA sequence, encoding polypeptide product useful for
 stimulating growth of early hematopoietic progenitor cells.

XX Example 3; Fig 12C; 167pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 8 universal
 CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicaemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
 Db 20 CTAATAAAAAAAAAAAAAAAAAA 1

RESULT 452
 AAS04214/C
 ID AAS04214 standard; DNA; 20 BP.

XX AAS04214;

DT 29-AUG-2001 (first entry)

DE Human SCF (stem cell factor) cDNA universal PCR primer 220-11.

XX Human; stem cell factor; SCF; early haematopoietic progenitor cell;
 KW blood disorder; leukaemia; Hodgkin's disease; lymphoma; splenomegaly;
 KW anaemia; Kala azar; septicaemia; malaria; hypopigmentation disorder;
 KW PCR primer; ss.

XX Homo sapiens.

PN US6218148-B1.

PD 17-APR-2001.

PF 21-DEC-1993; 93US-00172329.

PR 16-OCT-1989; 89US-00422383.

PR 11-JUN-1990; 90US-00537198.

PR 24-AUG-1990; 90US-00573616.

PR 01-OCT-1990; 90US-00589701.

PR 25-NOV-1992; 92US-00982255.

XX (AMGE-) AMGEN INC.

PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;

XX WPI; 2001-281051/29.

XX Isolated DNA sequence, encoding polypeptide product useful for
 stimulating growth of early hematopoietic progenitor cells.

XX Example 3; Fig 12C; 167pp; English.

XX The present sequence for universal PCR primer 220-11 is 1 of 8 universal
 CC oligonucleotides (AAS04211-AAS04218) used in the isolation of the human
 CC SCF (stem cell factor) cDNA sequence. The present invention relates to
 CC novel stem cell factors (AAU02761-AAU02767, AAU02770-AAU02775, AAU02797)
 CC and the polynucleotides encoding them. SCF stimulate primitive progenitor
 CC cells including early haematopoietic progenitor cells. The invention also
 CC describes SCF peptides (AAU02777-AAU02794) and the oligonucleotides
 CC (AAS04182-AAS04210) used in the isolation of human and rat SCF sequences.
 CC The polynucleotide encoding SCF is useful for producing SCF and useful in
 CC gene therapy. It is useful for treating disorders involving blood cells
 CC such as myelofibrosis, metastatic carcinoma, acute leukaemia, multiple
 CC myeloma, Hodgkin's disease, lymphoma, Gaucher's disease, anaemia,
 CC congestive splenomegaly, Kala azar, sarcoidosis, military tuberculosis,
 CC disseminated fungus disease, Fulminating septicaemia, malaria, vitamin B12
 CC and folic acid deficiency, pyridoxine deficiency, and hypopigmentation
 CC disorders such as piebaldism and vitiligo

SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
 Db 20 CGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 453

AAS10449/C
 ID AAS10449 standard; DNA; 20 BP.
 AC AAS10449;
 XX
 XX 24-OCT-2001 (first entry)

XX Human stem cell factor (SCF) cDNA universal PCR primer 220-11.
 XX Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX Homo sapiens.
 OS US6248319-B1.
 XX
 XX 19-JUN-2001.
 XX 24-MAY-1995; 95US-00449653.
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.

XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 WPI; 2001-407312/43.
 DR
 XX Increasing the number of early hematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell factor.
 XX Example 3; Fig 12C; 210pp; English.

XX The present sequence for universal PCR primer 220-11 is 1 of 19 PCR
 CC primers (AAS10435-AAS10453) used to amplify various portions of the human
 CC SCF cDNA sequence. The sequence is described in an invention relating to
 CC novel stem cell factors, the polynucleotides encoding them and methods
 CC for producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral blood
 CC by administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood disorders,
 CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS
 XX Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
 Db 20 CGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 454

AAS10448/C
 ID AAS10448 standard; DNA; 20 BP.
 XX AAS10448;
 XX
 XX 24-OCT-2001 (first entry)

XX Human stem cell factor (SCF) cDNA universal PCR primer 220-7.
 XX Human; stem cell factor; SCF; haematopoietic progenitor cell;
 KW blood disorder; Hodgkin's disease; vitamin B12; folic acid deficiency;
 KW hypopigmentation disorder; viral disorder; AIDS; PCR primer; ss.
 XX Homo sapiens.
 OS US6248319-B1.
 XX
 XX 19-JUN-2001.
 XX 24-MAY-1995; 95US-00449653.
 XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 01-OCT-1990; 90US-00589701.
 PR 10-APR-1991; 91US-00684535.
 PR 25-NOV-1992; 92US-00982255.
 PR 21-DEC-1993; 93US-00172329.
 XX (ZSEB/) ZSEBO K M.
 PA (BOSS/) BOSSELMAN R A.
 PA (SUGG/) SUGGS S V.
 PA (MART/) MARTIN F H.

XX Zeebo KM, Bosselman RA, Suggs SV, Martin FH;
 WPI; 2001-407312/43.
 DR
 XX Increasing the number of early hematopoietic progenitor cells in the
 PT peripheral blood useful for the treatment of blood disorders including
 PT Hodgkin's disease comprises the administration of human stem cell factor.
 XX Example 3; Fig 12C; 210pp; English.

XX The present sequence for universal PCR primer 220-7 is 1 of 19 PCR
 CC primers (AAS10435-AAS10453) used to amplify various portions of the human
 CC SCF cDNA sequence. The sequence is described in an invention relating to
 CC novel stem cell factors, the polynucleotides encoding them and methods
 CC for producing the stem cell factors. The methods involve increasing the
 CC number of early haematopoietic progenitor cells in human peripheral blood
 CC by administering a haematopoietically effective human stem cell factor
 CC polypeptide. The methods are useful for the treatment of blood disorders,
 CC including myelofibrosis, myelosclerosis, osteopetrosis, metastatic
 CC carcinoma, acute leukaemia, multiple myeloma, Hodgkin's disease,
 CC lymphoma, Gaucher's disease, Niemann-Pick disease, refractory anaemia,
 CC malaria, vitamin B12 and folic acid deficiency, hypopigmentation
 CC disorders i.e. piebaldism and viral induced disorders, including AIDS
 XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
 Db 20 CTAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 455

AAD35465/c
ID AAD35465 standard; DNA; 20 BP.
AC AAD35465;
XX
DT 25-JUL-2002 (first entry)
XX
DE Rat SCF 5' cDNA amplifying PCR primer, 220-7.
XX
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW infertility; neoplasia; myelofibrosis; myeloclerosis; osteopetrosis;
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myeloclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1754
Db 20 CTA AAAAAAAAAA AAAAAAAAAA 1
RESULT 456
AAD35466/c
ID AAD35466 standard; DNA; 20 BP.
XX
AC AAD35466;
XX
DT 25-JUL-2002 (first entry)
XX
DE Rat SCF 5' cDNA amplifying PCR primer, 220-11.
XX
KW Rat; stem cell factor; SCF protein; leucopaenia; thrombocytopaenia;
KW anaemia; myelosuppression; nerve damage; myeloproliferative disorder;
KW infertility; neoplasia; myelofibrosis; myeloclerosis; osteopetrosis;
KW metastatic carcinoma; acute leukaemia; multiple myeloma; sarcoidosis;
KW Hodgkin's disease; lymphoma; Gaucher's disease; Niemann-Pick disease;
KW Letterer-Siwe disease; refractory erythroblastic anaemia; Kala azar;
KW Di Guglielmo syndrome; congestive splenomegaly; splenic pancytopenia;
KW disseminated fungus disease; Fulminating septicaemia; piebaldism; AIDS;
KW acquired immune deficiency syndrome; malaria; military tuberculosis;
KW pyridoxine deficiency; vitamin B12 deficiency; folic acid deficiency;
KW Diamond Blackfan anaemia; hypopigmentation disorder; vitiligo; PCR;
KW primer; ss.
XX
OS Rattus sp.
XX
PN US2002018763-A1.
XX
PD 14-FEB-2002.
XX
PF 12-JAN-1998; 98US-00005243.
XX
PR 24-MAY-1995; 95US-00449653.
XX
PA (ZSEB/) ZSEBO K M.
PA (BOSS/) BOSSELMAN R A.
PA (SUGG/) SUGGS S V.
PA (MART/) MARTIN F H.
XX
PI Zsebo KM, Bosselman RA, Suggs SV, Martin FH;
XX WPI; 2002-350789/38.
XX
PT Novel non-naturally-occurring stem cell factor polypeptide, useful for
PT treating leucopenia, thrombocytopenia, anemia and for enhancing
PT engraftment of bone marrow during transplantation in a mammal.
XX
PS Example 3; Fig 12C; 217pp; English.
XX
CC The present invention relates to novel non-naturally-occurring stem cell
CC factor (SCF) polypeptides having an amino acid sequence sufficiently
CC duplicative of that of naturally-occurring SCF to allow possession of
CC haematopoietic biological activity of naturally occurring SCF. Sequences
CC of the invention are useful for treating leucopaenia, thrombocytopaenia,
CC anaemia and for enhancing bone marrow recovery in treatment of radiation,
CC engraftment of bone marrow during transplantation in mammals and chemical
CC or chemotherapeutic induced bone marrow aplasia or myelosuppression. They
CC are also useful for treating acquired immune deficiency in a human, nerve
CC damage, neoplasia, infertility, myeloproliferative disorder, intestinal
CC damage in a mammal. SCF sequences are useful for preparing biologically
CC active polymer polypeptide adduct, for enhancing transfection of early
CC haematopoietic progenitor cells with a gene, and transfer of a gene into
CC a mammal. They are useful for treating myelofibrosis, myeloclerosis,
CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
CC splenic pancytopenia, disseminated fungus disease, malaria, military
CC tuberculosis, Fulminating septicaemia, pyridoxine deficiency, vitamin B12
CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
CC and vitiligo. The present sequence is a PCR primer which is used for
CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
CC exemplification of the invention

CC osteopetrosis, metastatic carcinoma, acute leukaemia, multiple myeloma,
 CC Hodgkin's disease, lymphoma, Gaucher's disease, Niemann-Pick disease,
 CC Letterer-Siwe disease, refractory erythroblastic anaemia, Di Guglielmo
 CC syndrome, congestive splenomegaly, Kala azar, sarcoidosis, primary
 CC splenic pancytopenia, disseminated fungus disease, malaria, military
 CC tuberculosis, fulminating septicemia, pyridoxine deficiency, vitamin B12
 CC and folic acid deficiency, Diamond Blackfan anaemia, hypopigmentation
 CC disorders such as piebaldism, AIDS (acquired immune deficiency syndrome)
 CC and vitiligo. The present sequence is a PCR primer which is used for
 CC amplifying the 5' end of rat SCF cDNA. This sequence is used in the
 CC exemplification of the invention

XX
 SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA...AAAAA 1754
 Db 20 CAAAAA...AAAAA 1

RESULT 457
 ABS73849/c
 ID ABS73849 standard; DNA; 20 BP.

XX AC ABS73849;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE SCF universal oligonucleotide 220-7.
 XX
 KW Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculostatic;
 KW antianaemic; antifungal; antimalarial; dermatological; ss.
 XX
 OS Synthetic.

XX EPI241258-A2.
 XX
 PD 18-SEP-2002.
 XX
 PF 04-OCT-1990; 2002EP-00008587.

XX 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 28-SEP-1990; 90MO-US005548.
 PR 01-OCT-1990; 90US-00589701.
 PR 04-OCT-1990; 90EP-00310899.
 PR 04-OCT-1990; 95EP-00105391.

XX (AMGE-) AMGEN INC.

XX PI Zsebo KM, Suggs SV, Bosseelman RA, Martin FH;
 XX WPI; 2002-684093/74.

XX Production of a human stem cell factor (SCF) polypeptide for treating
 XX disorders involving blood cells, such as leukemia, comprises culturing
 XX mammalian cells comprising non-human SCF promoter DNA linked to DNA
 XX encoding the human SCF.

XX Example 3; Fig 12C; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic) system in
 CC mammals, particularly humans. The method of the invention is useful for

CC the production of human SCF. The stem cell factors are useful to treat
 CC disorders involving blood cells e.g. metastatic carcinoma, acute
 CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
 CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus
 CC disease, malaria, and vitiligo. The present sequence representing a
 CC universal oligonucleotide for SCF DNA is used in the examples of the
 CC present invention

SQ Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
 Best Local Similarity 95.0%; Pred. No. 2.5e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA...AAAAA 1754
 Db 20 CAAAAA...AAAAA 1

RESULT 458
 ABS73850/c
 ID ABS73850 standard; DNA; 20 BP.

XX AC ABS73850;
 XX
 DT 05-DEC-2002 (first entry)
 XX
 DE SCF universal oligonucleotide 220-11.

XX Stem cell factor; SCF; blood-forming system; blood cell disorder;
 KW haematopoietic system; metastatic carcinoma; acute leukaemia;
 KW multiple myeloma; Hodgkin's disease; lymphoma; malaria; vitiligo;
 KW refractory erythroblastic anaemia; miliary tuberculosis; cytostatic;
 KW disseminated fungus disease; haematopoietic; tuberculostatic;
 KW antianaemic; antifungal; antimalarial; dermatological; ss.
 XX
 OS Synthetic.

XX EPI241258-A2.
 XX
 PD 18-SEP-2002.

XX 04-OCT-1990; 2002EP-00008587.
 XX
 PF 16-OCT-1989; 89US-00422383.
 PR 11-JUN-1990; 90US-00537198.
 PR 24-AUG-1990; 90US-00573616.
 PR 28-SEP-1990; 90MO-US005548.
 PR 01-OCT-1990; 90US-00589701.
 PR 04-OCT-1990; 90EP-00310899.
 PR 04-OCT-1990; 95EP-00105391.

XX (AMGE-) AMGEN INC.

XX PI Zsebo KM, Suggs SV, Bosseelman RA, Martin FH;
 XX WPI; 2002-684093/74.

XX Production of a human stem cell factor (SCF) polypeptide for treating
 XX disorders involving blood cells, such as leukemia, comprises culturing
 XX mammalian cells comprising non-human SCF promoter DNA linked to DNA
 XX encoding the human SCF.

XX Example 3; Fig 12C; 120pp; English.

XX The present invention relates to novel stem cell factors (SCFs),
 CC polynucleotide sequences encoding the SCFs, and methods of producing
 CC them. SCFs are involved in the blood-forming (haematopoietic) system in
 CC mammals, particularly humans. The method of the invention is useful for
 CC the production of human SCF. The stem cell factors are useful to treat
 CC disorders involving blood cells e.g. metastatic carcinoma, acute
 CC leukaemia, multiple myeloma, Hodgkin's disease, lymphoma, refractory
 CC erythroblastic anaemia, miliary tuberculosis, disseminated fungus

CC disease, malaria, and vitiligo. The present sequence representing a
CC universal oligonucleotide for SCF DNA is used in the examples of the
CC present invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1735 CAAAAAATTTTTTTTTT 1754
Db 20 CAAAAAATTTTTTTTTT 1

RESULT 459
ABZ89546
ID ABZ89546 standard; DNA; 20 BP.
XX
AC ABZ89546;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.
XX
Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4788; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1732 TTACAAAAAATTTTTTTTTT 1751
Db 1 TTTAAAAAATTTTTTTTTT 20

RESULT 460
ABZ89085
ID ABZ89085 standard; DNA; 20 BP.
XX
AC ABZ89085;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIC-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
WPI; 2003-229219/22.
XX
Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4327; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 19 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1734 ACACAAAAA 1753
| | | | |
Db 1 AGAAAAA 20

RESULT 461
ABZ88694
ID ABZ88694 standard; DNA; 20 BP.

XX ABZ88694;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Disclosure; SEQ ID NO 3936; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1731 TTTACAAAAA 1750
| | | | |
Db 1 TTTAAAAA 20

RESULT 462
ABZ89240

ID ABZ89240 standard; DNA; 20 BP.

XX ABZ89240;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Disclosure; SEQ ID NO 4482; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC carcinoma, leukaemia and miliary tuberculosis. The SCF polypeptides are
 CC also used to expand haematopoietic progenitor cells for transplantation
 CC and to prepare such cells for transfection with a gene. The SCF
 CC polynucleotides can be used for recombinant expression of the
 CC polypeptides and also as probes for mapping of the SCF gene, for
 CC identifying SCF-related diseases and as a marker for neighbouring genes.
 CC Antibodies raised against the polypeptides are useful in diagnosis and to
 CC remove SCF from blood. This sequence represents SCF related DNA of the
 CC invention.

XX Sequence 20 BP; 1 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 20;

Best Local Similarity 95.0%; Pred. No. 2.5e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAATAAAAAAAAAA 1754

Db 20 CTAATAAAAAAAAAAAAAA 1

RESULT 465

AAQ75611/c

ID AAQ75611 standard; DNA; 21 BP.

XX AAQ75611;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 XX and using the aggregate of mRNAs as the template for each reverse
 XX transcription primer; (b) digesting each of the prepared aggregates of
 XX the double-stranded cDNAs with restriction enzyme and; (c)
 XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 2.7e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAATAAAAAAAAAA 1752

Db 20 TCCAAAAAATAAAAAAAAAA 1

RESULT 466

AAQ75630/c

ID AAQ75630 standard; DNA; 21 BP.

XX AAQ75630;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.

XX Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 XX and using the aggregate of mRNAs as the template for each reverse
 XX transcription primer; (b) digesting each of the prepared aggregates of
 XX the double-stranded cDNAs with restriction enzyme and; (c)
 XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;

Best Local Similarity 95.0%; Pred. No. 2.7e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAATAAAAAAAAAA 1752

Db 20 TCCAAAAAATAAAAAAAAAA 1

RESULT 467

AAQ75724/c

ID AAQ75724 standard; DNA; 21 BP.

XX AAQ75724;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX

```
PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 4 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. NO. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1750
DB 20 TTTAAAAA 1

RESULT 468
AAQ75661/c
ID AAQ75661 standard; DNA; 21 BP.
XX
XX AAQ75661;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
```

```
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. NO. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1752
DB 20 TGCAAAAA 1

RESULT 469
AAQ75671/c
ID AAQ75671 standard; DNA; 21 BP.
XX
XX AAQ75671;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. NO. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAA 1754
DB 20 CATAAAAA 1

RESULT 470
AAQ75675/c
ID AAQ75675 standard; DNA; 21 BP.
XX
XX AAQ75675;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
```

```

XX aggregate; restriction enzyme; ss.
OS Synthetic.
XX
XX JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PP 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 2.7e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1733 TACAAAAA 1752
XX |||||||
XX DB 20 TATAAAAAA 1
XX
XX RESULT 471
XX AAQ75771/c
XX ID AAQ75771 standard; DNA; 21 BP.
XX
XX AC AAQ75771;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PP 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 2.7e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1733 TACAAAAA 1752
XX |||||||
XX DB 20 TATAAAAAA 1
XX
XX RESULT 471
XX AAQ75771/c
XX ID AAQ75771 standard; DNA; 21 BP.
XX
XX AC AAQ75771;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PP 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 9; 11pp; Japanese.
XX

```

```

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 2.7e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1733 TACAAAAA 1752
XX |||||||
XX DB 20 TAGAAAAA 1
XX
XX RESULT 472
XX AAQ75627/c
XX ID AAQ75627 standard; DNA; 21 BP.
XX
XX AC AAQ75627;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PP 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18.4; DB 1; Length 21;
XX Best Local Similarity 95.0%; Pred. No. 2.7e+02;
XX Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1733 TACAAAAA 1752
XX |||||||
XX DB 20 TTCAAAAAA 1
XX
XX RESULT 473

```


Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. NO. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 476
AAQ75618/c
ID AAQ75618 standard; DNA; 21 BP.
XX AC AAQ75618;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
-CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. NO. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1752
Db 20 TACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 478
AAQ75725/c
ID AAQ75725 standard; DNA; 21 BP.
XX AC AAQ75725;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

XX Synthetic.
XX OS JP06303997-A.
XX FN 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PF 16-APR-1993; 93JP-00112515.
XX PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA WPI; 1995-018287/03.
XX DR Analysis of cDNA and gene expression - by amplification of mRNA followed
XX DR by digestion with restriction enzymes.
XX PT Disclosure; Page 6; 11pp; Japanese.
XX PS A method for the analysis of cDNA comprises (a) preparing an aggregate of
-CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. NO. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1752
Db 20 TACAAAAAAAAAAAAAAAAAAAAA 1

RESULT 478
AAQ75725/c
ID AAQ75725 standard; DNA; 21 BP.
XX AC AAQ75725;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX FN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTACAAAAA 1750
 |||||
 DB 20 TTAAAAA 1

RESULT 479
 AAQ75773/c
 ID AAQ75773 standard; DNA; 21 BP.

XX AC AAQ75773;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 9; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1752
 |||||
 DB 20 TAGAAAAA 1

RESULT 480
 AAQ75614/c

ID AAQ75614 standard; DNA; 21 BP.
 XX AC AAQ75614;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1752
 |||||
 DB 20 TCCAAAAA 1

RESULT 481
 AAQ75682/c
 ID AAQ75682 standard; DNA; 21 BP.

XX AC AAQ75682;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1752
 |||||
 DB 20 TCCAAAAA 1

RESULT 481
 AAQ75682/c
 ID AAQ75682 standard; DNA; 21 BP.

XX AC AAQ75682;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.
 XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.

Query Match 1.0%; Score 18.4; DB 1; Length 21;
 Best Local Similarity 95.0%; Pred. No. 2.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1752
 |||||
 DB 20 TAGAAAAA 1

RESULT 480
 AAQ75614/c

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PT
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 482
AAQ75767/C
ID AAQ75767 standard; DNA; 21 BP.
XX
XX AAQ75767;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1754
Db 20 CAAAAAAAAAAAAAAAAAAAAA 1
RESULT 483
AAQ75678/C
ID AAQ75678 standard; DNA; 21 BP.
XX
XX AAQ75678;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1733 TACAAAAAAAAAAAAAAAAAAAAA 1752
Db 20 TAAAAAAAAAAAAAAAAAAAAA 1
RESULT 484
AAQ75713/C
ID AAQ75713 standard; DNA; 21 BP.
XX
XX AAQ75713;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

```

OS Synthetic.
XX JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 7; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 0 C; 1 G; 19 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1734 ACAAAAAAAAAAAAAAAAAA 1753
DB 20 ACTAAAAAAAAAAAAAAAAA 1

RESULT 485
AAQ75615/c
ID AAQ75615 standard; DNA; 21 BP.
XX
XX AC AAQ75615;
XX
XX DT 04-AUG-1995 (first entry)
XX
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX OS Synthetic.
XX
XX PN JP06303997-A.
XX
XX PD 01-NOV-1994.
XX
XX PF 16-APR-1993; 93JP-00112515.
XX
XX PR 16-APR-1993; 93JP-00112515.
XX
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX DR WPI; 1995-018287/03.
XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1733 TACAAAAAAAAAAAAAAAAA 1752
DB 20 TCGAAAAAAAAAAAAAAAAA 1

RESULT 487
AAQ75680/c
ID AAQ75680 standard; DNA; 21 BP.

```

```

XX AC AAQ75680;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 488
AAQ75743/C
ID AAQ75743 standard; DNA; 21 BP.
XX AC AAQ75743;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
Db 20 AAAAAAAAAAAAAAAAAAAAAA 1

RESULT 488
AAQ75743/C
ID AAQ75743 standard; DNA; 21 BP.
XX AC AAQ75743;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAAAAAAAAAA 1753
Db 20 ACGAAAAAAAAAAAAAAAAAAAAA 1

RESULT 489
AAQ75714/C
ID AAQ75714 standard; DNA; 21 BP.
XX AC AAQ75714;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```



```

AC AAQ75617;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA
XX WPI; 1995-018287/03.
XX DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; lipp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ7547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 0 C; 2 G; 19 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAAAA 1753
DB 20 ACCAAAAAAAAAAAAAAA 1

RESULT 495
AAQ75768/c
ID AAQ75768 standard; DNA; 21 BP.
XX
XX AAQ75768;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX
XX JF06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX PF
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX PA
XX
```

```
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
      Query Match      1.0%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 2.7e+02;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1735 CAAGAAAAA 1754
DB 20 CAGAAAAA 1

RESULT 496
AAQ75777/c
ID AAQ75777 standard; DNA; 21 BP.
XX
AC AAQ75777;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
      Query Match      1.0%; Score 18.4; DB 1; Length 21;
      Best Local Similarity 95.0%; Pred. No. 2.7e+02;
      Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1733 TACAAAAA 1752
DB 20 TCGAAAAA 1

RESULT 498
AAQ75774/c
ID AAQ75774 standard; DNA; 21 BP.
XX
AC AAQ75774;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
```



```

PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1752
Db 20 TACAAAAA 1

RESULT 499
AAQ75613/C
ID AAQ75613 standard; DNA; 21 BP.
XX
AC AAQ75613;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse

```

```

CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1752
Db 20 TCCAAAAA 1

RESULT 500
AAQ75677/C
ID AAQ75677 standard; DNA; 21 BP.
XX
AC AAQ75677;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1752
Db 20 TATAAAAA 1

RESULT 501
AAQ75745/C
ID AAQ75745 standard; DNA; 21 BP.
XX
AC AAQ75745;

```

```
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA1754
DB 20 CAGAAAAA1

RESULT 503
AAQ75711/c
ID AAQ75711 standard; DNA; 21 BP.
XX
AC AAQ75711;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAA1753
DB 20 ACGAAAAA1

RESULT 502
AAQ75770/c
ID AAQ75770 standard; DNA; 21 BP.
XX
AC AAQ75770;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
```

Qy 1734 ACACAAAAA 1753
Db 20 ACTAAAAA 1

RESULT 504

AAZ26563
ID AAZ26563 standard; DNA; 21 BP.

XX AC AAZ26563;
XX 30-NOV-1999 (first entry)

XX DE Human polymorphic region 752.

XX KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
XX KW cell viability; loss of heterozygosity; precancerous condition; ASI;
XX KW allele specific inhibitor; somatic cell; diagnosis; prevention;
XX KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
XX KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
XX KW graft versus host disease; malignant cell removal; bone marrow; ss.

XX OS Homo sapiens.

XX PN WO9841648-A2.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US005419.

XX PR 20-MAR-1997; 97US-0041057P.

XX PA (VARI-) VARIAGENICS INC.

XX PI Housman D, Ledley FD, Stanton VP;
XX WPI; 1998-521232/44.

XX PT Identifying target genes for allele-specific drugs - used for diagnosis,
XX PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
XX PT dysplastic lesions, endometriosis or graft versus host disease.

XX PS Disclosure; Fig 7; 605pp; English.

XX CC This invention describes a novel method for identifying an inhibitor
XX CC potentially useful for treatment of cancer, where the inhibitor is active
XX CC on a gene vital for cell growth or viability, and where the gene is
XX CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
XX CC used for preventing the development of cancer in a patient having a
XX CC precancerous condition, by administering to the patient a first allele
XX CC specific inhibitor (ASI) targeted to an allele of a first essential gene
XX CC present in cells of the precancerous condition, where the normal somatic
XX CC cells of the patient are heterozygous for the first gene, the inhibitor
XX CC is active on at least one but less than all allelic forms of the gene
XX CC present in a population and targets only one allelic form present in the
XX CC normal somatic cells, and the first gene. The products and methods can be
XX CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
XX CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
XX CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
XX CC graft versus host disease. The method can also be used to remove
XX CC malignant cells from bone marrow transplants. AAZ25812-226825 represent
XX CC human polymorphic sites described in the method of the invention
XX CC Sequence 21 BP; 19 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACACAAAAA 1753
Db 2 ACACAAAAA 21

RESULT 505
AAF95716/C
ID AAF95716 standard; DNA; 21 BP.

XX AC AAF95716;
XX 06-JUN-2001 (first entry)

XX DE Human gene single nucleotide polymorphism #477.

XX KW Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX KW polymorphism; vascular disease; coronary artery disease; forensics;
XX KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
XX KW pulmonary embolism; paternity test; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX FT Variation replace(11,T)

XX FT /*tag= a
XX FT /standard_name= "single nucleotide polymorphism"

XX PN WO200118250-A2.

XX PD 15-MAR-2001.

XX PF 07-SEP-2000; 2000WO-US024503.

XX PR 10-SEP-1999; 99US-0153357P.

XX PR 26-JUL-2000; 2000US-0220947P.

XX PR 16-AUG-2000; 2000US-0225724P.

XX PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Lander ES, Gargill M, Ireland JS, Bolk S, Daley CQ, Mccarthy JJ;
XX WPI; 2001-226749/23.

XX PT Nucleic acids comprising single nucleotide polymorphisms, useful in
XX PT applications such as forensics, paternity testing, medicine, genetic
XX PT analysis and phenotype correlations to diseases such as diabetes and
XX PT atherosclerosis.

XX PS Example; Page 81; 242pp; English.

XX CC The present invention provides a method of diagnosing a vascular disease
XX CC in an individual, involving determining the sequence at various
XX CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
XX CC genes. The sequences at a number of polymorphic sites are also provided
XX CC in the specification. In particular, the method can be used in the
XX CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
XX CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
XX CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
XX CC useful in forensics, paternity testing, genetic analysis and phenotype
XX CC correlations to diseases. The present sequence is an example of one of
XX CC the human gene SNPs shown in the specification

XX SQ Sequence 21 BP; 1 A; 6 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 182 CCCCAGAGCAGCCGAGCCCC 201
Db 21 CCCCAGAGCAGCCGAGCCCC 2

RESULT 506

AAF24290/C
ID AAF24290 standard; DNA; 21 BP.

```
XX AAF24290;
XX 03-APR-2001 (first entry)
XX Complementary nucleic acid detection method related sequence #5.
XX Complementary nucleic acid; gene analysis; polymorphism; variation;
KW DNA chip; primer; ss.
XX Unidentified.
XX EP1065278-A2.
XX 03-JAN-2001.
XX 07-JUN-2000; 2000EP-00112235.
XX 07-JUN-1999; 99JP-00159339.
XX (FUUF ) FUJI PHOTO FILM CO LTD.
XX Makino Y, Abe Y, Ogawa M, Takagi M, Takenaka S, Yamashita K;
XX WPI; 2001-140003/15.
XX Determining complementarity of nucleotide fragment for gene analysis, by
XX comparing flow of electric current from or to electroconductive substrate
XX through DNA fragment, with reference obtained from its complement.
XX Example 1; Page 12; 28pp; English.
XX The present invention provides a method for analysing a nucleic acid
XX strand to determine the degree of complementarity between two sequences.
XX This involves the measurement of an electric current along the annealed
XX strands compared to a standard. This is useful in the analysis of genetic
XX polymorphisms and variation between genes
XX Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 21 AAAAAAAAAATAAAAAAAAAAA 2
RESULT 507
ABX79794/c
ID ABX79794 standard; cDNA; 21 BP.
XX ABX79794;
XX 17-APR-2003 (first entry)
XX EST polymorphic DNA repeat polynucleotide #119.
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX Homo sapiens.
XX US6472154-B1.
XX 29-OCT-2002.
XX 31-DEC-1999; 99US-00475947.
```

```
XX 31-DEC-1999; 99US-00475947.
XX (TEXA ) UNIV TEXAS SYSTEM.
XX Garner HR, Wren JD, Minna JD, Fondon JW;
XX WPI; 2003-208818/20.
XX Identifying a candidate polymorphic repeat within a coding sequence, for
XX understanding or treating genetic disease, comprises detecting tandem
XX repeats in a target coding sequence and scoring the repeats for
XX polymorphic probability.
XX Example; Col 495; 588pp; English.
XX The invention discloses a method for identifying a candidate polymorphic
XX repeat within a coding sequence (expressed sequence tag, EST), which
XX comprises detecting tandem repeats in a target coding sequence, scoring
XX the repeats for polymorphic probability and generating a dataset
XX correlating the repeats with polymorphic probability to identify a
XX candidate polymorphic repeat. The computational methods (polymorphic
XX marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
XX useful for identifying and detecting candidate polymorphic repeats in
XX human genes, which can be used to understand, treat or eliminate genetic
XX diseases, predispositions or adverse drug-treatment reactions. Examples
XX of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
XX syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
XX myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
XX spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
XX the polymorphic repeats identified for a search of human ESTs
XX Sequence 21 BP; 1 A; 0 C; 0 G; 20 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
DB 21 AAAAAAAAAATAAAAAAAAAAA 2
RESULT 508
AAT92356/c
ID AAT92356 standard; DNA; 22 BP.
XX AAT92356;
XX 26-JAN-1998 (first entry)
XX Amino modified oligodeoxyribonucleotide.
XX Amino modified oligodeoxyribonucleotide; oligonucleotide;
KW achiral linker reagent; 5-(aminomethyl)-1,3-benzenedimethanol;
KW N-fluoresceinyl-(5-aminomethyl)-1,3-benzenedimethanol;
KW hybridisation probe; PCR primer; nucleic acid sequencing;
KW affinity matrix; cloning recombinant DNA; in-vitro mutagenesis; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX misc_difference 11 /*tag= a
XX /*note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"
XX misc_difference 12 /*tag= b
XX /*note= "n = 5-(aminomethyl)-1,3-benzenedimethanol"
XX WO9705156-A1.
XX 13-FEB-1997.
XX
```

```

PF 26-JUL-1996; 96WO-DK000330.
PR 27-JUL-1995; 95DK-00000863.
XX
PA (BEHR/) BEHRENS C.
PA (PETE/) PETERSEN K H.
PA (EGHO/) EGHOLM M.
PA (NIEL/) NIELSEN J.
PA (DAHL/) DAHL O.
XX
PI Behrens C, Petersen KH, Egholm M, Nielsen J, Dahl O;
XX
DR WPI; 1997-145615/13.
XX
XX New achiral linker reagents - useful for incorporation of multiple amino
PT (gps. or reporter gps. into oligo:nucleotide(s)).
PT
XX
PS Disclosure; Page 20; 42pp; English.
XX
CC Achiral linker reagents have been developed for the incorporation of
CC multiple amino groups into oligonucleotides. The present sequence
CC represents a modified oligodeoxyribonucleotide. The achiral linker
CC reagents can be used for incorporation of multiple primary amino groups
CC or reporter groups into oligonucleotides. They are compatible with
CC conventional DNA synthesis following the phosphoramidite methodology, and
CC can be incorporated in good yields. The linker reagents may be used for
CC labelling of oligonucleotides. They may also be used for preparation of
CC oligonucleotides, e.g. for use as hybridisation probes, for use as
CC primers in the polymerase chain reaction or in nucleic acid sequencing
CC reactions, for production of affinity matrices for purification of DNA
CC binding proteins or other biomolecules, for production of affinity
CC matrices for detection of nucleic acid sequences, for cloning recombinant
CC DNA or for in-vitro mutagenesis
XX
SQ Sequence 22 BP; 0 A; 0 C; 0 G; 20 T; 0 U; 2 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAAAAAAAAAA 1755
DB 22 AAAAAAAAAAAAAAAAAAAAAA 1
RESULT 509
ABQ73084/c
ID ABQ73084 standard; DNA; 22 BP.
XX
AC ABQ73084;
XX
DT 25-SEP-2002 (first entry)
XX
DE Human zcytor19 PCR primer ZC37681 SEQ ID NO:27.
XX
KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;
KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;
KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;
KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;
KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;
KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;
KW mesangiol proliferative disease; chronic lymphocytic leukaemia; bronchitis;
KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;
KW haemolytic uraemic syndrome; renal neoplasms; urological neoplasms;
KW emphysema; chronic airway disease; chromosome 1; chromosome 1p36.11;
KW PCR primer; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200244209-A2.
XX

```

```

PD 06-JUN-2002.
XX
PF 28-NOV-2001; 2001WO-US044808.
XX
PR 28-NOV-2000; 2000US-0253561P.
PR 07-FEB-2001; 2001US-0267211P.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Xu W, Novak JE, Whitmore TE, Grant FJ;
XX
DR WPI; 2002-527700/56.
XX
XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating
PT immune responses in animals for producing antibodies, and for treating
PT autoimmune diseases, leukemia and asthma.
XX
PS Example 2; Page 187; 200pp; English.
XX
CC The present invention describes an isolated human zcytor19 protein (I),
CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,
CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory,
CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic
CC activities, and can be used in vaccines. (I) or an antibody binding (I)
CC can be used for suppressing the immune system for reducing rejection of
CC tissue or organ transplants and grafts and for treating T-cell specific
CC leukaemias or lymphomas and autoimmune diseases including rheumatoid
CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel
CC disease and Crohn's disease. The antibodies can also be used for treating
CC immunologic renal diseases, glomerulonephritis, mesangiol proliferative
CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or
CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related
CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the
CC antibodies can also be used for renal or urological neoplasms and
CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway
CC diseases. Human zcytor19 is located to chromosome 1, more specifically to
CC chromosome 1p36.11. The present sequence represents a PCR primer which is
CC used in an example from the present invention
XX
SQ Sequence 22 BP; 1 A; 13 C; 1 G; 7 T; 0 U; 0 Other;
Query Match 1.0%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 863 GAAGAGGAGGAGGAGCGAG 882
DB 21 GAGGAGGAGGAGGAGCGAG 2
RESULT 510
AAA29753/c
ID AAA29753 standard; DNA; 23 BP.
XX
AC AAA29753;
XX
DT 15-AUG-2000 (first entry)
XX
DE Synthetic oligonucleotide #1.
XX
KW Primer; destablise non-specific duplex formation; PCR; detection;
KW purification; sequencing; genetic marker; RACE; DNA synthesis; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 8 /*tag= a
FT /*mod_base= i
FT /*note= "inosine"
FT modified_base 18 /*tag= b
FT /*mod_base= i

```

```

FT XX /note= "inosine"
PN XX WO200020630-A1.
XX XX
PD XX 13-APR-2000.
XX XX
PF XX 06-OCT-1999; 99WO-CA000933.
XX XX
PR XX 07-OCT-1998; 98CA-02246623.
XX XX
PA (UYMC-) UNIV MCGILL.
XX XX
PI Pelletier J, Das M;
XX XX
DR WPI; 2000-328943/28.
XX XX
PT Novel method of stabilizing duplex formation, or destabilizing non-
PT specific duplex formation using primer containing modified nucleotide
PT analogs, useful for preventing mispriming during PCR, RACE, DNA synthesis
PT or sequencing.
PS
XX Example 1; Page 25; 46pp; English.
XX
CC The present invention describes a method for destabilising non-specific
CC duplex formation, between an oligonucleotide and a target nucleic acid
CC (NA), comprising incubating the target NA with a modified oligonucleotide
CC (I), comprising a homopolymeric sequence having a modification which
CC decreases or abrogates H-bonding between the modified oligonucleotide and
CC the non-specific target NA. The modified oligonucleotide is used to
CC improve discrimination between the targeted homopolymeric sequence and a
CC non-homopolymeric target sequence. It is used to increase the proportion
CC of full length cDNA clones for a library, to reduce mispriming during
CC sequencing, 5' or 3' RACE (rapid amplification of cDNA ends) or DNA
CC synthesis or to generate bona fide genetic markers. The present sequence
CC represents an oligonucleotide which is used in the exemplification of the
CC present invention
XX
SQ Sequence 23 BP; 0 A; 0 C; 0 G; 21 T; 0 U; 2 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 23;
Best Local Similarity 86.4%; Pred. No. 2.8e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 ACACAAAAA 1755
Db 23 AAAAAAAAAAAAAAAAAA 2

RESULT 511
AAH24266/c
ID AAH24266 standard; DNA; 24 BP.
XX
AC AAH24266;
XX
DT 11-SEP-2001 (first entry)
XX
DE Human phosphatase 79 RT-PCR primer, SEQ ID NO:4.
XX
KW Phosphatase 79; human; BAC clone CTB-54D4-encoded protein homologue;
KW recombinant production; malignant tumour; cancer; blood disease;
KW HIV infection; human immunodeficiency virus; immune disorder;
KW inflammatory condition; cytostatic; anti-HIV; antiinflammatory;
KW immunomodulator; reverse transcription-PCR; RT-PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200138385-A1.
XX
PD 31-MAY-2001.
XX
PF 20-NOV-2000; 2000WO-CN000459.
XX
PR 22-NOV-1999; 99CN-00124059.

```

```

XX (BIOR-) BIOROAD GENE DEV LTD SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
DR WPI; 2001-355903/37.
XX
PT Human phosphatase 79 and encoded polynucleotide, applicable in diagnosis
PT and treatment of malignant tumor, hemopathy, HIV infection, immunological
PT diseases and various inflammation.
XX
PS Example 3; Page 12; 38pp; Chinese.
XX
CC The invention relates to human phosphatase 79 (AAB73700), nucleic acids
CC encoding it (AAH24264), and a method for the recombinant production of
CC human phosphatase 79. The present invention additionally discloses an
CC agonist of phosphatase 79 for therapeutic use, and an antibody which
CC specifically binds to human phosphatase 79. Human phosphatase 79, and
CC nucleotides which encode it may be used for treating a variety of
CC diseases, such as malignant tumours, blood diseases, HIV (human
CC immunodeficiency virus) infection, immune disorders and inflammatory
CC conditions. The protein may also be used to screen for modulators of its
CC activity or for peptide fingerprinting identification. The polynucleotide
CC can be used as a primer for nucleic acid amplification reaction or as a
CC probe for hybridisation reactions, or in producing gene chips or
CC microarrays. Sequences AAH24265-AAH24266 represent reverse transcription-
CC PCR (RT-PCR) primers used in an exemplification of the invention to
CC isolate human phosphatase 79 cDNA
XX
SQ Sequence 24 BP; 2 A; 0 C; 0 G; 22 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 24;
Best Local Similarity 95.0%; Pred. No. 2.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAA 1755
Db 24 AAAAAAAAAAAAAAAAAATAA 5

RESULT 512
AAH44623/c
ID AAH44623 standard; DNA; 24 BP.
XX
AC AAH44623;
XX
DT 16-NOV-2001 (first entry)
XX
DE Human FD 17 PCR primer 2 SEQ ID NO:4.
XX
KW Human; FD 17; cytostatic; virucidal; immunomodulatory; haemostatic;
KW antiinflammatory; gene therapy; malignant tumour; haemopathy;
KW human immunodeficiency virus infection; HIV infection;
KW immunological disease; inflammation; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200164729-A1.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-CN000221.
XX
PR 02-MAR-2000; 2000CN-00111868.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
XX
DR WPI; 2001-550164/61.
XX
XX New human polypeptide FD 17 for diagnosing and treating malignant tumor,
PT hemopathy, human immunodeficiency virus (HIV) infection, immunological

```

PT diseases and inflammations.

PS Example 2; Page 11; 36pp; Chinese.

CC The present invention describes the human PD 17 protein (I). (I) has

CC cytostatic, virucidal, immunomodulatory, antiinflammatory and haemostatic

CC activities. The polynucleotide encoding (I) can be used in gene therapy.

CC (I) and the polynucleotide encoding it are applicable in the diagnosis

CC and treatment of malignant tumour, haemopathy, human immunodeficiency

CC virus (HIV) infection, immunological diseases and various inflammations.

CC The present sequence represents a PCR primer for human PD 17, which is

CC used in an example from the present invention

XX

SQ Sequence 24 BP; 0 A; 2 C; 1 G; 21 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 24;

Best Local Similarity 95.0%; Pred. No. 2.9e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAGAAAAA 1754

Db 24 CAAAAAAGAAAAA 5

RESULT 513

ABK13715/c

ID ABK13715 standard; DNA; 24 BP.

XX

AC ABK13715;

XX

DT 23-APR-2002 (first entry)

XX

DE RT-PCR primer #2 for human transcriptional activation subunit 14 cDNA.

XX

KW Human; transcriptional activation subunit 14; malignant neoplasm;

KW haematopathy; cytostatic; HIV infection; human immunodeficiency virus;

KW immunological disease; inflammation; virucide; immunomodulatory;

KW antiinflammatory; reverse transcriptase-PCR; RT-PCR; primer; ss.

XX

OS Homo sapiens.

XX

XX WO200194403-A1.

PN

XX

PD 13-DEC-2001.

XX

XX 14-MAY-2001; 2001WO-CN000753.

PF

XX

XX 16-MAY-2000; 2000CN-00115720.

PR

XX

PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.

XX

XX Mao Y, Xie Y;

PI

XX

DR WPI; 2002-090139/12.

XX

PT Human transcriptional activation subunit 14 and encoding polynucleotide,

PT used in diagnosis and treatment of malignant tumors, hemopathy, human

PT immunodeficiency virus infection, immunological diseases and

PT inflammation.

XX

PS Example 2; Page 17; 36pp; Chinese.

XX

CC The present invention relates to the isolation of human transcriptional

CC activation subunit 14, and the polynucleotide encoding it. Also described

CC is the process for preparing the protein by DNA recombination and the

CC application of the polypeptide and polynucleotide in treating various

CC diseases such as malignant neoplasms, haematopathy, human

CC immunodeficiency virus (HIV) infection, immunological diseases, and

CC various inflammations. Antagonists against the polypeptide can also be

CC used in treating such diseases. The present sequence for reverse

CC transcriptase (RT)-PCR primer #2 is used with RT-PCR primer #1 (ABK13714)

CC for isolating cDNA encoding human transcriptional activation subunit 14

XX

SQ Sequence 24 BP; 0 A; 2 C; 2 G; 20 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 24;

Best Local Similarity 95.0%; Pred. No. 2.9e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAGAAAAA 1754

Db 23 CAAAAAAGAAAAA 4

RESULT 514

ABK12409

ID ABK12409 standard; DNA; 24 BP.

XX

AC ABK12409;

XX

DT 18-JUN-2002 (first entry)

XX

DE RT-PCR primer #1 for cDNA encoding polypeptide-laminin B210.67.

XX

KW Polypeptide-laminin B210.67; embryo development teratogenesis;

KW cytostatic; reverse transcriptase-PCR; RT-PCR; primer; ss.

XX

OS Unidentified.

XX

XX CN1328013-A.

PN

XX

PD 26-DEC-2001.

XX

PF 14-JUN-2000; 2000CN-00116514.

XX

XX 14-JUN-2000; 2000CN-00116514.

PR

XX

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

XX Mao Y, Xie Y;

PI

XX

DR WPI; 2002-270054/32.

XX

XX Polypeptide-laminin B210.67, useful for treating diseases such as embryo

XX development teratogenesis.

PT

XX

PS Example 2; Page 18 (disclosure); 33pp; Chinese.

XX

CC The present invention relates to the isolation of polypeptide-laminin

CC B210.67, and the polynucleotide encoding it. Also described is the

CC process for preparing the protein by DNA recombination. The polypeptide

CC is useful for treating diseases such as embryo development teratogenesis.

CC The present sequence for reverse transcriptase (RT)-PCR primer #1 is used

CC with RT-PCR primer #2 (ABK12410) for isolating cDNA encoding polypeptide-

CC laminin B210.67

XX

SQ Sequence 24 BP; 19 A; 2 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 1.0%; Score 18.4; DB 1; Length 24;

Best Local Similarity 95.0%; Pred. No. 2.9e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAAAGAAAAA 1751

Db 5 TTAAGAAAAAAGAAAAA 24

RESULT 515

AAK06572/c

ID AAK06572 standard; DNA; 19 BP.

XX

XX AAK06572;

AC

XX

DT 06-APR-1999 (first entry)

XX

DE (-)-limonene-6-hydroxylase primer 3.B.

XX (-)-limonene-6-hydroxylase; (-)-limonene-3-hydroxylase; L3H; L6H;
 KW spear mint; peppermint; enzyme; limonene hydroxylase; trans-carveol;
 KW trans-isopiperitenol; pathogen defense mechanism; attractant;
 KW environmental signal; monoterpene hydroxylase; PCR primer; ss.
 XX Synthetic.
 OS Mentha spicata.
 XX
 PN W09859042-A1.
 XX
 PD 30-DEC-1998.
 XX
 PF 15-JUN-1998; 98WO-US012581.
 XX
 PR 24-JUN-1997; 97US-00881784.
 XX
 PA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Croteau RB, Lupien SL, Karp F;
 XX
 DR WPI; 1999-105618/09.
 XX
 DR New isolated limonene hydroxylase nucleic acids - which encode limonene-6
 PT -hydroxylase and limonene-3-hydroxylase, which can be used to produce
 PT trans-carveol and trans-isopiperitenol.
 XX
 PS Example 4; Page 27; 80pp; English.
 XX
 CC The invention relates to nucleotide sequences encoding spearmint (-)-
 CC limonene-6-hydroxylase (L6H) and peppermint (-)-limonene-3- hydroxylase
 CC (L3H). Host cells containing a vector comprising the nucleotide sequences
 CC can be used for the recombinant production of limonene hydroxylases or of
 CC primary enzyme products. The primary enzyme products are trans-carveol in
 CC the case of (-)-L6H or trans-isopiperitenol in the case of (-)-L3H, which
 CC are of subsequent use, to obtain enhanced expression of limonene
 CC hydroxylase in plants to attain enhanced trans- carveol or trans-
 CC isopiperitenol production as a predator or pathogen defense mechanism,
 CC attractant or environmental signal. The limonene hydroxylase cDNAs also
 CC provide a useful tool for isolating other monoterpene hydroxylase genes
 CC and for examining the developmental regulation of monoterpene
 CC biosynthesis. Sequences AA06584-73 represent primers for the PCR
 CC amplification of (-)-limonene-6-hydroxylase cDNA
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAAAAAAAAAA 1754
 :|||||
 DB 19 DAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 516
 AAZ99489/c
 ID AAZ99489 standard; DNA; 19 BP.
 XX
 AC AAZ99489;
 XX
 DT 03-JUL-2000 (first entry)
 XX
 DE Primer HOOK for cDNA encoding a C-20 oxidase polypeptide.
 XX
 KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
 KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
 KW seed germination; seedling growth; gibberellin biosynthetic pathway;
 KW transgenic plant; hypocotyl; epicotyl; PCR primer; ss.
 XX
 OS Cucurbita maxima.
 XX
 PN W0200009722-A2.

XX 24-FEB-2000.
 PD
 XX 10-AUG-1999; 99WO-US018066.
 PF
 XX 10-AUG-1998; 98US-0096111P.
 PR
 XX 07-JUN-1999; 99US-0137977P.
 PR
 XX (MONS) MONSANTO CO.
 PA
 XX Brown SM, Eich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
 PI Filler KJ, Rao S, Ream JE;
 PI
 XX WPI; 2000-224351/19.
 DR
 XX Obtaining transgenic plant useful for controlling seed germination and
 PT seedling growth comprises transgene comprising a sequence expressing
 PT altered levels of an essential hormone.
 XX
 PS Example 17; Page 262; 267pp; English.
 XX
 CC The present primer was used to reverse transcribe cDNA encoding a C-20
 CC oxidase. The amplifie fragment is used in the method of the invention.
 CC The specification describes methods for the inhibition and control of
 CC gibberellic acid levels. Gibberellic acid levels may be inhibited or
 CC controlled by use of a chimeric expression construct expressing a RNA or
 CC protein which suppresses the gibberellin biosynthetic pathway sequence,
 CC diverts substrate from the pathway, or degrades pathway substrates or
 CC products. The methods uses copalyl diphosphate synthase, 3beta-
 CC hydroxylase, 2-oxidase, phytoene synthase, C-20 oxidase, and a
 CC 2beta,3beta-hydroxylase polynucleotides to achieve this. The method is
 CC used to control seed germination and seedling growth especially to
 CC regulate gene products of gibberellin biosynthetic pathway and
 CC restoration of normal seed germination, in transgenic plants. The plants
 CC produced are gibberellin deficient, and have shortened hypocotyl and/or
 CC epicotyl phenotypes compared to normal plants
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
 :|||||
 DB 19 BAAAAAAAAAAAAAAAAAAAAA 1
 RESULT 517
 AAD15201/c
 ID AAD15201 standard; DNA; 19 BP.
 XX
 AC AAD15201;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE 3' sequencing primer #1 to identify and characterise polynucleotides.
 XX
 KW Fatty lesion development; atherosclerosis; Alzheimer's disease;
 KW nervous system disorder; Parkinson's disease; immune system disorder;
 KW ischaemia; lymphopaenia; leukocyte adhesion deficiency syndrome;
 KW haemoglobinuria; anaemia; hyperproliferative disorder; Gaucher's disease;
 KW coagulation disorder; blood platelet disorder; autoimmune disorder;
 KW dermatitis; herpes simplex; Addison's disease; rheumatoid arthritis;
 KW Grave's disease; gene therapy; antiarteriosclerotic; immunostimulant;
 KW cardiovascular; antiviral; primer; ss.
 XX
 OS Unidentified.
 XX
 PN W0200154651-A2.
 XX
 PD 02-AUG-2001.
 XX

PF 25-JAN-2001; 2001WO-US002439.
 PR 25-JAN-2000; 2000US-0177963P.
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX Leonardi A, Sartani A, Glass JR, Sutcliffe JG, Hasel KW;
 XX WPI; 2001-514526/56.
 DR New polynucleotides regulated by fatty lesion development and their
 PT encoded polypeptides, useful for preventing, treating or ameliorating
 PT atherosclerosis, as well as for immune or hyperproliferative disorders.
 XX Example 1; Page 79; 188pp; English.
 XX The present invention relates to an isolated nucleic acid regulated by
 CC fatty lesion development, which comprises any of 55 polynucleotide
 CC sequences from *Oryctolagus cuniculus*. The polynucleotide, polypeptide or
 CC antibody is useful for preventing, treating, modulating or ameliorating a
 CC medical condition, particularly atherosclerosis. The invention is used as
 CC a marker or detector of nervous system disorder or disease (e.g.
 CC Parkinson's disease, Alzheimer's disease, ischaemia, dementia). The
 CC invention may also be useful for treating deficiencies or disorders of
 CC the immune system (e.g. lymphopenia, leukocyte adhesion deficiency
 CC syndrome or haemoglobinuria, anaemia), hyperproliferative disorders
 CC (e.g. Gaucher's disease), infectious disease (e.g. herpes simplex),
 CC coagulation disorders, blood platelet disorders and autoimmune disorders
 CC (Addison's disease, rheumatoid arthritis, dermatitis, Grave's disease).
 CC The polynucleotide sequence is also used in gene therapy. The present
 CC sequence is a 3' sequencing primer used in the identification and
 CC characterisation of polynucleotides up-regulated by fatty lesion
 CC development
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA...AAAAAAAAA 1753
 Db 19 BAAAAA...AAAAAAAAA 1
 RESULT 518
 AAH21968/C
 ID AAH21968 standard; DNA; 19 BP.
 XX AAH21968;
 XX
 XX 16-AUG-2001 (first entry)
 XX
 DE Mouse total gene expression analysis (TOGA) 3' sequencing primer SEQ:92.
 XX Mouse; human; total gene expression analysis; TOGA; DST; EST;
 KW digital sequence tag; expressed sequence tag; neuroleptic; antimanic;
 KW central nervous system; antidepressant; gene therapy; diagnosis;
 KW neuropsychiatric disorder; schizophrenia; bipolar disorder;
 KW addiction-related behaviour; chromosome identification; immune response;
 KW PCR primer; probe; ss.
 XX
 XX Mus musculus.
 OS
 XX
 XX WO2000130972-A2.
 PN
 XX
 XX 03-MAY-2001.
 PD
 XX
 XX 26-OCT-2000; 2000WO-US029690.
 PF
 XX
 XX 26-OCT-1999; 99US-0161379P.
 PR
 XX
 XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush B, Hasel KW;
 XX WPI; 2001-300499/31.
 DR New neuroleptic-regulated polynucleotides expressed in the central
 PT nervous system for diagnosing and treating neuropsychiatric disorders
 PT such as schizophrenia, bipolar disorder and addiction-related behavior.
 XX
 XX Example 1; Page 87; 210pp; English.
 XX The present invention describes isolated neuroleptic-regulated nucleic
 CC acid molecules. (I) have neuroleptic, antimanic and antidepressant
 CC activities, and can be used in gene therapy. (I), polypeptides (II)
 CC encoded by (I), or a host cell (III) comprising (I), are useful for
 CC preventing, treating, modulating or ameliorating a medical condition such
 CC as a neuropsychiatric disorder. (I) are useful as diagnostic agents for
 CC diagnosing a pathological condition or susceptibility to a pathological
 CC condition such as neuropsychiatric disorder e.g. schizophrenia, a bipolar
 CC disorder or addiction-related behaviour. (I) are useful for detecting the
 CC presence of a nucleic acid encoding a protein in a mammalian tissue
 CC sample. (I) can be used as probes and primers, for chromosome
 CC identification, to control gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy to treat the above mentioned
 CC disorders, identifying individuals from minute biological samples, as an
 CC alternative to restriction fragment length polymorphism (RFLP) and as
 CC polymorphic markers for forensic purposes. (I) is also useful as
 CC molecular weight markers on Southern gels, diagnostic probes for the
 CC presence of specific mRNA in a particular cell type, as a probe to
 CC subtract-out known sequences in the process of discovering novel
 CC polynucleotides, for selecting and making oligomers for attachment to a
 CC gene chip or other support, to raise anti-DNA antibodies using DNA
 CC immunisation technique, and as an antigen to elicit an immune response.
 CC AAH21877 to AAH21984, AAB98083 and AAB98084 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA...AAAAAAAAA 1753
 Db 19 BAAAAA...AAAAAAAAA 1
 RESULT 519
 AAF76617/C
 ID AAF76617 standard; DNA; 19 BP.
 XX AAF76617;
 XX
 XX 15-MAY-2001 (first entry)
 DT
 XX
 DE Spearmint (-)-limonene-6-hydroxylase PCR primer SEQ ID NO: 18.
 KW Spearmint; peppermint; (-)-limonene-6-hydroxylase;
 KW (-)-limonene-3-hydroxylase; flavour; aroma; probe; PCR primer; ss.
 XX
 XX Mentha spicata.
 OS
 XX
 XX US6194185-B1.
 PN
 XX
 XX 27-FEB-2001.
 PD
 XX
 XX 14-APR-1999; 99US-00292768.
 PF
 XX
 XX 24-JUN-1997; 97US-00881784.
 PR
 XX
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 PA
 XX
 XX Croteau RB, Lupien SL, Karp F;

XX WPI; 2001-243405/25.
XX Novel isolated limonene hydroxylase encoding nucleic acid molecule,
PT useful for altering production of limonene-6-hydroxylase or limonene-3-
PT hydroxylase in suitable host cell.
XX
XX Example 4; Col 55; 57pp; English.
XX
XX The present invention provides the protein and coding sequences of the
CC peppermint and spearmint (-)-limonene-3-hydroxylase and the spearmint (-)
CC -limonene-6-hydroxylase. Also provided are a number of probes and PCR
CC primers which were used to isolate the sequences. These are useful in the
CC production of transgenic plants with altered flavour and aroma
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. NO. 2.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB :|||||
19 DAAAAAAAAAAAAAAAAA 1

RESULT 520
AAS06525/C
ID AAS06525 standard; DNA; 19 BP.
XX
AC AAS06525;
XX
DT 07-SEP-2001 (first entry)
XX
DE Mouse microglia and macrophage regulatory gene primer #60.
XX
KW Mouse; microglia; macrophage; regulatory gene; digital sequence tag; DST;
KW PCR-based total gene expression analysis; TOGA; infectious disorder;
KW neuroinflammatory pathology; neurodegenerative disease; gene therapy;
KW hyperproliferative disorder; autoimmune; inflammatory disorder; primer;
KW ss.
XX
OS Mus musculus.
XX
PN WO200134770-A2.
XX
PD 17-MAY-2001.
XX
PF 06-NOV-2000; 2000WO-US030585.
XX
PR 12-NOV-1999; 99WO-US026824.
PR 03-MAR-2000; 2000US-0186770P.
PR 19-JUN-2000; 2000US-0212465P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Carson MJ, Sutcliffe JG, Almazan MT, Tobal GW;
XX
DR WPI; 2001-308782/32.
XX
PT New regulated genes of microglia and macrophages, useful for diagnosing,
PT preventing or treating neuroinflammatory pathology and neurodegenerative
PT disease.
XX
PS Example 1; Page 88; 244pp; English.
XX
CC The present sequence represents a primer used to isolate novel mouse
CC microglia and macrophage regulatory gene DST (digital sequence tag)
CC sequences. AAS06401-AAS06590 represent these novel sequences and the
CC primer sequences used to isolate them. The PCR-based total gene
CC expression analysis (TOGA) system is used to examine the expression
CC pattern of molecules corresponding to genes that are regulated in
CC unstimulated microglia, activated microglia, unstimulated macrophage and

CC activated macrophage. The polynucleotides of the invention, the
CC polypeptides encoded by them and antibodies that bind to these
CC polypeptides are useful for the diagnosis, prevention,
CC treatment or amelioration of a medical condition, preferably a
CC neuroinflammatory pathology or a neurodegenerative disease such as
CC Alzheimer's disease, senile dementia, Parkinson's disease, obsessive
CC compulsive disorders, epilepsy, schizophrenia, multiple sclerosis,
CC depression and bipolar manic-depressive disorder. The sequences and
CC methods of the invention can also be used for detecting or treating
CC infectious disorders (e.g. AIDS), hyperproliferative disorders (e.g.
CC cancer), immune disorders (e.g. severe combined immunodeficiency, SCID)
CC autoimmune diseases (e.g. insulin dependent diabetes mellitus),
CC inflammatory disorders (e.g. arthritis). The polynucleotides can be used
XX for gene therapy
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. NO. 2.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
DB :|||||
19 BAAAAAAAAAAAAAAAAA 1

RESULT 521
ABK71509/c
ID ABK71509 standard; DNA; 19 BP.
XX
AC ABK71509;
XX
DT 30-JUL-2002 (first entry)
XX
DE CNS related 3' sequencing primer.
XX
KW Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
KW neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
KW Pick's disease; Binswanger's disease; senile dementia; encephalopathy;
KW Parkinson's disease; obsessive compulsive disorder; epilepsy; ischaemia;
KW addiction; multiple sclerosis; depression; manic-depressive disorder;
KW primer; ss.
XX
OS Synthetic.
XX
PN WO200226936-A2.
XX
PD 04-APR-2002.
XX
PF 01-OCT-2001; 2001WO-US030695.
XX
PR 29-SEP-2000; 2000US-0236790P.
PR 18-JAN-2001; 2001US-0263084P.
XX
PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX
PI Thomas EA, Sutcliffe JG, Pribyl TM, Hilbush BS, Hasel KW;
XX
DR WPI; 2002-383271/41.
XX
PT New polynucleotide useful in gene therapy for preventing, treating
PT modulating or ameliorating a medical condition such as psychoses or a
PT neuro psychiatric disorder e.g. schizophrenia, or a bipolar disorder in a
PT mammal.
XX
PS Example 1; Page 40; 254pp; English.
XX
CC This invention relates to the cDNA sequences of novel isolated
CC polynucleotides associated with psychoses or other neuropsychiatric
CC disorders. The sequences of the invention may act as blockers of D-2
CC receptors in the meso-limbic dopamine system. The nucleotide sequences of
CC the invention and the polypeptides encoded by them are useful in the
CC manufacture of a medicament useful for preventing, treating, modulating

CC or ameliorating a medical condition e.g. a neuropsychiatric disorder. An
 CC antibody that binds the proteins of the invention is useful for
 CC preventing, treating, modulating or ameliorating neurological disorders
 CC such as psychoses or other neuropsychiatric disorders in a subject. The
 CC sequences are also useful for diagnosing neurological disorders or a
 CC susceptibility to a neurological disorder such as psychoses and other
 CC neuro psychiatric disorders in a subject by determining the presence or
 CC absence of mutation in the nucleotide sequence of apolipoprotein B or by
 CC determining the alteration (increase or decrease) in the expression of
 CC apolipoprotein B. The sequences of the invention are useful in treating
 CC deficiencies or disorders of the central nervous system or peripheral
 CC nervous system by activating or inhibiting the proliferation,
 CC differentiation or mobilisation (chemotaxis) of neuroblasts, stem cells
 CC or glial cells. The sequences are useful as a marker or detector of a
 CC particular nervous system disease or disorder such as Alzheimer's
 CC disease, Pick's disease, Binswanger's disease, other senile dementia,
 CC Parkinson's disease, obsessive compulsive disorders, epilepsy,
 CC encephalopathy, ischaemia, addiction, multiple sclerosis, depression and
 CC manic-depressive disorder. The present sequence represents an
 CC oligonucleotide primer used in the identification of the cDNA sequences
 CC of the invention
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA...AAAAA 1753
 :|||||
 Db 19 BAAAAA...AAAAA 1

RESULT 522
 ABO73231/C
 ID ABO73231 standard; DNA; 19 BP.
 XX
 AC ABO73231;
 XX
 DT 27-SEP-2002 (first entry)
 XX
 DE Rabbit atherosclerosis related TOGA primer SEQ ID NO.26.
 XX
 KW Rabbit; Oryctolagus cuniculus; atherosclerosis; intimal hyperplasia;
 KW TOGA primer; ss.
 OS
 OS Oryctolagus cuniculus.
 OS Synthetic.
 XX
 FN WO200242420-A2.
 XX
 PD 30-MAY-2002.
 XX
 PF 21-NOV-2001; 2001WO-US044072.
 XX
 PR 21-NOV-2000; 2000US-0252216P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Leonardi A, Sartani A, Glass JR, Hasel KW;
 XX
 DR WPI; 2002-575233/61.

XX New polynucleotides related to regulated genes characteristic of
 PT atherosclerosis, useful for diagnosing, preventing, treating, modulating
 PT or ameliorating atherosclerosis in a mammalian subject.
 XX
 PS Disclosure; Page 28; 130pp; English.
 XX
 CC The present invention describes an isolated polynucleotide (I) and its
 CC complements, and degenerate variants, comprising a sequence selected from
 CC those given in ABO73206 to ABO73222 (NS), which is a digital sequence tag
 CC (DST) corresponding to mRNAs whose expression is regulated by

CC proliferative lesion development caused by mechanically induced intimal
 CC hyperplasia, or by lercanidipine treatment, or by proliferative lesions
 CC and reversed by lercanidipine treatment. (I) has antiatherosclerotic
 CC activity and can be used in gene therapy. (I) can be used for diagnosing
 CC a medical condition (e.g. atherosclerosis) in a subject which involves
 CC determining the presence or absence of a mutation in (I) and diagnosing
 CC the medical condition based on the presence or absence of the mutation.
 CC (I) is also useful for diagnosing atherosclerosis, or the susceptibility
 CC to atherosclerosis in a subject which involves detecting an alteration
 CC (an increase or decrease) in amount of expression of (I). (I) is also
 CC useful for diagnosing or monitoring the effects of treating a subject
 CC with dihydropyridine calcium antagonist e.g., lercanidipine. (I) can also
 CC be used for preventing, treating, modulating, or ameliorating a medical
 CC condition such as atherosclerosis in a mammalian subject. The present
 CC sequence represents a TOGA primer which is used in the exemplification of
 CC the present invention
 XX

SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA...AAAAA 1753
 :|||||
 Db 19 BAAAAA...AAAAA 1

RESULT 523
 AAD34663/C
 ID AAD34663 standard; DNA; 19 BP.
 XX
 AC AAD34663;
 XX
 DT 16-JUL-2002 (first entry)
 XX
 DE PCR primer #4 used for direct sequencing of TOGA generated PCR products.
 XX
 KW Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virucide;
 KW acute hepatitis; therapeutic; gene therapy; vaccine; infectious disease;
 KW TOGA; Total Gene Expression Analysis; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 FN WO200222783-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 17-SEP-2001; 2001WO-US029123.
 XX
 PR 15-SEP-2000; 2000US-0233176P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Chisari FV, Wieland SF, Guidotti LGDM, Mueller R, Hilbush BS;
 XX
 DR WPI; 2002-339865/37.

XX Preventing and treating hepatitis viral infection in a mammal, comprises
 PT administering nucleic acid molecules that up- or down-regulate in
 PT hepatitis B virus infection or polypeptides encoded by the nucleic acid
 PT molecules.
 XX
 PS Disclosure; Page 28; 125pp; English.
 XX
 CC The present invention relates to a method for preventing, treating,
 CC modulating or ameliorating a medical condition. The method involves
 CC administering one or more nucleic acid molecules up- or down-regulated in
 CC hepatitis B virus (HBV) infection or polypeptides encoded by the nucleic
 CC acid molecules or antibodies that bind to the polypeptide. The method is
 CC useful for preventing, treating, modulating or ameliorating a medical
 CC condition. It is also useful for determining the presence or absence of a
 CC mutation in the nucleic acid molecules or detecting an alteration in

expression of the polypeptide which is useful for the diagnosis of hepatitis viral infection. The method is useful for assessing the stage of hepatitis viral infection (e.g., acute hepatitis versus chronic hepatitis) or assessing the efficacy or toxicity of therapeutic treatment for hepatitis viral infection and a gene expression profile is useful for identifying polypeptides and polynucleotides which are associated with hepatitis viral infection. Sequences of the invention are used in gene therapy and as vaccines. Nucleic acid sequences are useful as a diagnostic markers for HBV infection and for treating infectious diseases. The present DNA sequence is a PCR primer which is used for direct sequencing of TOGA (Total Gene Expression Analysis) generated PCR products

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
:|||||
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 524
AAD40279/c
ID AAD40279 standard; DNA; 19 BP.
AC AAD40279;
XX
DT 22-OCT-2002 (first entry)
XX
DE HOOK PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA.
XX
KW Gibberellin; transgenic plant; seed germination; seedling growth; GA;
KW transgenic; 2beta-3beta hydroxylase; enzyme; pumpkin; PCR; primer; ss.
XX
OS Cucurbita pepo.
XX
PN US2002053095-A1.
XX
PD 02-MAY-2002.
XX
PF 10-AUG-1999; 99US-00371307.
XX
PR 10-AUG-1999; 99US-00371307.
XX
PA (BROW/) BROWN S M.
XX
PI Brown SM, Elich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
PI Piller KJ, Rao S, Ream JE;
XX
DR WPI; 2002-489107/52.
XX
XX Control of gibberellin levels in plants useful to avoid unfavorable conditions in crops to increase yields, using transgenic plants having reduced seed germination and early seedling growth then treatment to restore these properties.
XX
XX Example 19; Page 104; 155pp; English.
XX
XX The invention relates to control of gibberellin (GA) levels in plants. The method involves producing transgenic plants having a phenotype of reduced seed germination and reduced early seedling growth, then restoring seed germination and early seedling growth by treating plants with an appropriate compound when conditions are favourable. The method is useful to control seed germination and/or early seedling growth in agricultural production so that unfavorable environmental conditions normally reducing agronomic output can be avoided and yields increased. Plants also demonstrate increased uniformity of germination, emergence and seedling vigor, so increasing yields at harvest. The method is especially useful in crop plants such as e.g. canola, soybean, cotton, etc., and is also useful in storage and transport of seeds to reduce

premature germination which may affect agronomic or food quality of the seeds. The present sequence is a PCR primer used to isolate pumpkin 2beta-3beta hydroxylase cDNA. This primer is used in the exemplification of the invention

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
:|||||
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 525
ABZ68389/c
ID ABZ68389 standard; DNA; 19 BP.
XX
AC ABZ68389;
XX
DT 22-APR-2003 (first entry)
XX
DE Reverse transcription primer used to produce yeast cDNA.
XX
KW Histone acetyltransferase; histone deacetylase; gene expression profile; chromatin-associated protein; gene expression; primer; ss.
XX
OS Synthetic.
XX
PN WO2003000715-A1.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019750.
XX
PR 22-JUN-2001; 2001US-0300135P.
XX
PA (CERE-) CERES INC.
XX
PI Dang V, Okamuro J;
XX
DR WPI; 2003-175280/17.
XX
PT New chimeric polypeptide comprising a histone acetyltransferase polypeptide segment and a segment comprising a histone deacetylase chromatin-associated protein complex subunit, useful for modulating gene expression in cells.
XX
PS Example 10; Page 54; 85pp; English.
XX
XX The specification describes chimeric histone acetyltransferase polypeptides. The chimeric polypeptides comprise a polypeptide segment that exhibits histone acetyltransferase activity, and a polypeptide segment having 40% or greater sequence identity to a subunit of a histone deacetylase chromatin-associated protein complex. The chimeric polypeptides are useful for determining gene expression profiles in specific cells, for modulating gene expression in specific cells, and for making genetically modified eukaryotes. The present sequence represents a reverse transcription primer used in the method of the invention

Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAAAAAA 1753
:|||||
Db 19 BAAAAAAAAAAAAAAAAAAAAA 1

RESULT 526
 ID ACC79402/c standard; DNA; 19 BP.
 AC ACC79402;
 DT 04-AUG-2003 (first entry)
 XX
 DE M13 sequencing primer 3' primer SEQ ID NO:84.
 XX
 KW Pathological condition; ataxia telangiectasia; AT; tumour; cancer;
 KW cytostatic; vaccine; gene therapy; PCR primer; ss.
 XX
 OS Enterobacteria phage M13.
 OS Synthetic.
 XX
 PN WO2003033668-A2.
 XX
 PD 24-APR-2003.
 XX
 PF 17-OCT-2002; 2002WO-US033311.
 XX
 PR 17-OCT-2001; 2001US-0330206P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Barlow C, Winrow CJ, Callahan MLA, Pankratz DG, Vibat CRT;
 PI Warren AJ;
 XX
 DR WPI; 2003-393520/37.
 XX
 XX Preventing or treating a pathological condition e.g., ataxia
 PT telangiectasia (AT), AT tumors or other cancers comprises administering
 PT polynucleotides.
 XX
 PS Example 1; Page 76; 184pp; English.
 XX
 CC The present invention describes a method for preventing or treating a
 CC pathological condition (comprising ataxia telangiectasia (AT), AT tumors
 CC or other cancers), which comprises administering to a mammalian subject
 CC at least one of: (a) a first polynucleotide comprising a sequence having
 CC 38-889 bp (consisting of the sequences in ACC79319 to ACC79392 (I)) or a
 CC second polynucleotide at least 95% identical to the first polynucleotide;
 CC (b) a third polynucleotide comprising at least 10-bp sequence that is
 CC hybridisable to the first polynucleotide under stringent conditions; or
 CC (c) a gene corresponding to any of (1)-(2) or another gene at least 95%
 CC identical to the gene. (I) have cytostatic activities, and can be used in
 CC vaccines and in gene therapy. The method is useful for preventing or
 CC treating e.g., ataxia telangiectasia (AT), AT tumors or other cancers.
 CC ACC79393 to ACC79423 represent primers used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAA 1753
 Db :||||| AAAAAAAAAA 1
 19 BAAAAA AAAAAAAAAA 1
 RESULT 527
 AAD49149/c
 ID AAD49149 standard; DNA; 19 BP.
 XX
 AC AAD49149;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE 3' sequencing primer #1 used in the invention.
 XX
 KW Gene expression; drug interaction mechanism; drug screening; primer;
 KW genomic mapping; ss.

KW Atherosclerosis; vaccine; nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; multiple sclerosis; immune disorder; gene therapy;
 KW autoimmune disorder; rheumatoid arthritis; hyperproliferative disorder;
 KW haemolytic anaemia; graft-versus-host disease; inflammation; infection;
 KW epilepsy; Addison's disease; neoplasm; tissue regeneration; chemotaxis;
 KW food additive; food preservative; primer; ss.
 XX
 OS Unidentified.
 XX
 PN WO200281726-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 15-NOV-2001; 2001WO-US043741.
 XX
 PR 15-NOV-2000; 2000US-0248892P.
 XX
 PR 28-NOV-2000; 2000US-0253623P.
 XX
 PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
 XX
 PI Leonardi A, Sartani A, Glass J, Sutcliffe JG, Hasel KW;
 XX WPI; 2003-058561/05.
 DR
 XX New polypeptide associated with atherosclerosis, useful for treating
 PT atherosclerosis, nervous system disorders, immune disorders,
 PT hyperproliferative disorders and infectious diseases.
 XX
 PS Disclosure; Page 139; 146pp; English.
 XX
 CC The invention relates to polynucleotides and polypeptides associated with
 CC atherosclerosis. Polynucleotides of the invention are useful for delivery
 CC of genes, DNA vaccines, diagnostic reagents, peptides, proteins or
 CC macromolecules. Sequences of the invention are useful for treating
 CC nervous system disorders (e.g., Alzheimer's disease, Parkinson's disease,
 CC multiple sclerosis, epilepsy), immune disorders (e.g., autoimmune
 CC disorders such as rheumatoid arthritis, Addison's disease, haemolytic
 CC anaemia, graft-versus-host disease, inflammation), hyperproliferative
 CC disorders (e.g., neoplasms) and infectious diseases (e.g., viral,
 CC bacterial, fungal or parasite infection). They are used for regeneration
 CC of tissues, to repair or replace or protect damage tissues, for increasing
 CC chemotaxis activity of cells, for increasing or decreasing the
 CC differentiation or proliferation of embryonic stem cells from a lineage,
 CC for modulating mammalian characteristics, (such as body weight or
 CC height), for modulating mammalian metabolism affecting catabolism,
 CC anabolism, processing utilisation and storage of energy, to change a
 CC mammal's mental or physical state, or as a food additive or preservative.
 CC The invention is useful in gene therapy. The present sequence is a
 CC sequencing primer used in the invention
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
 Query Match 1.0%; Score 18.2; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 2.6e+02;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAA 1753
 Db :||||| AAAAAAAAAA 1
 19 BAAAAA AAAAAAAAAA 1
 RESULT 528
 AAD50267/c
 ID AAD50267 standard; DNA; 19 BP.
 XX
 AC AAD50267;
 XX
 DT 24-MAR-2003 (first entry)
 XX
 DE 3' sequencing primer #1 used to illustrate the method of the invention.
 XX
 KW Gene expression; drug interaction mechanism; drug screening; primer;
 KW genomic mapping; ss.

XX OS Unidentified.
XX PN WO200261045-A2.
XX PD 08-AUG-2002.
XX PF 01-FEB-2002; 2002WO-US002666.
XX PR 01-FEB-2001; 2001US-00775217.
XX PA (DIGI-) DIGITAL GENE TECHNOLOGIES INC.
XX PI (QUAN/) QUAN J.
XX PI Quan J., Hilbush BS, Hasel KWPD, Sutcliffe GJ, Chang HW;
XX PI Callahan MA;
XX DR WPI; 2003-092784/08.
XX PT Simplified TOGA method for simultaneous sequence-specific identification
XX PT of multiple mRNA molecules in mRNA population, useful for determining
XX PT tissue-specific patterns of gene expression or mechanisms of drug
XX PT interaction.
XX PS Disclosure; Page 39; 93pp; English.
XX CC The present invention relates to a novel simplified TOGA (RTM) method for
XX CC simultaneous sequence-specific identification of multiple mRNA molecules
XX CC in a RNA population. The method involves characterising each of the
XX CC sequence-specific polymerase chain reaction (PCR) products by partial
XX CC sequence and length. The method is useful for determining tissue-specific
XX CC patterns of gene expression or mechanisms of drug interaction. It is also
XX CC useful for drug screening, studying physiological processes, genomic
XX CC mapping or manufacture of diagnostic, prognostic or therapeutic reagents.
XX CC The present sequence is a primer used to illustrate the method of the
XX CC invention
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1753
DB 19 BAAAAA AAAAAAAAAA 1
RESULT 529
ADC21495/c
ID ADC21495 standard; DNA; 19 BP.
XX AC ADC21495;
XX DT 18-DEC-2003 (first entry)
XX DE Human PRDI-BF1 RT-PCR primer.
XX KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
XX KW multiple myeloma cell; human; PRDI-BF1;
XX KW positive regulatory domain I-binding factor-1; MHC;
XX KW major histocompatibility complex Class I; cytostatic; vaccine; ss;
XX KW primer; PCR.
XX OS Homo sapiens.
XX PN WO2003029282-A2.
XX PD 10-APR-2003.
XX PF 24-SEP-2002; 2002WO-EP010701.
XX PR 29-SEP-2001; 2001DE-01048236.

XX PA (IMMU-) IMMUGENICS AG.
XX PI Theobald M, Lotz C;
XX DR WPI; 2003-354724/33.
XX PT New tumor-associated oligopeptide, useful particularly for treating
XX PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also
XX PT derivatives and related nucleic acid.
XX PS Disclosure; Page 22; 64pp; German.
XX CC This invention describes a novel tumor-associated oligopeptide that is
XX CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
XX CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
XX CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
XX CC regulatory domain I-binding factor-1) which is able to induce an MHC
XX CC (major histocompatibility complex) Class I allele variant A2-restricted
XX CC immune response of CD8+ CTL against tumor cells. The products of the
XX CC invention have cytostatic activity and can be used in a vaccine. The
XX CC peptide of the invention, also related retro-inverse and pseudopeptides,
XX CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
XX CC and T cell receptors specific for PRDI-BF1 peptides are useful for
XX CC treating diseases associated with PRDI-BF1, particularly tumors. The
XX CC products of the invention are also useful as diagnostic, therapeutic and
XX CC prophylactic agents for detecting, modifying, generating, expanding
XX CC and/or regulating activation and functional status of T cells, and for
XX CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell
XX CC receptors and their functional equivalents. This sequence represents an
XX CC RT-PCR primer used to amplify the human PRDI-BF1 gene described in the
XX CC invention.
XX SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
Query Match 1.0%; Score 18.2; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 2.6e+02;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1753
DB 19 BAAAAA AAAAAAAAAA 1
RESULT 530
AAZ09197/c
ID AAZ09197 standard; DNA; 20 BP.
XX AC AAZ09197;
XX DT 19-OCT-1999 (first entry)
XX DE Oligonucleotide 9 for DNA analysis.
XX KW Primer; DNA analysis; amplification; hybridisation; ss.
XX OS Synthetic.
XX PN JP11196874-A.
XX PD 27-JUL-1999.
XX PF 14-JAN-1998; 98JP-000053399.
XX PR 14-JAN-1998; 98JP-000053399.
XX PA (HITA) HITACHI LTD.
XX DR WPI; 1999-496652/42.
XX PT Analysis of DNA fragment - comprises addition of known common
XX PT oligonucleotide, amplification of resultant DNA fragment and analysis and
XX PT labelling of amplified DNA.

XX Example 5; Page 12; 17pp; Japanese.

PS This invention describes a novel method for the analysis of a DNA fragment

CC which comprises: (i) addition of a known common oligonucleotide sequence

CC to at least one terminal of each DNA fragment, (ii) amplification of the

CC resultant DNA fragment as a primer using a first common primer containing

CC a complementary nucleotide sequence to the above mentioned known common

CC oligonucleotide sequence, a second common primer containing a

CC complementary nucleotide sequence to the prepared known common

CC oligonucleotide sequence optionally having been introduced with

CC complementary nucleotide sequence at a terminal, and a specific primer

CC capable of hybridisation with a DNA fragment containing whole or part of

CC the gene having known sequence, to give amplified DNA, (iii) analysis of

CC the amplified DNA to find the information of the DNA fragment, in which

CC the specific primer is designed to prepare fragments of the common first

CC and second primers and to give short fragment of amplified DNA and (iv)

CC labelling them to make their differentiation. Differentiation of

CC informations of known and unknown genes readily provides information of

CC unknown gene and simultaneous monitoring of signals derived from minor

CC genes. Furthermore, labelling of DNAs according to functions of known

CC genes can be performed. AAQ09189-209201 represent oligonucleotide primers

CC used to illustrate the method of the invention

XX SQ Sequence 20 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 2 Other;

Query Match 1.0%; Score 18.2; DB 1; Length 20;

Best Local Similarity 94.7%; Pred. No. 2.7e+02;

Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1753

Db 19 BAAAAA AAAAAAAAAA 1

RESULT 531

AAQ34110

ID AAQ34110 standard; DNA; 18 BP.

XX AC AAQ34110;

XX 25-MAR-2003 (revised)

DT 02-FEB-1993 (first entry)

XX Sequence of a microsatellite from clone TGLA60B.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;

KW genetic mapping; traits; amplification; ss.

XX Bos taurus.

OS

XX WO9213102-A1.

PN 06-AUG-1992.

FD 15-JAN-1992; 92WO-US000340.

XX 15-JAN-1991; 91US-00642342.

PR (GENM-) GENMARK.

XX Georges M, Massey JM;

PI WPI; 1992-284684/34.

DR Polymorphic bovine DNA markers - used in genetic identification, gene

PT mapping, and selective breeding.

XX Table 7; Page 375; 517pp; English.

PS The sequence is that of a bovine microsatellite sequence obd. by

CC screening a library of bovine MboI DNA fragments of between 250 and 500

CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50

CC

CC clones cross-hybridised. Assuming independent distribution of

CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites

CC in the bovine genome is estimated at >100, 000. The sequence information

CC for ca. 230 such bovine microsatellites is summarised in the

CC specification and indexed herein (see below). The sequences upstream and

CC downstream of the microsatellite sequence were used to generate the

CC required PCR primers for in vitro amplification of the corresp.

CC microsatellite (using the program OPTIPRIM). The microsatellites may be

CC used to identify individuals, for parentage testing, and in the genetic

CC mapping of economic trait loci, or genes involved the determination of

CC economically important traits esp. in cattle, to allow selective

CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA AAAAAAAAAA 1753

Db 1 AAAAAA AAAAAAAAAA 18

RESULT 532

AAQ75025/C

ID AAQ75025 standard; RNA; 18 BP.

XX AC AAQ75025;

XX 25-MAR-2003 (revised)

DT 03-AUG-1995 (first entry)

XX PCR primer.

DE Synthetic oligo; solid phase immunoassay; ss.

XX Synthetic.

OS WO9426932-A1.

PN 24-NOV-1994.

FD 13-MAY-1994; 94WO-US005407.

PF 13-MAY-1993; 93US-00061694.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Fields HA, Khudyakov YE;

PI WPI; 1995-006819/01.

DR Solid phase immunoassay using oligo:nucleotide as label - also new

XX conjugates of oligo:nucleotide coupled to antigenic peptide, partic. for

PT diagnosing hepatitis C or E virus infection.

XX Example; Page 12; 34pp; English.

PS AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.

CC They are used in a method for detecting an antigen in a subject. The

CC method involves binding the antigen to a solid support and then reacting

CC it with an immunoreactive ligand (L) bound to an oligo; removing any

CC unreacted L, and then detecting the presence of the oligo. A similar

CC method can be used to detect Abs, in which case the ligand is an oligo-

CC labelled Ag. The use of an amplifiable oligo as the label allows Ag or Ab

CC to be detected at very low levels. An exemplary oligo is AAQ75024 which

CC can be covalently attached by the 5'-terminus to the N- or C-terminal of

CC a synthetic peptide. In the example, peptide AAR62941 was coupled to

CC oligo AAQ75024 using disuccinimidyl suberate. Serum samples suspected to

CC contain HEV Abs were immobilised on plastic tubes or wells, then

CC incubated for 30-60 mins with the peptide-oligo product. The vessels were

RESULT 534


```

XX DT 14-JUN-1999 (first entry)
XX DE Primer SEQ ID NO:3 from JP11075880.
XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX OS Synthetic.
XX PN JP11075880-A.
XX PD 23-MAR-1999.
XX PF 10-JUL-1998; 98JP-00195719.
XX PR 14-JUL-1997; 97JP-00205378.
XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 1999-257710/22.
XX PT Labelling of an oligonucleotide - useful for detecting genes.
XX PS Example 1; Page 7; 10pp; Japanese.
XX CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1736 AAAAAAAAAAAAAAAAAA 1753
XX Db 18 AAAAAAAAAAAAAAAAAA 1
XX RESULT 536
XX AAX19942
XX ID AAX19942 standard; DNA; 18 BP.
XX AC AAX19942;
XX DT 14-JUN-1999 (first entry)
XX DE Primer SEQ ID NO:2 from JP11075880.
XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX OS Synthetic.
XX PN JP11075880-A.
XX PD 23-MAR-1999.
XX PF 10-JUL-1998; 98JP-00195719.
XX PR 14-JUL-1997; 97JP-00205378.
XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 1999-257710/22.
XX DT 14-JUN-1999 (first entry)
XX DE Primer SEQ ID NO:3 from JP11075880.
XX KW Primer; oligonucleotide; labelling; detection; self-priming; PCR; ss.
XX OS Synthetic.
XX PN JP11075880-A.
XX PD 23-MAR-1999.
XX PF 10-JUL-1998; 98JP-00195719.
XX PR 14-JUL-1997; 97JP-00205378.
XX PA (KAGA) ZH KAGAKU & KESSEI RYOHO KENKYUSHO.
XX DR WPI; 1999-257710/22.
XX
XX PT Labelling of an oligonucleotide - useful for detecting genes.
XX PS Example 1; Page 7; 10pp; Japanese.
XX CC A method has been developed for labelling an oligonucleotide having a
CC repeated sequence of (XY)n (where X and Y consists of a combination of
CC adenine and thymine or uracil or guanine and cytosine, and n is an
CC integer of 1 or more) at the 3'-terminal side in which the repeated
CC sequence is added and extended using a labelled body of the nucleotide
CC constituting the repeated sequence and a DNA polymerase lacked in 5' to
CC 3' exonuclease activity. The method can be used for detecting a gene. The
CC method can detect a gene in a sensitivity up to ten times higher than
CC prior art methods. The present sequence represents a primer used in an
CC example from the present invention
XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 18; DB 1; Length 18;
XX Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX Qy 1736 AAAAAAAAAAAAAAAAAA 1753
XX Db 18 AAAAAAAAAAAAAAAAAA 1
XX RESULT 537
XX AAZ87161
XX ID AAZ87161 standard; RNA; 18 BP.
XX AC AAZ87161;
XX DT 08-MAY-2000 (first entry)
XX DE Oligoarabinonucleotide SEQ ID NO:2.
XX KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
XX reverse transcription; viral replication; RNase H cleavage;
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT modified_base 1..18
XX FT /*tag= a
XX FT /note= "Ribose moiety replaced by beta-D-arabinose"
XX PN WO9967378-A1.
XX XX 29-DEC-1999.
XX PF 17-JUN-1999; 99WO-CA000571.
XX PR 19-JUN-1998; 98CA-02241361.
XX PA (UYMC-) UNIV MCGILL.
XX PI Danha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
XX DR WPI; 2000-160584/14.
XX PT Therapeutic composition containing antisense oligonucleotides that
XX include arabinose sugars, particularly for inhibiting viral replication.
XX PS Example 1; Page 29; 91pp; English.
XX CC The invention relates to a new composition for selective, sequence-
XX specific inhibition of gene transcription and expression in a host. The
XX composition comprises oligonucleotides containing arabinose sugars that
XX can hybridise to either a single-stranded (ss) RNA to induce RNase H
XX cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
XX helix, thereby inhibiting DNA replication and/or transcription. The
XX oligoarabinonucleotides are used for antisense inhibition of gene

```

CC expression or to prevent DNA replication, or reverse transcription of RNA
 CC by retroviruses. The compositions are therefore particularly used to
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be
 CC used, in combination with RNase H, as reagents for sequence-specific
 CC cleavage or RNA mapping, and additionally for the study and control of
 CC gene expression in cells. The oligoarabinonucleotides have excellent
 CC affinity for RNA, increased resistance to nucleases and show little if
 CC any non-specific binding to cellular or serum proteins. They target ss
 CC RNA, but not complementary ss DNA, so may be useful for targeting
 CC retroviral genomic RNA to inhibit the early stages of viral replication.
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
 CC with significantly higher thermal stability than those produced by normal
 CC oligonucleotides. Sequences AA287160-287164 represent
 CC oligoarabinonucleotides containing beta-D-arabinose used in an
 CC exemplification of the present invention
 XX
 SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
 |||||
 DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 538
 AA287162/c
 ID AA287162 standard; RNA; 18 BP.
 AC AA287162;
 DT 08-MAY-2000 (first entry)
 XX
 DE Oligoarabinonucleotide SEQ ID NO:3.
 XX
 KW Beta-D-arabinose; antisense; inhibition; transcription; expression;
 KW reverse transcription; viral replication; RNase H cleavage;
 KW triple helix formation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..18
 FT /tag= a
 FT /note= "Ribose moiety replaced by beta-D-arabinose"
 XX
 PN WO9967378-A1.
 XX
 XX 29-DEC-1999.
 XX
 PF 17-JUN-1999; 99WO-CA000571.
 XX
 PR 19-JUN-1998; 98CA-02241361.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
 XX
 DR WPI; 2000-160584/14.
 XX
 PT Therapeutic composition containing antisense oligonucleotides that
 PT include arabinose sugars, particularly for inhibiting viral replication.
 XX
 PS Example 1; Page 29; 91pp; English.
 XX

CC The invention relates to a new composition for selective, sequence-
 CC specific inhibition of gene transcription and expression in a host. The
 CC composition comprises oligonucleotides containing arabinose sugars that
 CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
 CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
 CC helix, thereby inhibiting RNA replication and/or transcription. The

CC oligoarabinonucleotides are used for antisense inhibition of gene
 CC expression or to prevent DNA replication, or reverse transcription of RNA
 CC by retroviruses. The compositions are therefore particularly used to
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be
 CC used, in combination with RNase H, as reagents for sequence-specific
 CC cleavage or RNA mapping, and additionally for the study and control of
 CC gene expression in cells. The oligoarabinonucleotides have excellent
 CC affinity for RNA, increased resistance to nucleases and show little if
 CC any non-specific binding to cellular or serum proteins. They target ss
 CC RNA, but not complementary ss DNA, so may be useful for targeting
 CC retroviral genomic RNA to inhibit the early stages of viral replication.
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
 CC with significantly higher thermal stability than those produced by normal
 CC oligonucleotides. Sequences AA287160-287164 represent
 CC oligoarabinonucleotides containing beta-D-arabinose used in an
 CC exemplification of the present invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 0 T; 18 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
 |||||
 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 539
 AA287166/c
 ID AA287166 standard; DNA; 18 BP.
 AC AA287166;
 XX
 DT 08-MAY-2000 (first entry)
 XX
 DE Deoxyarabinonucleotide SEQ ID NO:7.
 XX
 KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
 KW transcription; expression; reverse transcription; viral replication;
 KW RNase H cleavage; triple helix formation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..18
 FT /tag= a
 FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
 fluoro-beta-D-arabinose"
 XX
 PN WO9967378-A1.
 XX
 XX 29-DEC-1999.
 XX
 PF 17-JUN-1999; 99WO-CA000571.
 XX
 PR 19-JUN-1998; 98CA-02241361.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Arion D;
 XX
 DR WPI; 2000-160584/14.
 XX
 PT Therapeutic composition containing antisense oligonucleotides that
 PT include arabinose sugars, particularly for inhibiting viral replication.
 XX
 PS Example 2; Page 31; 91pp; English.
 XX

CC The invention relates to a new composition for selective, sequence-
 CC specific inhibition of gene transcription and expression in a host. The
 CC composition comprises oligonucleotides containing arabinose sugars that
 CC can hybridise to either a single-stranded (ss) RNA to induce RNase H

CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
 CC helix, thereby inhibiting DNA replication and/or transcription. The
 CC oligoarabinonucleotides are used for antisense inhibition of gene
 CC expression or to prevent DNA replication, or reverse transcription of RNA
 CC by retroviruses. The compositions are therefore particularly used to
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be
 CC used, in combination with RNase H, as reagents for sequence-specific
 CC cleavage or RNA mapping, and additionally for the study and control of
 CC gene expression in cells. The oligoarabinonucleotides have excellent
 CC affinity for RNA, increased resistance to nucleases and show little if
 CC any non-specific binding to cellular or serum proteins. They target ss
 CC RNA, but not complementary ss DNA, so may be useful for targeting
 CC retroviral genomic RNA to inhibit the early stages of viral replication.
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
 CC with significantly higher thermal stability than those produced by normal
 CC oligodeoxynucleotides. Sequences AAZ87165-287169 represent
 CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
 CC arabinose used in an exemplification of the present invention
 XX
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 540

AAZ87167
 ID AAZ87167 standard; DNA; 18 BP.

AC AAZ87167;

DT 08-MAY-2000 (first entry)

DE Deoxyarabinonucleotide SEQ ID NO:8.

KW 2'-deoxy-2'-fluoro-beta-D-arabinose; antisense; inhibition;
 KW transcription; expression; reverse transcription; viral replication;
 KW RNase H cleavage; triple helix formation; ss.

OS Synthetic.

FH Key Location/Qualifiers
 FT modified_base 1..18

FT /tag= a
 FT /note= "Deoxyribose moiety replaced by 2'-deoxy-2'-
 FT fluoro-beta-D-arabinose"

PN WO9967378-A1.

PD 29-DEC-1999.

PF 17-JUN-1999; 99WO-CA000571.

PR 19-JUN-1998; 98CA-02241361.

PA (UWMC-) UNIV MCGILL.

PI Damha MJ, Parniak MA, Noronha AM, Wilds C, Borkow G, Azion D;

DR WPI; 2000-160584/14.

XX Therapeutic composition containing antisense oligonucleotides that
 PT include arabinose sugars, particularly for inhibiting viral replication.

PS Example 2; Page 31; 91pp; English.

XX The invention relates to a new composition for selective, sequence-
 CC specific inhibition of gene transcription and expression in a host. The

CC composition comprises oligonucleotides containing arabinose sugars that
 CC can hybridise to either a single-stranded (ss) RNA to induce RNase H
 CC cleavage activity, or to a DNA/DNA or DNA/RNA duplex to form a triple
 CC helix, thereby inhibiting DNA replication and/or transcription. The
 CC oligoarabinonucleotides are used for antisense inhibition of gene
 CC expression or to prevent DNA replication, or reverse transcription of RNA
 CC by retroviruses. The compositions are therefore particularly used to
 CC inhibit retroviral replication. The oligoarabinonucleotides can also be
 CC used, in combination with RNase H, as reagents for sequence-specific
 CC cleavage or RNA mapping, and additionally for the study and control of
 CC gene expression in cells. The oligoarabinonucleotides have excellent
 CC affinity for RNA, increased resistance to nucleases and show little if
 CC any non-specific binding to cellular or serum proteins. They target ss
 CC RNA, but not complementary ss DNA, so may be useful for targeting
 CC retroviral genomic RNA to inhibit the early stages of viral replication.
 CC Oligoarabinonucleotides containing pyrimidine bases form triple helices
 CC with significantly higher thermal stability than those produced by normal
 CC oligonucleotides. Sequences AAZ87165-287169 represent
 CC oligodeoxyarabinonucleotides containing 2'-deoxy-2'-fluoro-beta-D-
 CC arabinose used in an exemplification of the present invention
 XX
 XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753

Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 541

AAZ03565/C

ID AAZ03565 standard; DNA; 18 BP.

AC AAZ03565;

DT 19-JUN-2001 (first entry)

DE Oligonucleotide #6 used for the preparation of normalised cDNA libraries.

KW Rat; secreted factor; clone P00188 D12; cardiant; antiinflammatory;
 KW antiarrhythmic; antiarteriosclerotic; antiatherosclerotic; nephropathic;
 KW antidiabetic; immunosuppressive; antiasthmatic; antirheumatoid;
 KW antibacterial; osteopathic; cerebroprotective; vasotropic; antitumor;
 KW neurotropic; neuroprotective; congestive heart failure; myocardial;
 KW hypertrophic cardiomyopathy; angina pectoris; myocardial infarction;
 KW kidney disease; acute renal failure; renal glucosuria; renal infarction;
 KW polycystic kidney disease; hereditary nephritis; inflammatory disease;
 KW tumour angiogenesis; osteoarthritis; toxic shock syndrome; psoriasis;
 KW stroke; neural trauma; cerebral malaria; Crohn's disease; osteoporosis;
 KW ulcerative colitis; Alzheimer's disease; gene therapy; ss.

OS Rattus norvegicus.

PN W0200123564-A1.

PD 05-APR-2001.

PF 27-SEP-2000; 2000WO-US026544.

PR 27-SEP-1999; 99US-0156280P.

PA (SCIO-) SCIOS INC.

PI Stanton LW, Kapoun AM;

DR WPI; 2001-266159/27.

XX Novel secreted factor encoded by clone P00188D12 which is differentially
 PT expressed in certain disease states, useful in diagnosing and treating
 CC cardiac, renal or inflammatory diseases.

XX Example 1; Page 42; 71pp; English.

XX The patent discloses novel secreted factor protein encoded by clone

CC P00188_D12. The secreted factor is differentially expressed in certain

CC disease states. Secreted protein, its antibodies, antagonists or

CC compositions comprising them are useful in the diagnosis and treatment of

CC cardiac diseases such as congestive heart failure, myocarditis,

CC hypertrophic cardiomyopathy, angina pectoris, myocardial infarction,

CC cardiac arrhythmia, arteriosclerosis, kidney diseases such as acute renal

CC failure, renal glucosuria, renal infarction, nephrogenic diabetes

CC insipidus, polycystic kidney diseases, hereditary nephritis and

CC inflammatory diseases such as asthma, autoimmune diabetes, tumour

CC angio genesis, rheumatoid arthritis, osteoarthritis, toxic shock syndrome,

CC asthma, stroke, neural trauma, psoriasis, cerebral malaria, osteoporosis,

CC Crohn's disease, ulcerative colitis, Alzheimer's disease. Secreted

CC protein DNA is useful in antisense-mediated gene inhibition and in gene

CC therapy. An array comprising one or more oligonucleotides complementary

CC to reference RNA or DNA encoding the secreted factor is useful for

CC detecting cardiac, kidney and inflammatory disease. The present DNA

CC sequence is an oligonucleotide which is used in the preparation of a

CC normalised cDNA library containing secreted factor DNAs. The normalised

CC cDNA libraries are used in the identification of differentially expressed

CC rat secreted factor F00188_D12 gene

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e+02; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753

DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 542

AAAD17014

ID AAD17014 standard; DNA; 18 BP.

AC AAD17014;

XX 29-NOV-2001 (first entry)

XX Oligonucleotide A18-2PEG linker.

XX Scaffold protein; antibody mimic; fibronectin type III domain;

KW randomised loop; randomised beta-sheet; diagnostic purpose;

KW protein designing; ss.

XX Unidentified.

OS Key Location/Qualifiers

FH misc_feature 18

FT /*tag= a

FT /note= "Linked to (PEG)2CCPuromycin"

XX WO200164942-A1.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US006414.

XX 29-FEB-2000; 2000US-00515260.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2001-557782/62.

XX Fibronectin scaffold protein array for obtaining a protein/compound which

PT binds to a compound/protein, comprises a fibronectin type III domain

PT having a randomized loop, a randomized beta-sheet or their combination.

XX Disclosure; Page 25; 67pp; English.

XX The present invention relates to an array of proteins (antibody mimics)

CC comprising a fibronectin type III domain having a randomised loop, a

CC randomised beta-sheet, or their combination, and has the capacity to bind

CC to a compound that is not bound by a corresponding naturally-occurring

CC fibronectin, immobilised onto a solid support. The antibody mimics is

CC useful for detecting a compound preferably a protein, in a biological

CC sample. It is also useful to detect one or more different analytes

CC simultaneously in a sample. Hence is useful for diagnostic purposes. It

CC is also useful for the purpose of designing proteins capable of binding

CC to virtually any compound of interest. The present sequence is an

CC oligonucleotide A18-2PEG linker used in an exemplification of the

CC invention

XX SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753

DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 543

AAF75597/C

ID AAF75597 standard; DNA; 18 BP.

XX AAF75597;

XX 10-MAY-2001 (first entry)

XX Binary encoded sequence tag method anchored primer #2.

XX Binary encoded sequence tag; BEST; nucleic acid analysis;

KW gene expression; adaptor; PCR primer; ss.

XX Synthetic.

XX WO200112855-A2.

XX 22-FEB-2001.

XX 11-AUG-2000; 2000WO-US022164.

XX 13-AUG-1999; 99US-0148870P.

XX 06-APR-2000; 2000US-00544713.

XX (UYVA) UNIV YALE.

XX Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;

XX WPI; 2001-202878/20.

XX Producing binary sequence tags, useful for analyzing nucleic acid

PT sequence tags, gene expression or gene-expression patterns, involves

PT generating nucleic acid fragments, which are mixed with offset adaptors

PT and adaptor-indexers.

XX Disclosure; Page 100; 101pp; English.

XX The present invention describes a method of producing binary sequence

CC tags from nucleic acid fragments in a sample, involving incubating the

CC sample with cleaving reagents, mixing offset adaptors with the sample,

CC incubating with more cleaving reagents and mixing the sample with adaptor

CC -indexers where the adaptors are coupled to binary sequence tags. The

CC method is useful in sequence analysis, including analysis and comparison

CC of gene expression, nucleic acid samples and genomes

```

SQ Sequence 18 BP; 0 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 ACAAAAAAAAAAAAAAAAAA 1751
DB 18 ACAAAAAAAAAAAAAAAAAA 1

RESULT 544
AAF99708/c
ID AAF99708 standard; DNA; 18 BP.
XX
AC AAF99708;
XX
DT 12-JUN-2001 (first entry)
XX
DE Immunostimulatory nucleic acid #824.
XX
KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic;
KW immunostimulatory; tumour; viral infection; bacterial infection;
KW fungal infection; parasitic infection; cancer; asthma;
KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200122972-A2.
XX
PD 05-APR-2001.
XX
PF 25-SEP-2000; 2000WO-US026383.
XX
PR 25-SEP-1999; 99US-0156113P.
PR 27-SEP-1999; 99US-0156135P.
PR 23-AUG-2000; 2000US-0227436P.
XX
PA (IOWA ) UNIV IOWA RES FOUND.
PA (COLE-) COLEY PHARM GMBH.
XX
PI Krieg AM, Schetter C, Vollmer J;
XX
DR WPI; 2001-273485/28.
XX
PT Vaccinating against tumors, infectious diseases, allergies and asthma
PT using immunostimulatory Py-rich and TG nucleic acids.
XX
PS Claim 101; Page 56; 338pp; English.
XX
CC The present invention relates to a method for stimulating an immune
CC response. The method comprises administering an immunostimulatory nucleic
CC acid to a non-rodent subject in sufficient quantity to stimulate an
CC immune response. The present sequence is one such immunostimulatory
CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich
CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects
CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae
CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,
CC haemophilus, campylobacter, clostridium, Escherichia coli and/or
CC staphylococcus), fungal antigens and/or parasitic antigens. The method is
CC also useful for preventing cancer, asthma, infectious disease, allergy or
CC immune deficiency. The present sequence can also be used to redirect a
CC Th2 to a Th1 immune response and to activate immune cells. Note: the
CC present sequence may have a phosphorothioate backbone
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 546
AAF82472/c
ID AAF82472 standard; DNA; 18 BP.
XX
AC AAF82472;

```

XX 29-JUN-2001 (first entry)
 DT Phagemid vector pCR2.1 polylinker oligonucleotide #6.
 DE
 XX Phagemid vector; pCR2.1; rat; secreted factor; P00210D09; cardiant;
 KW nephrotropic; antiinflammatory; gene therapy; cardiac disease;
 KW renal disease; inflammatory disease; polylinker; ss.
 XX
 OS Synthetic.
 XX
 PN WO200123419-A2.
 XX
 PD 05-APR-2001.
 XX
 XX 27-SEP-2000; 2000WO-US026582.
 PF
 XX 27-SEP-1999; 99US-0156277P.
 PR
 XX (SCIO-) SCIOS INC.
 PA
 XX Stanton LW, Kapoun AM;
 PI
 XX WPI; 2001-328177/34.
 DR
 XX Novel secreted factor encoded by clone P00210D09 useful for diagnosing,
 PT treating and/or preventing various cardiac, renal and inflammatory
 PT diseases.
 PT
 XX Example 1; Page 41; 69pp; English.
 PS
 XX The present sequence corresponds to polylinker DNA of the phagemid vector
 CC pCR2.1. It was used in the construction of a normalised rat cDNA library,
 CC which was used in an example demonstrating differential expression of a
 CC rat gene referred to as clone P00210D09. The invention relates to a
 CC polypeptide comprising a sequence of at least 80% identity to residues 22
 CC -122 of the present sequence, or a sequence encoded by a nucleic acid
 CC hybridising under stringent conditions to the complement of the coding
 CC region comprising 1031 nucleotides, and having at least one biological
 CC activity of the polypeptide encoded by clone P00210D09. The polypeptides
 CC and polynucleotides of the invention are useful for the treatment of
 CC cardiac, renal and inflammatory diseases. The polynucleotides are useful
 CC in antisense mediated gene inhibition and in gene therapy. The
 CC polypeptides are useful in assays for identifying lead compounds that may
 CC be used as therapeutic agents in the treatment of cardiac, kidney or
 CC inflammatory diseases
 CC
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1
 RESULT 547
 AAS94743/c
 ID AAS94743 standard; DNA; 18 BP.
 XX
 AC AAS94743;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX Rat secreted factor DNA oligonucleotide probe #5.
 DE
 XX Rat; secreted factor polypeptide; cardiac disease; renal disease; kidney;
 KW inflammatory disease; congestive heart failure; myocarditis; asthma; ss;
 KW dilated congestive cardiomyopathy; angina pectoris; cardiac arrhythmia;
 KW myocardial infarction; pulmonary hypertension; arteriosclerosis; stroke;
 KW atherosclerosis; cardiac tumour; glomerulonephritis; nephrotic syndrome;

KW renal infarction; hereditary nephritis; polycystic kidney disease;
 KW chronic renal failure; renal vein thrombosis; medullary sponge kidney;
 KW rheumatoid arthritis; osteoarthritis; psoriasis; restenosis; PCR primer;
 KW graft versus host reaction; Crohn's disease; ulcerative colitis; probe;
 KW Alzheimer's disease; gene therapy.
 XX
 OS Synthetic.
 XX
 PN WO200174901-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 23-MAR-2001; 2001WO-US009555.
 PF
 XX 31-MAR-2000; 2000US-0193548P.
 PR
 XX 14-MAR-2001; 2001US-00809545.
 PR
 XX (SCIO-) SCIOS INC.
 PA
 XX Stanton LW, White RT;
 PI
 XX WPI; 2002-010779/01.
 DR
 XX Novel secreted factor polypeptide useful for treating cardiac diseases
 PT such as arteriosclerosis, myocardial infarction, inflammatory diseases
 PT such as asthma, stroke, and rheumatoid arthritis and renal diseases.
 PT
 XX Example 1; Page 51; 189pp; English.
 PS
 XX The invention relates to rat secreted factor polypeptides and the
 CC polynucleotides encoding them. The sequences are useful for treating
 CC cardiac, renal or inflammatory diseases. These include cardiac diseases
 CC such as congestive heart failure, myocarditis, dilated congestive
 CC cardiomyopathy, angina pectoris, myocardial infarction, cardiac
 CC arrhythmia, pulmonary hypertension, arteriosclerosis, atherosclerosis and
 CC cardiac tumours, renal diseases such as glomerulonephritis, nephrotic
 CC syndrome, renal infarction, hereditary nephritis, polycystic kidney
 CC disease, chronic renal failure, renal vein thrombosis and medullary
 CC sponge kidney and inflammatory diseases such as asthma, rheumatoid
 CC arthritis, osteoarthritis, stroke, psoriasis, restenosis, graft versus
 CC host reaction, Crohn's disease, ulcerative colitis and Alzheimer's
 CC disease. Sequences AAS94693-AAS94745 represent cDNA clones, which encode
 CC the secreted factor polypeptides of the invention, and oligonucleotide
 CC probes and PCR primers
 CC
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1
 RESULT 548
 ABS78455/c
 ID ABS78455 standard; DNA; 18 BP.
 XX
 AC ABS78455;
 XX
 XX 13-DEC-2002 (first entry)
 DT
 XX Angiogenesis inhibitory oligonucleotide #939.
 DE
 XX Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Weber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;

KW scleroderma; hypertrophic scar.
 XX Synthetic.
 OS
 PN WO200253141-A2.
 XX
 XX 11-JUL-2002.
 PD
 XX
 XX 14-DEC-2001; 2001WO-US048458.
 PF
 XX 14-DEC-2000; 2000US-0255534P.
 PR
 XX (COLE-) COLEY PHARM GROUP INC.
 PA
 XX Bratzler RL;
 PI
 XX WPI; 2002-566690/60.
 DR
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PT
 XX Claim 2; Page 36; 276pp; English.
 PS
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 XX administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1
 RESULT 549
 ABS78429/C
 ID ABS78429 standard; DNA; 18 BP.
 XX
 AC ABS78429;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Angiogenesis inhibitory oligonucleotide #913.
 XX
 KW Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;
 KW tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;
 KW diabetic retinopathy; retinopathy of prematurity; macular degeneration;
 KW corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;
 KW rubeosis; Osler-Webber Syndrome; myocardial angiogenesis;
 KW plaque neovascularisation; telangiectasia; haemophilic joint;
 KW angiofibroma; wound granulation; intestinal adhesion; atherosclerosis;
 KW scleroderma; hypertrophic scar.
 XX
 OS Synthetic.
 XX
 PN WO200253141-A2.
 XX
 XX 11-JUL-2002.

XX 14-DEC-2001; 2001WO-US048458.
 PF
 XX 14-DEC-2000; 2000US-0255534P.
 PR
 XX (COLE-) COLEY PHARM GROUP INC.
 PA
 XX Bratzler RL;
 PI
 XX WPI; 2002-566690/60.
 DR
 XX Inhibiting angiogenesis in a subject, involves administering at least one
 PT antiangiogenic nucleic acid molecule to the subject.
 PT
 XX Claim 2; Page 35; 276pp; English.
 PS
 XX The invention relates to inhibiting angiogenesis in a subject, comprising
 XX administering at least one antiangiogenic nucleic acid molecule. Also
 CC included is a kit comprising a first container housing the antiangiogenic
 CC nucleic acids, and instructions for administering them to a subject
 CC having a condition characterised by unwanted angiogenesis. The method is
 CC useful for inhibiting angiogenesis associated with solid tumour growth,
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,
 CC rubeosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque
 CC neovascularisation, telangiectasia, haemophilic joints, angiofibroma,
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic
 CC acid of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1
 RESULT 550
 ABL39401/C
 ID ABL39401 standard; DNA; 18 BP.
 XX
 AC ABL39401;
 XX
 DT 16-APR-2002 (first entry)
 XX
 DE Immunostimulatory nucleic acid SEQ ID NO: 837.
 XX
 KW Antibody-induced cell lysis; cancer; immunostimulatory; CD20;
 KW angiogenesis; metastasis; cytostatic; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..18
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "phosphorothioate backbone"
 XX
 PN WO200197843-A2.
 XX
 PD 27-DEC-2001.
 XX
 XX 22-JUN-2001; 2001WO-US020154.
 PR
 XX 22-JUN-2000; 2000US-0213346P.
 PR
 XX (IOWA) UNIV IOWA RES FOUND.
 PA
 XX

PI Weiner G, Hartmann G;
 XX WPI; 2002-154611/20.
 XX Treating or preventing cancer, such as basal cell carcinoma, comprises
 PT administering immunostimulatory nucleic acids that induce expression of
 PT cell surface antigens and antibodies to a subject having or at risk of
 PT developing cancer.
 XX Disclosure; Page 308; 312pp; English.
 XX The present invention relates to methods for treating or preventing
 CC cancer, involving administering to a subject having or at risk of
 CC developing cancer immunostimulatory nucleic acids that induce expression
 CC of cell surface antigens and antibodies. The methods are useful for
 CC treating or preventing cancer such as basal cell carcinoma, bladder
 CC cancer, bone cancer, brain and central nervous system (CNS) cancer,
 CC breast cancer, cervical cancer, colon and rectum cancer, connective
 CC tissue cancer, oesophageal cancer, eye cancer, kidney cancer, larynx
 CC cancer, leukaemia, liver cancer, lung cancer, Hodgkin's lymphoma, non-
 CC Hodgkin's lymphoma, melanoma, myeloma, oral cavity cancer, ovarian
 CC cancer, pancreatic cancer, prostate cancer, rhabdomyosarcoma, skin
 CC cancer, stomach cancer, testicular cancer, and uterine cancer. The
 CC present sequence is an immunostimulatory oligonucleotide described in the
 CC exemplification of the invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1
 RESULT 551
 AAD41497/C
 ID AAD41497 standard; DNA; 18 BP.
 XX
 AC AAD41497;
 XX
 DT 30-OCT-2002 (first entry)
 DE Oligonucleotide used for amplifying sea hare cytoplasm L DNA.
 XX
 KW Apoptosis; ion channel modulator; hyperproliferative disease; tumour;
 KW therapy; leukaemia; carcinoma; sarcoma; degenerative disease; melanoma;
 KW Alzheimer's disease; Parkinson's disease; arteriosclerosis;
 KW heart disease; stroke; vascular disease; neurotropic; neuroprotective;
 KW cerebroprotective; cardiant; cytotoxic protein; cytoplasm L; ss.
 XX
 OS Unidentified.
 XX
 PN WO200231144-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-BF011837.
 XX
 PR 13-OCT-2000; 2000EP-00122466.
 XX
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA Butzke D, Machuy N, Rudel T, Meyer TF;
 XX WPI; 2002-537205/57.
 XX
 DR Novel polypeptide having cytotoxic activity obtainable from Aplysia,
 PT useful for destroying tumors, for identifying novel targets for the
 PT development of anti-tumor agents, and as specific ion channel modulators.
 XX

PS Example 5; Page 37; 87pp; English.
 XX The present invention relates to novel polypeptides having cytotoxic
 CC activity obtainable from sea hare Aplysia. Sequences of the invention are
 CC useful for the manufacture of cytotoxic agents against apoptosis-
 CC resistant cells, where the agents are useful for diagnosis, prevention,
 CC treatment of disorders associated with dysfunctions of GAP-SH3 binding
 CC protein, factors for generating or detoxifying reactive oxygen species
 CC (ROS) and factors for blocking and/or by-passing of caspases. They are
 CC useful for tumour therapy. Cytotoxic proteins of the invention are useful
 CC for destroying tumors and/or selectively killing cells in tissues, for
 CC identifying novel targets for the development of pharmaceutical agents,
 CC preferably anti-tumour agents and as specific ion channel modulators,
 CC e.g., blockers or openers for therapy, diagnostic or research. They are
 CC useful for the diagnosis and therapy of hyperproliferative diseases,
 CC preferably tumors, e.g., leukaemia, carcinoma, sarcoma and melanoma.
 CC They are also useful for development of drugs for the treatment of
 CC degenerative diseases such as Alzheimer's disease, Parkinson's disease,
 CC arteriosclerosis, heart diseases, stroke and vascular diseases. The
 CC present sequence is an oligonucleotide which is used for amplifying sea
 CC hare cytoplasm L DNA. This sequence is used in the exemplification of the
 CC invention
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 18 AAAAAAAAAAAAAAAAAA 1
 RESULT 552
 ABS53437/C
 ID ABS53437 standard; DNA; 18 BP.
 XX
 AC ABS53437;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Poly d(T) primer.
 XX
 KW Terminal continuation; TC; ss; second strand cDNA synthesis; primer;
 KW poly d(T).
 XX
 OS Synthetic.
 XX
 PN WO200265093-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 14-FEB-2002; 2002WO-US005713.
 XX
 PR 14-FEB-2001; 2001US-0268645P.
 PR 14-FEB-2001; 2001US-0268664P.
 PR 18-JUL-2001; 2001US-0306216P.
 PR 07-NOV-2001; 2001US-0344557P.
 PR 07-NOV-2001; 2001US-0348242P.
 PR 09-NOV-2001; 2001US-0350176P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 PA (REME-) RES FOUND MENTAL HYGIENE INC.
 XX
 PI Ginsberg SD, Che S;
 XX WPI; 2002-567050/60.
 XX
 DR Increasing efficiency of second strand cDNA synthesis using terminal
 PT continuation model before performing further RNA amplification by RNA
 PT transcription.
 XX

PS Example 7; Page 80; 128pp; English.

CC This invention relates to a novel method for increasing the efficiency of

CC second strand cDNA synthesis through a mechanism of terminal

CC continuation. In the method an RNA molecule is obtained and a first

CC primer is added that comprises a region that hybridises to a

CC complementary region of the molecule before a second primer is added

CC comprising at least one riboguanine at the 3' end of the primer. A first

CC complementary nucleic acid molecule is synthesised, the RNA molecule and

CC second primer are removed and a second complementary nucleic acid

CC molecule is synthesised to form a second hybrid with an extension product

CC of the third primer bound to the first complementary molecule. The method

CC of the invention is useful for increasing the efficiency of second strand

CC cDNA synthesis and may be used for linear amplification of genetic

CC signals from histologically stained tissue. The present sequence

CC represents a poly d(T) PCR primer used in the method of the invention

XX

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 553

ABA93239/c

ID ABA93239 standard; DNA; 18 BP.

AC ABA93239;

DT 18-APR-2002 (first entry)

DE Adaptor oligonucleotide SEQ ID NO:2.

KW Detection; comparative detection; adaptor; ss.

OS Synthetic.

PN JP2001333800-A.

PD 04-DEC-2001.

PF 30-MAY-2000; 2000JP-00160324.

PR 30-MAY-2000; 2000JP-00160324.

PA (UNIT-) UNITECH CO LTD.

DR WPI; 2002-135950/18.

XX Comparative detection of the amounts of RNA and DNA.

PS Disclosure; Page 9; 9pp; Japanese.

CC The present invention describes a method for the comparative detection of

CC the amount of an RNA. The method comprises: (a) cDNAs obtained by

CC transcribing respectively from at least two tissue RNAs are respectively

CC fragmented by using a same restriction enzyme; (b) each different adaptor

CC and a common adaptor are added to each of the cDNA fragments derived from

CC the same or different tissues by the step (a); (c) the resultant adaptor-

CC added cDNAs are mixed together; (d) an adaptor primer having the common

CC sequence to said different adaptor and a gene-specific adaptor are used

CC to amplify said adaptor-added cDNAs containing no region derived from

CC polyadenylic acid of the mRNA before the addition of the adaptor among

CC the adaptor-added cDNAs prepared by the step (b); (e) the ratios of the

CC cDNA amounts are measured between the tissues; (f) the RNA is detected

CC from the measured result; (g) each different adaptor and a common adaptor

CC are added to each of the genomic DNA fragments derived from a same or

CC different individuals; (h) the resultant adaptor-added genomic DNAs are

CC mixed together; (i) the adaptor-added genomic DNAs are amplified by using

CC an adaptor primer having the common sequence to the different adaptor and

CC a sequence-specific adaptor; and (j) the ratios of the amplified amounts

CC of the genomic DNAs are measured between the individuals. The method is

CC used for the detection of the amounts of RNA and DNA. The present

CC sequence represents an oligonucleotide which is used in the

XX exemplification of the present invention

SQ Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753

Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 554

AAD56466

ID AAD56466 standard; RNA; 18 BP.

XX AAD56466;

DT 07-AUG-2003 (first entry)

DE Target RNA #1 used in the exemplification of the invention.

KW Acyclic linker; gene expression; gene therapy; ss.

OS Unidentified.

PN WO2003037909-A1.

PD 08-MAY-2003.

PF 29-OCT-2002; 2002WO-CA001628.

PR 29-OCT-2001; 2001US-0330719P.

PA (UTMC-) UNIV MCGILL.

PI Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;

DR WPI; 2003-421516/39.

XX Novel acyclic linker-containing oligonucleotide useful for preventing or

PT decreasing translation, reverse transcription and/or replication of a

PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX Example 2; Fig 5; 104pp; English.

PS The invention relates to an acyclic linker-containing oligonucleotide

CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of

CC the invention are useful for preventing or decreasing translation,

CC reverse transcription and/or replication of a target RNA in a system.

CC They are useful for selectively preventing gene expression in a cellular

CC specific manner, for hybridising to complementary RNA such as cellular

CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary

CC RNA. They are also useful therapeutically in formulations or medicaments

CC to prevent or treat a disease characterised by the expression of a

CC particular target RNA. The invention is used in gene therapy. The present

CC sequence is a target RNA, used in the exemplification of the invention

XX

SQ Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753

```
Db      1 AAAAAAAAAAAAAAAAAAAAA 18
RESULT 555
AAD56440/c
ID      AAD56440 standard; DNA; 18 BP.
XX
AC      AAD56440;
XX
DT      07-AUG-2003 (first entry)
XX
DE      Antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
KW      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW      antisense; ss.
XX
OS      Unidentified.
XX
PN      WO2003037909-A1.
XX
PD      08-MAY-2003.
XX
PF      29-OCT-2002; 2002WO-CA001628.
XX
PR      29-OCT-2001; 2001US-0330719P.
XX
PA      (UYMC-) UNIV MCGILL.
XX
PI      Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX      WPI; 2003-421516/39.
XX
XX      Novel acyclic linker-containing oligonucleotide useful for preventing or
PT      decreasing translation, reverse transcription and/or replication of a
PT      target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS      Example 2; Fig 9; 104pp; English.
XX
XX      The invention relates to an acyclic linker-containing oligonucleotide
CC      comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC      the invention are useful for preventing or decreasing translation,
CC      reverse transcription and/or replication of a target RNA in a system.
CC      They are useful for selectively preventing gene expression in a sequence-
CC      specific manner, for hybridising to complementary RNA such as cellular
CC      mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC      RNA. They are also useful therapeutically in formulations or medicaments
CC      to prevent or treat a disease characterised by the expression of a
CC      particular target RNA. The invention is used in gene therapy. The present
CC      sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC      H degradation of target RNA. This sequence is used in the exemplification
CC      of the invention
XX
SQ      Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAA 1753
Db      18 AAAAAAAAAAAAAAAAAAAAA 1
RESULT 556
AAD56446/c
ID      AAD56446 standard; DNA; 18 BP.
XX
AC      AAD56446;
XX
DT      07-AUG-2003 (first entry)
XX
DE      2'F-ANA antisense oligo #1, to elicit RNase H degradation of target RNA.
XX
```

```
KW      Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
KW      antisense; ss.
XX
OS      Unidentified.
XX
FH      Key      Location/Qualifiers
FT      modified_base      1..18
FT      /*tag= a
FT      /mod_base= OTHER
FT      /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX
PN      WO2003037909-A1.
XX
PD      08-MAY-2003.
XX
PF      29-OCT-2002; 2002WO-CA001628.
XX
PR      29-OCT-2001; 2001US-0330719P.
XX
PA      (UYMC-) UNIV MCGILL.
XX
PI      Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
XX      WPI; 2003-421516/39.
XX
XX      Novel acyclic linker-containing oligonucleotide useful for preventing or
PT      decreasing translation, reverse transcription and/or replication of a
PT      target RNA in a system, comprises a modified deoxyribonucleotide.
XX
PS      Example 2; Fig 7; 104pp; English.
XX
XX      The invention relates to an acyclic linker-containing oligonucleotide
CC      comprising at least one modified deoxyribonucleotide. Oligonucleotides of
CC      the invention are useful for preventing or decreasing translation,
CC      reverse transcription and/or replication of a target RNA in a system.
CC      They are useful for selectively preventing gene expression in a sequence-
CC      specific manner, for hybridising to complementary RNA such as cellular
CC      mRNA or viral RNA, to hybridise to and induce cleavage of complementary
CC      RNA. They are also useful therapeutically in formulations or medicaments
CC      to prevent or treat a disease characterised by the expression of a
CC      particular target RNA. The invention is used in gene therapy. The present
CC      sequence is an antisense oligo used to elicit human RNase (ribonuclease)
CC      H degradation of target RNA. This sequence is used in the exemplification
CC      of the invention
XX
SQ      Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736 AAAAAAAAAAAAAAAAAAAAA 1753
Db      18 AAAAAAAAAAAAAAAAAAAAA 1
RESULT 557
ACH03247/c
ID      ACH03247 standard; DNA; 18 BP.
XX
AC      ACH03247;
XX
DT      25-SEP-2003 (first entry)
XX
DE      Immunostimulatory nucleic acid #882.
XX
KW      Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;
KW      antiulcer; gene therapy; vaccine; non-allergic inflammatory disease;
KW      psoriasis; eczema; allergic contact dermatitis; latex dermatitis;
KW      inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.
XX
OS      Synthetic.
XX
```

```

PN  US2003050268-A1.
PD  13-MAR-2003.
XX
PF  29-MAR-2002; 2002US-00112653.
XX
PR  29-MAR-2001; 2001US-0279642P.
XX
XX  (KRIE/) KRIEG A M.
PA  (BERG/) BERG D J.
XX
PI  Krieg AM, Berg DJ;
XX
DR  WPI; 2003-521815/49.
XX
XX  Treating non-allergic inflammatory diseases, such as psoriasis, eczema,
PT  allergic contact dermatitis, latex dermatitis or inflammatory bowel
PT  disease by administering an immunostimulatory nucleic acid.
XX
XX  Disclosure; Page 33; 229pp; English.
XX
XX  The invention describes a method of treating non-allergic inflammatory
CC  disease comprising administering to a subject having or at risk of
CC  developing a non-allergic inflammatory disease an immunostimulatory
CC  nucleic acid for prevention or treatment of the disease. The method is
CC  useful for treating non-allergic inflammatory diseases, such as
CC  psoriasis, eczema, allergic contact dermatitis, latex dermatitis or
CC  inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.
CC  This sequence represents an immunostimulatory nucleic acid
XX
XX  Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1736 AAAAAAAAAAAAAAAAAA 1753
Db  18 AAAAAAAAAAAAAAAAAA 1

RESULT 558
AAD57871/c
ID  AAD57871 standard; DNA; 18 BP.
XX
AC  AAD57871;
XX
XX  20-NOV-2003 (first entry)
XX
XX  Antisense oligo #1 used in the exemplification of the invention.
XX
XX  Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX  hepatitis B; gene therapy; virucide; anti-HIV; antisense; ss.
XX
XX  Unidentified.
XX
XX  WO2003064441-A2.
XX
XX  07-AUG-2003.
XX
XX  31-JAN-2003; 2003WO-CA000129.
XX
XX  01-FEB-2002; 2002US-0352873P.
XX
XX  (UYMC-) UNIV MCGILL.
XX
XX  Damha MJ, Parniak MA;
XX
XX  WPI; 2003-689523/65.
XX
XX  New oligonucleotide, useful for preventing or treating a disease related
PT  to a target RNA in a system, e.g., AIDS or hepatitis B.
XX

```

```

PS  Example 2; Page 35; 73pp; English.
XX
XX  The present invention relates to a new oligonucleoside which comprises
CC  alternating first and second segments. The first segment comprises at
CC  least one sugar modified nucleoside. The second segment comprises at
CC  least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC  each of the first and second segments, so that it comprises at least 4
CC  alternating segments. The oligonucleotide is useful for preparing a
CC  composition for inducing RNase H-mediated cleavage of a target RNA in a
CC  system, preventing or decreasing translation, transcription or
CC  replication of a target RNA in a system, detecting the presence of a
CC  target RNA in a system, validating a gene target corresponding to a
CC  target RNA in a system or preventing or treating a disease related to a
CC  target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC  or hepatitis B. The invention is useful in gene therapy. The present
CC  sequence is an antisense oligonucleotide used in the exemplification of
XX  the invention
XX
XX  Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1736 AAAAAAAAAAAAAAAAAA 1753
Db  18 AAAAAAAAAAAAAAAAAA 1

RESULT 559
AAD57878/c
ID  AAD57878 standard; DNA; 18 BP.
XX
AC  AAD57878;
XX
XX  20-NOV-2003 (first entry)
XX
XX  Antisense DNA-RNA hybrid #2 used in the exemplification of the invention.
XX
XX  Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX  hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
XX  ss.
XX
XX  Unidentified.
XX
XX  Key      Location/Qualifiers
XX  misc_RNA 1..3
XX              /*tag= a
XX              /label= RNA
XX              /note= "2'-O-methyl-D-uridine"
XX  misc_RNA 7..9
XX              /*tag= b
XX              /label= RNA
XX              /note= "2'-O-methyl-D-uridine"
XX  misc_RNA 13..15
XX              /*tag= c
XX              /label= RNA
XX              /note= "2'-O-methyl-D-uridine"
XX
XX  WO2003064441-A2.
XX
XX  07-AUG-2003.
XX
XX  31-JAN-2003; 2003WO-CA000129.
XX
XX  01-FEB-2002; 2002US-0352873P.
XX
XX  (UYMC-) UNIV MCGILL.
XX
XX  Damha MJ, Parniak MA;
XX
XX  WPI; 2003-689523/65.
XX

```

```
PT New oligonucleotide, useful for preventing or treating a disease related
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 560
AAD57879/c
ID AAD57879 standard; DNA; 18 BP.
XX
AC AAD57879;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #3 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1..6
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 13..18
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
XX WO2003064441-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-CA000129.
XX
PR 01-FEB-2002; 2002US-0352873P.
XX
PA (UYMC-) UNIV MCGILL.
XX
PI Damba MJ, Parniak MA;
XX
PI WPI; 2003-689523/65.
XX
PR New oligonucleotide, useful for preventing or treating a disease related
```

```
PT to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
PS Example 2; Page 35; 73pp; English.
XX
CC The present invention relates to a new oligonucleoside which comprises
CC alternating first and second segments. The first segment comprises at
CC least one sugar modified nucleoside. The second segment comprises at
CC least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
CC each of the first and second segments, so that it comprises at least 4
CC alternating segments. The oligonucleotide is useful for preparing a
CC composition for inducing RNase H-mediated cleavage of a target RNA in a
CC system, preventing or decreasing translation, transcription or
CC replication of a target RNA in a system, detecting the presence of a
CC target RNA in a system, validating a gene target corresponding to a
CC target RNA in a system or preventing or treating a disease related to a
CC target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
CC or hepatitis B. The invention is useful in gene therapy. The present
CC sequence is an antisense DNA-RNA hybrid used in the exemplification of
CC the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 6 T; 12 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 561
AAD57877/c
ID AAD57877 standard; DNA; 18 BP.
XX
AC AAD57877;
XX
DT 20-NOV-2003 (first entry)
XX
DE Antisense DNA-RNA hybrid #1 used in the exemplification of the invention.
XX
KW Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
KW hepatitis B; gene therapy; virucide; anti-HIV; antisense; DNA-RNA hybrid;
KW ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT misc_RNA 1
FT /*tag= a
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 3
FT /*tag= b
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 5
FT /*tag= c
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 7
FT /*tag= d
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 9
FT /*tag= e
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 11
FT /*tag= f
FT /label= RNA
FT /note= "2'-O-methyl-D-uridine"
FT
FT misc_RNA 13
```

```
FT      /*tag= 9
FT      /label= RNA
FT      /note= "2'-O-methyl-D-uridine"
FT      15
FT      misc_RNA
FT      /*tag= h
FT      /label= RNA
FT      /note= "2'-O-methyl-D-uridine"
FT      17
FT      misc_RNA
FT      /*tag= i
FT      /label= RNA
FT      /note= "2'-O-methyl-D-uridine"
XX
XX
XX      WO2003064441-A2.
XX
XX      07-AUG-2003.
XX
XX      31-JAN-2003; 2003WO-CA000129.
XX
XX      01-FEB-2002; 2002US-0352873P.
XX      (UYMC-) UNIV MCGILL.
XX
XX      Damha MJ, Parniak MA;
XX
XX      WPI; 2003-689523/65.
XX
XX      New oligonucleotide, useful for preventing or treating a disease related
XX      to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX      Example 2; Page 35; 73pp; English.
XX
XX      The present invention relates to a new oligonucleoside which comprises
XX      alternating first and second segments. The first segment comprises at
XX      least one sugar modified nucleoside. The second segment comprises at
XX      least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
XX      each of the first and second segments, so that it comprises at least 4
XX      alternating segments. The oligonucleotide is useful for preparing a
XX      composition for inducing RNase H-mediated cleavage of a target RNA in a
XX      system, preventing or decreasing translation, transcription or
XX      replication of a target RNA in a system, detecting the presence of a
XX      target RNA in a system, validating a gene target corresponding to a
XX      target RNA in a system or preventing or treating a disease related to a
XX      target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
XX      or hepatitis B. The invention is useful in gene therapy. The present
XX      sequence is an antisense DNA-RNA hybrid used in the exemplification of
XX      the invention
XX
XX      Sequence 18 BP; 0 A; 0 C; 0 G; 9 T; 9 U; 0 Other;
XX
XX      Query Match      1.0%; Score 18; DB 1; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      1736 AAAAAAAAAAAAAAAAAA 1753
XX      Db      18 AAAAAAAAAAAAAAAAAA 1
XX
XX      RESULT 562
XX      AAD57890
XX      ID      AAD57890 standard; RNA; 18 BP.
XX
XX      AC      AAD57890;
XX
XX      XX      20-NOV-2003 (first entry)
XX
XX      DE      Target RNA #1 used in RNase H assay.
XX
XX      KW      Sugar-modified nucleoside; acquired immune deficiency syndrome; AIDS;
XX      hepatitis B; gene therapy; virucide; anti-HIV; ss.
XX
XX      OS      Unidentified.
XX
```

```
PN      WO2003064441-A2.
XX
XX      07-AUG-2003.
XX
XX      31-JAN-2003; 2003WO-CA000129.
XX
XX      01-FEB-2002; 2002US-0352873P.
XX      (UYMC-) UNIV MCGILL.
XX
XX      Damha MJ, Parniak MA;
XX
XX      WPI; 2003-689523/65.
XX
XX      New oligonucleotide, useful for preventing or treating a disease related
XX      to a target RNA in a system, e.g., AIDS or hepatitis B.
XX
XX      Example 4; Page 38; 73pp; English.
XX
XX      The present invention relates to a new oligonucleoside which comprises
XX      alternating first and second segments. The first segment comprises at
XX      least one sugar modified nucleoside. The second segment comprises at
XX      least one 2'-deoxynucleoside. The oligonucleoside comprises at least 2 of
XX      each of the first and second segments, so that it comprises at least 4
XX      alternating segments. The oligonucleotide is useful for preparing a
XX      composition for inducing RNase H-mediated cleavage of a target RNA in a
XX      system, preventing or decreasing translation, transcription or
XX      replication of a target RNA in a system, detecting the presence of a
XX      target RNA in a system, validating a gene target corresponding to a
XX      target RNA in a system or preventing or treating a disease related to a
XX      target RNA in a system, e.g., acquired immune deficiency syndrome (AIDS)
XX      or hepatitis B. The invention is useful in gene therapy. The present
XX      sequence is a target RNA used in RNase H assay. This sequence is used in
XX      the exemplification of the invention
XX
XX      Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
XX      Query Match      1.0%; Score 18; DB 1; Length 18;
XX      Best Local Similarity 100.0%; Pred. No. 2.6e+02;
XX      Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      Qy      1736 AAAAAAAAAAAAAAAAAA 1753
XX      Db      1 AAAAAAAAAAAAAAAAAA 18
XX
XX      RESULT 563
XX      ADB37210/C
XX      ID      ADB37210 standard; DNA; 18 BP.
XX
XX      AC      ADB37210;
XX
XX      DT      04-DEC-2003 (first entry)
XX
XX      DE      Immunostimulatory nucleic acid #824.
XX
XX      KW      ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
XX      hypo-responsive subject; immunostimulatory.
XX
XX      OS      Synthetic.
XX
XX      PN      US2003087848-A1.
XX
XX      PD      08-MAY-2003.
XX
XX      PF      02-FEB-2001; 2001US-00776479.
XX
XX      PR      03-FEB-2000; 2000US-0179991P.
XX
XX      (BRAT/) BRATZLER R L.
XX      (PETE/) PETERSEN D M.
XX      (FOUR/) FOURON Y.
XX
```

PI Bratzler RL, Petersen DM, Fouron Y;
 DR WPI; 2003-657977/62.
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 PS Disclosure; Page 17; 221pp; English.
 XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1753
 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 564
 ADB37236/C
 ID ADB37236 standard; DNA; 18 BP.
 XX ADB37236;
 XX 04-DEC-2003 (first entry)
 DE Immunostimulatory nucleic acid #850.
 XX ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;
 KW hypo-responsive subject; immunostimulatory.
 XX Synthetic.
 OS US2003087848-A1.
 PN 08-MAY-2003.
 PD 02-FEB-2001; 2001US-00776479.
 XX 03-FEB-2000; 2000US-0179991P.
 PA (BRAT/) BRATZLER R L.
 PA (PETE/) PETERSEN D M.
 PA (FOUR/) FOURON Y.
 PI Bratzler RL, Petersen DM, Fouron Y;
 DR WPI; 2003-657977/62.
 XX Treating and/or preventing allergy or asthma using an immunostimulatory
 PT nucleic acid alone or in combination with an asthma/allergy medicament.
 PS Disclosure; Page 18; 221pp; English.
 XX The invention relates to a method of treating or preventing allergy or
 CC asthma which comprises administering to a subject a poly-G nucleic acid
 CC in an aerosol formulation. The methods and compositions of the present
 CC invention are useful for diagnosing and/or treating asthma and allergy
 CC especially in a hypo-responsive subject. The present sequence represents
 CC an immunostimulatory nucleic acid of the invention.
 XX Sequence 18 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 SQ

Query Match 1.0%; Score 18; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1753
 DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 565
 ADE77617
 ID ADE77617 standard; DNA; 18 BP.
 XX ADE77617;
 XX 29-JAN-2004 (first entry)
 DE Human probe NEG for elongation mediated multiplexed analysis of HLA-DR.
 XX probe; ss; negative control; CFTR; human leukocyte antigen; HLA;
 KW genetic testing; carrier screening; genotyping; profiling; polymorphic;
 KW multiplexed elongation assay; enzymatic recognition;
 KW cystic fibrosis conductance transmembrane regulator.
 XX Synthetic.
 OS Homo sapiens.
 XX WO2003034029-A2.
 PN 24-APR-2003.
 PD 15-OCT-2002; 2002WO-US033012.
 XX 15-OCT-2001; 2001US-0329427P.
 PR 15-OCT-2001; 2001US-0329428P.
 PR 15-OCT-2001; 2001US-0329619P.
 PR 15-OCT-2001; 2001US-0329620P.
 PR 14-MAR-2002; 2002US-0364416P.
 XX (BIOA-) BIOARRAY SOLUTIONS LTD.
 PI Li AX, Hashmi G, Seoul M;
 XX WPI; 2003-393553/37.
 XX Concurrent interrogation of a number of polymorphic sites, useful for
 PT genetic testing, carrier screening, genetic profiling, and identity
 PT testing, comprises conducting a multiplexed elongation assay using
 PT probes.
 XX Example 9; Page 46; 143pp; English.
 PS This invention relates to a novel method for the concurrent interrogation
 CC of a number of polymorphic sites in the presence of, and without
 CC interference from, non-designated polymorphic sites. Specifically, it
 CC comprises conducting a multiplexed elongation assay by applying one or
 CC more temperature cycles to achieve linear amplification of the target or
 CC a combination of annealing and elongation steps under temperature-
 CC controlled conditions. Furthermore, this detection method uses probe
 CC extension or elongation and relies on enzymatic recognition, a superior
 CC technique that no longer depends on differential hybridisation. The
 CC present invention describes probes and methods useful for identifying or
 CC detecting polymorphisms at one or more designated sites, such that they
 CC can identify mutations within the cystic fibrosis conductance
 CC transmembrane regulator (CFTR) or the human leukocyte antigen (HLA)
 CC genes. In addition, concurrent interrogation of a multiplicity of
 CC polymorphic sites is useful for genetic testing, carrier screening,
 CC genotyping or genetic profiling, and identity testing. This
 CC oligonucleotide is the negative control probe used for the elongation
 CC mediated multiplexed analysis of HLA-DR, in an exemplification of the
 CC invention.
 XX Sequence 18 BP; 18 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ

```
Query Match      1.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18

RESULT 566
AAQ75548/c
ID AAQ75548 standard; DNA; 19 BP.
XX
AC AAQ75548;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match      1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 567
AAQ75547/c
ID AAQ75547 standard; DNA; 19 BP.
XX
AC AAQ75547;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
```

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AA075547-075798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

XX Sequence 19 BP; 0 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.8e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CAAGAAAAA 1752
 |||||

DB 18 CAAGAAAAA 1752
 |||||

RESULT 569

ABL51521

ID ABL51521 standard; DNA; 19 BP.

XX ABL51521;

XX 01-JUL-2002 (first entry)

XX Tailoring reaction related exemplary primer dA18U SEQ ID NO:2.

XX Tailoring reaction; tailed primer; primer; probe; identification;

XX detection; linear amplification scheme; chain extending enzyme;

XX telomerase; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_RNA 19

FT /*tag= a

XX US2002031776-A1.

XX 14-MAR-2002.

XX 26-JUL-2001; 2001US-00917138.

XX 28-MAY-1999; 99US-0136545P.

XX 25-MAY-2000; 2000US-00580358.

XX (TULL/) TULLIS R H.

XX (STRE/) STREIFEL J A.

XX Tullis RH, Streifel JA;

XX WPI; 2002-361176/39.

XX Identifying and detecting nucleic acids, particularly DNA hybridization
 PT probes, involves employing chain extending enzymes (e.g. telomerase) to
 PT elongate probes to render them readily detectable.

PS Example 1; Page 5; 10pp; English.

XX The present invention describes a method for detecting a nucleic acid
 CC probe, which comprises using chain extending enzymes to elongate probes.
 CC The method comprises: (a) treating the sample with a chain terminating
 CC reagent to prevent polynucleotide chain growth from the nucleic acid in
 CC the sample; (b) contacting the sample with the probe containing a
 CC terminus capable of elongation by a chain extending enzyme, where the
 CC probe hybridises to the nucleic acid in the sample; (c) contacting the
 CC sample with a chain extending enzyme and its substrates, which elongates
 CC the probe; and (d) detecting the elongated hybridised probe. Also
 CC described is a method comprising: (a) treating nucleic acid molecules or
 CC modified nucleic acids in a sample with a reagent or reagents that render
 CC the nucleic acid chains unextendable by a non-template-dependent enzyme;

CC (b) hybridising the treated molecules with a nucleic acid probe that
 CC includes an extendable terminus, under conditions where hybrids form; and
 CC (c) treating any hybrids formed with a non-template dependent chain
 CC elongating enzyme and its substrates, where any hybridised probe is
 CC extended. The method is useful for identifying and detecting nucleic
 CC acids, particularly DNA hybridisation probes. The present sequence
 CC represents a tailing reaction exemplary primer, which is used in an
 CC example from the present invention
 XX

XX Sequence 19 BP; 18 A; 0 C; 0 G; 0 T; 1 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAA 1753
 |||||

DB 1 AAAAAA 18
 |||||

RESULT 570

ABZ75398/C

ID ABZ75398 standard; DNA; 19 BP.

XX ABZ75398;

XX 07-MAY-2003 (first entry)

XX Synthetic nuclease-resistant oligomeric compound #54.

XX Nuclease resistant; ds; pharmaceutical; topical administration;

XX transdermal patch; enzymatic degradation resistant.

XX Synthetic.

XX Key Location/Qualifiers

FT modified_base 19

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phenoxazine"

XX WO2003004602-A2.

XX 16-JAN-2003.

XX 01-JUL-2002; 2002WO-US020934.

XX 03-JUL-2001; 2001US-0302682P.

XX 28-NOV-2001; 2001US-00996292.

XX 10-DEC-2001; 2001US-00013295.

XX (ISIS-) ISIS PHARM INC.

XX Manoharan M, Maier MA, Prakash TP, Rajeev KG;

XX WPI; 2003-256318/25.

XX Nuclease-resistant oligomeric compound useful as pharmaceuticals for
 PT topical administration such as transdermal patches.

PS Disclosure; Page 234; 234pp; English.

XX The invention relates to novel nuclease-resistant oligomeric compounds.
 CC The compounds of the invention are useful as pharmaceuticals for topical
 CC administration such as transdermal patches. The oligomeric compound is
 CC resistant to enzymatic degradation. The sequences shown in ABZ75345-
 CC ABZ75399 represent the nuclease-resistant compounds of the invention
 XX

XX Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;

Query Match 1.0%; Score 18; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.8e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 18 AAAAAAAAAAAAAAAAAA 1

RESULT 571
ABZ75399/c
ID ABZ75399 standard; DNA; 19 BP.
XX
AC ABZ75399;
XX
DT 07-MAY-2003 (first entry)
XX
DE Synthetic nuclease-resistant oligomeric compound #55.
XX
KW Nuclease resistant; ds; pharmaceutical; topical administration;
KW transdermal patch; enzymatic degradation resistant.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 19
FT /*tag= a
FT /mod_base= OTHER
FT /note= "G-clamp modification"
XX
FN WO2003004602-A2.
XX
PD 16-JAN-2003.
XX
PF 01-JUL-2002; 2002WO-US020934.
XX
PR 03-JUL-2001; 2001US-0302682P.
PR 28-NOV-2001; 2001US-00956292.
PR 10-DEC-2001; 2001US-00013295.
XX
FA (ISIS-) ISIS PHARM INC.
XX
PI Manoharan M, Maier MA, Prakash TP, Rajeev KG;
XX
WPI; 2003-256318/25.
XX
Nuclease-resistant oligomeric compound useful as pharmaceuticals for
topical administration such as transdermal patches.
XX
PS Disclosure; Page 234; 234pp; English.
XX
CC The invention relates to novel nuclease-resistant oligomeric compounds.
CC The compounds of the invention are useful as pharmaceuticals for topical
CC administration such as transdermal patches. The oligomeric compound is
CC resistant to enzymatic degradation. The sequences shown in ABZ75345-
CC ABZ75399 represent the nuclease-resistant compounds of the invention
XX
SQ Sequence 19 BP; 0 A; 0 C; 0 G; 18 T; 0 U; 1 Other;
Query Match 1.0%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
Db 18 AAAAAAAAAAAAAAAAAA 1

RESULT 572
AAQ75566/c
ID AAQ75566 standard; DNA; 20 BP.
XX
AC AAQ75566;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 573
AAQ75574/c
ID AAQ75574 standard; DNA; 20 BP.
XX
AC AAQ75574;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
WPI; 1995-018287/03.
XX
Analysis of cDNA and gene expression - by amplification of mRNA followed
by digestion with restriction enzymes.
PT

```

```
XX Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match          1.0%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 2.9e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
RESULT 574
AAQ75559/c
ID AAQ75559 standard; DNA; 20 BP.
XX
AC AAQ75559;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 0 C; 3 G; 17 T; 0 U; 0 Other;
    Query Match          1.0%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 2.9e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
RESULT 575
AAQ75563/c
ID AAQ75563 standard; DNA; 20 BP.
XX
AC AAQ75563;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match          1.0%; Score 18; DB 1; Length 20;
    Best Local Similarity 100.0%; Pred. No. 2.9e+02;
    Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
RESULT 576
AAQ75565/c
ID AAQ75565 standard; DNA; 20 BP.
XX
AC AAQ75565;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
```

```

XX SQ Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match      1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 578
AAQ75573/c
ID ID AAQ75573 standard; DNA; 20 BP.
XX AC AC
XX AC AC
XX AC AC
DT 04-AUG-1995 (first entry)
DE DE
DE DE
XX XX
XX Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS OS
XX OS
XX PN JP06303997-A.
XX PN
XX PD 01-NOV-1994.
XX PF
XX PF 16-APR-1993; 93JP-00112515.
XX PR
XX PR 16-APR-1993; 93JP-00112515.
XX PA
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PS by digestion with restriction enzymes.
XX Disclosure; Page 5; lipp; Japanese.
XX CC
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 20 BP; 0 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match      1.0%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1

RESULT 579
AAQ75571/c
ID ID AAQ75571 standard; DNA; 20 BP.
XX AC AC
XX AC AC
XX AC AC
DT 04-AUG-1995 (first entry)
DE DE
DE DE
XX XX
XX Reverse transcription primer used in cDNA analysis technique.

```

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

XX Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 20 BP; 0 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CAAAAA...AAAAA 1752
 DB 18 CAAAAA...AAAAA 1

RESULT 580

ABZ85312/c

ID ABZ85312 standard; DNA; 20 BP.

XX ABZ85312;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

XX Claim 15; SEQ ID NO 554; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAA...AAAAA 1753
 DB 18 AAAAAA...AAAAA 1

RESULT 581

ABZ88938

ID ABZ88938 standard; DNA; 20 BP.

XX ABZ88938;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX WO200285308-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013135.

XX 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Disclosure; SEQ ID NO 4180; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAA 1752
 Db 3 CAAAAAAAAAAAAAAAAA 20
 RESULT 582
 ABZ89301
 ID ABZ89301 standard; DNA; 20 BP.
 XX
 AC ABZ89301;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200285308-A2.
 XX
 XX 31-OCT-2002.
 PD
 XX
 XX 23-APR-2002; 2002WO-US013135.
 PF
 XX
 XX 24-APR-2001; 2001US-0286137P.
 PR
 XX
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 XX Disclosure; SEQ ID NO 4543; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 17 A; 2 C; 0 G; 1 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.9e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAA 1752
 Db 3 CAAAAAAAAAAAAAAAAA 20
 RESULT 583
 AAQ75622/C
 ID AAQ75622 standard; DNA; 21 BP.
 XX
 AC AAQ75622;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 XX JP06303997-A.
 PN
 XX
 PD 01-NOV-1994.
 XX
 XX 16-APR-1993; 93JP-00112515.
 PF
 XX
 XX 16-APR-1993; 93JP-00112515.
 PR
 XX
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX
 XX WPI; 1995-018287/03.
 DR
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX

```

PS Disclosure; Page 6; 1lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
RESULT 584
AAQ75633/c
ID AAQ75633 standard; DNA; 21 BP.
XX AC AAQ75633;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
OS JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 1lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
RESULT 586
AAQ75609/c
ID AAQ75609 standard; DNA; 21 BP.
XX AC AAQ75609;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
OS JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX

```

```

RESULT 585
AAQ75670/c
ID AAQ75670 standard; DNA; 21 BP.
XX AC AAQ75670;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
OS JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 1lpp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
RESULT 586
AAQ75609/c
ID AAQ75609 standard; DNA; 21 BP.
XX AC AAQ75609;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX
OS JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX

```

```
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 5; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX XX
XX SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1735 CAAAAAAAAAAAAAAAAA 1752
XX DB 18 CAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 587
XX AAQ75620/c
XX ID AAQ75620 standard; DNA; 21 BP.
XX AC AAQ75620;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX XX
```

```
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1735 CAAAAAAAAAAAAAAAAA 1752
XX DB 18 CAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 588
XX AAQ75626/c
XX ID AAQ75626 standard; DNA; 21 BP.
XX AC AAQ75626;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX XX
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX
XX DR WPI; 1995-018287/03.
XX XX
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX XX
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX XX
XX SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 18; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 3e+02;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1735 CAAAAAAAAAAAAAAAAA 1752
XX DB 18 CAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 589
XX AAQ75657/c
XX ID AAQ75657 standard; DNA; 21 BP.
XX AC AAQ75657;
XX XX
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX XX
```

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752

DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 590

AAQ75664/c

ID AAQ75664 standard; DNA; 21 BP.

XX AAQ75664;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752

DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 591

AAQ75663/c

ID AAQ75663 standard; DNA; 21 BP.

XX AAQ75663;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752

DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 592
AAQ75631/c
ID AAQ75631 standard; DNA; 21 BP.
XX
XX
AC AAQ75631;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
SQ Sequence 21 BP; 1 A; 0 C; 2 G; 18 T; 0 U; 0 Other;
XX
XX
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1
XX
RESULT 593
AAQ75668/c
ID AAQ75668 standard; DNA; 21 BP.
XX
XX
AC AAQ75668;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
XX

PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Oy 1735 CAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAA 1
XX
RESULT 594
AAQ75607/c
ID AAQ75607 standard; DNA; 21 BP.
XX
XX
AC AAQ75607;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 0 C; 4 G; 17 T; 0 U; 0 Other;
XX

```
Query Match      1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1752
Db 18 CAAAAA...AAAAA 1

RESULT 595
AAQ75625/c
ID AAQ75625 standard; DNA; 21 BP.
AC AAQ75625;
XX
XX
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1752
Db 18 CAAAAA...AAAAA 1

RESULT 597
AAQ75665/c
ID AAQ75665 standard; DNA; 21 BP.
AC AAQ75665;
XX
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX

Query Match      1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAA 1752
Db 18 CAAAAA...AAAAA 1

RESULT 596
AAQ75634/c
ID AAQ75634 standard; DNA; 21 BP.
AC AAQ75634;
XX
XX
XX 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX
```

```

AAQ75608/c
ID   AAQ75608 standard; DNA; 21 BP.
XX
AC   AAQ75608;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
XX   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993; 93JP-00112515.
XX
PR   16-APR-1993; 93JP-00112515.
XX
PA   (NITE ) NIPON TELEGRAPH & TELEPHONE CORP.
XX
XX   WPI; 1995-018287/03.
XX
XX   Analysis of cDNA and gene expression - by amplification of mRNA followed
XX   by digestion with restriction enzymes.
XX
XX   Disclosure; Page 5; 11pp; Japanese.
XX
XX   A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX   double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX   labelled reverse transcription primers (GENESQ files AAQ75547-075798)
XX   and using the aggregate of mRNAs as the template for each reverse
XX   transcription primer; (b) digesting each of the prepared aggregates of
XX   the double-stranded cDNAs with restriction enzyme and; (c)
XX   electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX   method can be used to analyse gene expression rapidly and easily
XX
SQ   Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. NO. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 600
AAQ75655/c
ID   AAQ75655 standard; DNA; 21 BP.
XX
AC   AAQ75655;
XX
DT   04-AUG-1995 (first entry)
XX
DE   Reverse transcription primer used in cDNA analysis technique.
XX
KW   Analysis; gene expression; reverse transcription; primer; cDNA;
XX   aggregate; restriction enzyme; ss.
XX
OS   Synthetic.
XX
PN   JP06303997-A.
XX
PD   01-NOV-1994.
XX
PF   16-APR-1993; 93JP-00112515.
XX
PR   16-APR-1993; 93JP-00112515.
XX

```

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
XX
RESULT 601
ID AAQ75663 standard; DNA; 21 BP.
XX
XX AAQ75663;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
XX

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
XX
RESULT 602
ID AAQ75636 standard; DNA; 21 BP.
XX
XX AAQ75636;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 6; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1735 CAAAAAAAAAAAAAAAAA 1752
DB 18 CAAAAAAAAAAAAAAAAA 1
XX
RESULT 603
ID AAQ75610 standard; DNA; 21 BP.
XX
XX AAQ75610;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX JN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

XX PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1752
 |||||
 Db 18 CAAAAA AAAAAAAAAA 1

RESULT 604
 AAQ75632/c
 ID AAQ75632 standard; DNA; 21 BP.

XX AC AAQ75632;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

XX Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

XX PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1752
 |||||
 Db 18 CAAAAA AAAAAAAAAA 1

RESULT 604
 AAQ75632/c
 ID AAQ75632 standard; DNA; 21 BP.

XX AC AAQ75632;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

XX Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

XX PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of

CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1752
 |||||
 Db 18 CAAAAA AAAAAAAAAA 1

RESULT 605
 AAQ75619/c
 ID AAQ75619 standard; DNA; 21 BP.

XX AC AAQ75619;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA; aggregate; restriction enzyme; ss.

XX Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.

XX PS Disclosure; Page 6; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily.

XX Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1752
 |||||
 Db 18 CAAAAA AAAAAAAAAA 1

RESULT 606
 AAQ75621/c


```

Best Local Similarity 100.0%; Pred. No. 3e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 609
AAQ75637/c
ID AAQ75637 standard; DNA; 21 BP.
XX
AC AAQ75637;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 610
AAQ75666/c
ID AAQ75666 standard; DNA; 21 BP.
XX
AC AAQ75666;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

```

```

OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAAAAAA 1752
Db 18 CAAAAAAAAAAAAAAAAAAAAA 1

RESULT 611
AAQ75623/c
ID AAQ75623 standard; DNA; 21 BP.
XX
AC AAQ75623;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 6; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

```

CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752
 DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 612
 AAQ75635/c
 ID AAQ75635 standard; DNA; 21 BP.

AC AAQ75635;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02; 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752
 DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 613
 AAQ75658/c
 ID AAQ75658 standard; DNA; 21 BP.

XX
 AC AAQ75658;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 6; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX

SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1752
 DB 18 CAAAAAAAAAAAAAAAAA 1

RESULT 614
 AAQ75638/c
 ID AAQ75638 standard; DNA; 21 BP.

AC AAQ75638;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 6; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAA 1752
 Db 18 CAAAAAAAAAAAAAAAAA 1
 RESULT 615
 AAQ64706/C
 ID AAQ64706 standard; cDNA to mRNA; 22 BP.
 XX
 AC AAQ64706;
 XX
 XX 25-MAR-2003 (revised)
 DT 04-JAN-1995 (first entry)
 XX
 XX 2',5'-linked tetraadenylate-antisense oligonucleotide chimeric mol.
 DE antisense; 2',5'-tetraadenylate; 2-5A dependent RNase activator;
 KW RNA cleavage; antiviral therapy; chimeric molecule; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..4
 FT /tag= a
 FT /label= 2',5'-linked tetraadenylate
 FT /note= "nucleotides linked through phosphodiester bonds
 FT at hydroxyl groups of 2' and 5' carbons"
 FT 5..22
 FT misc_feature /tag= b
 FT /note= "antisense region"
 FT
 XX
 XX WO9409129-A2.
 XX
 XX 28-APR-1994.
 PD
 XX
 XX 20-OCT-1993; 93WO-US010103.
 PP
 XX
 XX 21-OCT-1992; 92US-00965666.
 PR
 XX 17-SEP-1993; 93US-00123449.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (CLEV-) CLEVELAND CLINIC RES INST.
 XX
 XX Torrence P, Silverman R, Maitra R, Lesiak K;
 PI WPI; 1994-151315/18.
 XX
 DR Specific cleavage of RNA, useful partic. for treating viral infection,
 PT cancers, etc. - by using anti-sense oligo:nucleotide coupled to activator
 PT of 2-5A dependent RNase.

XX
 PS Example 1; Page 68; 86pp; English.
 XX
 CC This sequence is an example of a 2-5A-antisense oligonucleotide chimeric
 CC molecule. The antisense region targets the chimeric molecule to a
 CC particular region of RNA to be specifically cleaved and the 2',5'-linked
 CC tetraadenylate tail activates the 2-5A RNase. Typical applications are
 CC treatment of viral infections (esp. for cleavage of an RNA virus genome),
 CC cancer; leukaemia, cardiovascular disorders (e.g. restenosis after
 CC angioplasty), genetic disorders, osteoarthritis or rheumatoid arthritis.
 CC (Updated on 25-MAR-2003 to correct EN field.)
 XX
 SQ Sequence 22 BP; 4 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 22 AAAAAAAAAAAAAAAAAA 5
 RESULT 616
 ABX94933
 ID ABX94933 standard; DNA; 22 BP.
 XX
 AC ABX94933;
 XX
 XX 25-AUG-2003 (first entry)
 DT
 XX
 DE Renilla luciferase associated PCR primer #198forw.
 XX
 KW Luciferase; ubiquitin promoter; glucocorticoid receptor; PCR; primer;
 KW transrepression protein-protein reciprocal effect; immunosuppressive;
 KW transactivation deficient inflammation; ss.
 XX
 OS Renilla reniformis.
 XX
 XX DE10222714-A1.
 XX
 XX 02-JAN-2003.
 PD
 XX
 XX 23-MAY-2002; 2002DE-01022714.
 PF
 XX 28-MAY-2001; 2001DE-01024575.
 PF
 XX (GESL) FORSCHUNGSZENTRUM KARLSRUHE GMBH.
 PA Goettlicher M, Heilbock C, Herrlich P, Litfin M, Schneider S;
 XX WPI; 2003-291460/29.
 XX
 FT A genetically modified glucocorticoid receptor which is transactivation
 FT deficient is used to identify cofactors which will be useful to provide
 FT inflammation-inhibiting and immunosuppressive treatment.
 FT
 XX Disclosure; Col 12; 12pp; German.
 XX
 CC This invention describes a novel genetically modified glucocorticoid
 CC receptor, which has transrepression protein-protein reciprocal effects
 CC and is transactivation deficient. The invention also describes (1) a gene
 CC construct comprising at least a nucleic acid encoding the glucocorticoid
 CC receptor, operably linked with regulatory sequences of a reporter gene,
 CC preferably a DNA-binding domain for a reporter gene; (2) identifying a
 CC gene encoding a cofactor involved in glucocorticoid receptor modulation
 CC of at least another transcription factor comprising: (a) using the above
 CC construct with an expression bank of a eukaryotic cell expressed in a
 CC yeast two hybrid system; (b) detecting a specific protein-protein complex
 CC or the receptor and a cofactor through growth in a selective medium for
 CC the reporter and (c) isolating and characterising the nucleic acid
 CC encoding the cofactor in the cDNA clone; (3) a cofactor with
 CC transrepression specific for the glucocorticoid receptor which in a

CC protein-protein interaction achieves a reciprocal effect, whereby within
CC a downstream segment the N-terminal AF-1 and the DNA-binding domain of
CC the receptors are bound; (4) identifying an agent which affects the
CC reciprocal effect of the glucocorticoid receptor with other transcription
CC factors and/or cofactors, whereby the receptor or construct is contacted
CC with a potential agent and modulation of the interaction of the protein
CC partner is measured by expression of the reporter gene or detecting
CC protein-protein complex binding; (5) an agent for modulating interaction
CC of the glucocorticoid receptor with a cofactor which binds either at the
CC binding site of a physiological hormone or at a separate binding place
CC and (6) a compound with an inflammation-inhibiting or immunosuppressive
CC effect comprising the above agent. The genetically modified
CC glucocorticoid receptor is useful to identify coreceptors which are used
CC to produce an inflammation-inhibiting or immunosuppressive treatment.
CC This sequence represents a PCR primer #198forw used to amplify a Renilla
CC reniformis luciferase gene which is then cloned into a reporter construct
CC behind a ubiquitin promoter
XX
SQ Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 151 TTCCAGGCCCATGTCGGGG 168
Db 5 TTCCAGGCCCATGTCGGGG 22

RESULT 617
AAD33503
ID AAD33503 standard; DNA; 23 BP.
XX
AC AAD33503;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.
XX
KW Molecular array; probe; ss.

OS Unidentified.
PN EP1186673-A2.
XX
PD 13-MAR-2002.
XX
PF 10-SEP-2001; 2001BP-00307665.
XX
PR 11-SEP-2000; 2000US-00659173.
XX
PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX
PI Wobler PK, Delenstarr GC;
XX
DR WPI; 2002-282886/33.
XX
PT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.
XX
PS Disclosure; Page 14; 32pp; English.
XX

CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibrations probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data
XX

SQ Sequence 23 BP; 18 A; 3 C; 0 G; 2 T; 0 U; 0 Other;
Query Match 1.0%; Score 18; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 1 AAAAAAAAAAAAAAAAAA 18
RESULT 618
ASN85073/C
ID ASN85073 standard; DNA; 24 BP.
XX
AC ASN85073;
XX
DT 05-SEP-2002 (first entry)
XX
DE Human S4 ribosomal protein 13.97 PCR primer #2.
XX
KW Human; S4 ribosomal protein 13.97; malignant tumour; haemopathy;
KW HIV infection; immunological disease; inflammation; cytostatic; anti-HIV;
KW PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN CN1333268-A.
XX
PD 30-JAN-2002.
XX
PF 07-JUL-2000; 2000CN-00117077.
XX
PR 07-JUL-2000; 2000CN-00117077.
XX
PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-292916/34.
XX
PT Human S4 ribosomal protein 13.97 polypeptide and encoding polynucleotide,
PT useful for treating malignant tumor, inflammation, hemopathy, human
PT immunodeficiency virus infection, immunological disease and inflammation.
XX
PS Example 2; Page 16 (Disclosure); 33pp; Chinese.
XX
CC The present invention relates to human S4 ribosomal protein 13.97 (see
CC ABB83379). The ribosomal protein and its coding sequence are useful for
CC treating malignant tumours, haemopathy, HIV infection, immunological
CC diseases and various inflammations. The present sequence is a PCR primer,
CC which was used in an example from the invention
XX
SQ Sequence 24 BP; 1 A; 2 C; 1 G; 20 T; 0 U; 0 Other;

Query Match 1.0%; Score 18; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1753
Db 24 AAAAAAAAAAAAAAAAAA 7
RESULT 619
AAD33505
ID AAD33505 standard; DNA; 24 BP.
XX
AC AAD33505;
XX
DT 01-JUL-2002 (first entry)
XX
DE T7T18Apad_PS12-24-0001 probe for calibration of molecular array data.

XX Molecular array; probe; ss.
 XX Unidentified.
 XX EPI186673-A2.
 XX 13-MAR-2002.
 XX 10-SEP-2001; 2001EP-00307665.
 XX 11-SEP-2000; 2000US-00659173.
 XX (AGIL-) ACILENT TECHNOLOGIES INC.
 XX Wobler PK, Delenstarr GC;
 XX WPI; 2002-282886/33.
 XX Calibration of molecular array data by employing calibration probes that generate signals proportional to total concentrations of labeled target molecules, and molecular arrays incorporating sets of calibration probes.
 XX Disclosure; Page 14; 32pp; English.
 XX The invention relates to a method for calibrating data scanned from a molecular array. The method involves employing calibrations probes that generate signals proportional to the total concentrations of labeled target molecules to which the molecular array probes are directed over an entire range of sample solutions and molecular arrays incorporating sets of calibration probes. Method is useful for calibrating different types of signals scanned from a molecular array, or calibrating signals scanned from different molecular arrays. The present sequence is poly (A)
 XX normalisation probe used in calibration of molecular array data
 XX
 XX Sequence 24 BP; 18 A; 4 C; 0 G; 2 T; 0 U; 0 Other;
 Query Match 1.0%; Score 18; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 1 AAAAAAAAAAAAAAAAAA 18
 RESULT 620
 AAQ75748/c
 ID AAQ75748 standard; DNA; 21 BP.
 AC AAQ75748;
 XX
 XX 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 XX 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
 XX Disclosure; Page 8; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily
 XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1729 AGTTTACAAAAAAAAAAAAA 1749

PT Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
 XX Disclosure; Page 8; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily
 XX Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1733 TACAAAAAAAAAAAAAAAAA 1753
 Db 21 TCGGAAAAAAAAAAAAAAAAA 1
 RESULT 621
 AAQ75733/c
 ID AAQ75733 standard; DNA; 21 BP.
 AC AAQ75733;
 XX
 XX 04-AUG-1995 (first entry)
 DT Reverse transcription primer used in cDNA analysis technique.
 XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX Synthetic.
 XX JP06303997-A.
 XX 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 XX 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX WPI; 1995-018287/03.
 XX
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed by digestion with restriction enzymes.
 XX Disclosure; Page 8; 11pp; Japanese.
 XX A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse transcription primer; (b) digesting each of the prepared aggregates of the double-stranded cDNAs with restriction enzyme and; (c) electrophoresing the digested aggregate of cDNAs in separate lanes. The method can be used to analyse gene expression rapidly and easily
 XX Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1729 AGTTTACAAAAAAAAAAAAA 1749

```
Db      21  ACTTAAAAAATAAAAAAAAAA 1
||||| | ||||| ||||| |||||
RESULT 622
AAQ75736/c
ID  AAQ75736 standard; DNA; 21 BP.
XX
XX
AC  AAQ75736;
XX
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 8; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY  1733 TACAAAAAATAAAAAAAAAA 1753
    ||||| ||||| ||||| |||||
Db      21  TCCGAAAAAATAAAAAAAAAA 1
||||| ||||| ||||| |||||
RESULT 623
AAQ75730/c
ID  AAQ75730 standard; DNA; 21 BP.
XX
XX
AC  AAQ75730;
XX
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 9; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY  1733 TACAAAAAATAAAAAAAAAA 1753
    ||||| ||||| ||||| |||||
Db      21  TCCGAAAAAATAAAAAAAAAA 1
||||| ||||| ||||| |||||
RESULT 624
AAQ75780/c
ID  AAQ75780 standard; DNA; 21 BP.
XX
XX
AC  AAQ75780;
XX
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 9; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY  1730 GTTACAAAAAATAAAAAAAAAA 1750
    ||||| ||||| ||||| |||||
Db      21  GATTAAAAAATAAAAAAAAAA 1
||||| ||||| ||||| |||||
RESULT 624
AAQ75780/c
ID  AAQ75780 standard; DNA; 21 BP.
XX
XX
AC  AAQ75780;
XX
XX
DT  04-AUG-1995 (first entry)
XX
DE  Reverse transcription primer used in cDNA analysis technique.
XX
KW  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
OS  Synthetic.
XX
PN  JP06303997-A.
XX
PD  01-NOV-1994.
XX
PF  16-APR-1993; 93JP-00112515.
XX
PR  16-APR-1993; 93JP-00112515.
XX
PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR  WPI; 1995-018287/03.
XX
PT  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
PS  Disclosure; Page 9; 11pp; Japanese.
XX
CC  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
SQ  Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX
QY  1730 GTTACAAAAAATAAAAAAAAAA 1750
    ||||| ||||| ||||| |||||
Db      21  GATTAAAAAATAAAAAAAAAA 1
||||| ||||| ||||| |||||
```

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 XX method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1752
 Db 21 TGAGAAAAA 1

RESULT 625
 AAQ75781/c
 ID AAQ75781 standard; DNA; 21 BP.

AC AAQ75781;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 9; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 0 A; 2 C; 0 G; 19 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;
 Best Local Similarity 90.5%; Pred. No. 3.2e+02;
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACAAAAAA 1754
 Db 21 AGAGAAAAA 1

RESULT 626

AAQ75684/c

ID AAQ75684 standard; DNA; 21 BP.

AC AAQ75684;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 3.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1752
 Db 21 TGAGAAAAA 1

RESULT 627

AAQ75695/c

ID AAQ75695 standard; DNA; 21 BP.

AC AAQ75695;

DT 04-AUG-1995 (first entry)

DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed

```
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          1.0%; Score 17.8; DB 1; Length 21;
    Best Local Similarity 90.5%; Pred. No. 3.2e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 CAAAAA...AAAAAAAAA 1755
   || |||||
Db 21 CAGTAAAAA...AAAAAAAAA 1

RESULT 628
AAQ75753/c
ID AAQ75753 standard; DNA; 21 BP.
XX
AC AAQ75753;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
    Query Match          1.0%; Score 17.8; DB 1; Length 21;
    Best Local Similarity 90.5%; Pred. No. 3.2e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1730 GTTACAAAA...AAAAAAAAA 1750
   || |||||
Db 21 GTGTAAAAA...AAAAAAAAA 1

RESULT 630
AAQ75728/c
ID AAQ75728 standard; DNA; 21 BP.
XX
AC AAQ75728;
XX
XX 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.

PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
    Query Match          1.0%; Score 17.8; DB 1; Length 21;
    Best Local Similarity 90.5%; Pred. No. 3.2e+02;
    Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAAAAA...AAAAAAAAA 1754
   || |||||
```

```
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1753
Dy 21 TATTAAAAA 1
RESULT 631
AAQ75758/c
ID AAQ75758 standard; DNA; 21 BP.
XX AC AAQ75758;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 3 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1753
Dy 21 TATTAAAAA 1
RESULT 631
AAQ75758/c
ID AAQ75758 standard; DNA; 21 BP.
XX AC AAQ75758;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
```

```
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1730 GTTACAAAAA 1750
Dy 21 GTTCAAAAAA 1
RESULT 632
AAQ75788/c
ID AAQ75788 standard; DNA; 21 BP.
XX AC AAQ75788;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX XX WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1732 TTACAAAAA 1752
Dy 21 TTGAAAAA 1
RESULT 633
AAQ75791/c
ID AAQ75791 standard; DNA; 21 BP.
XX AC AAQ75791;
XX DT 04-AUG-1995 (first entry)
XX XX
```

```
DE Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS JP06303997-A.
PN 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
PF 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
PT
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. NO. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1735 CAAAAAAGAAAAA 1755
DB 21 CAGGAAAAA 1
RESULT 634
AAQ75716/c
ID AAQ75716 standard; DNA; 21 BP.
XX AC AAQ75716;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. NO. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1735 CAAAAAAGAAAAA 1755
DB 21 CAGGAAAAA 1
RESULT 634
AAQ75716/c
ID AAQ75716 standard; DNA; 21 BP.
XX AC AAQ75716;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. NO. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1735 CAAAAAAGAAAAA 1755
DB 21 CATTAAAAA 1
RESULT 635
AAQ75727/c
ID AAQ75727 standard; DNA; 21 BP.
XX AC AAQ75727;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. NO. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1735 CAAAAAAGAAAAA 1755
DB 21 CATTAAAAA 1
```



```

RESULT 636
AAQ75740/c
ID AAQ75740 standard; DNA; 21 BP.
XX
AC AAQ75740;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1752
DB 21 TTCGAAAAA 1

RESULT 637
AAQ75779/c
ID AAQ75779 standard; DNA; 21 BP.
XX
AC AAQ75779;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1752
DB 21 TTCGAAAAA 1

RESULT 638
AAQ75689/c
ID AAQ75689 standard; DNA; 21 BP.
XX
AC AAQ75689;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 CAAAAA 1755
DB 21 CGAGAAAAA 1

RESULT 639
AAQ75689/c
ID AAQ75689 standard; DNA; 21 BP.
XX
AC AAQ75689;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1735 CAAAAA 1755
DB 21 CGAGAAAAA 1

```

```

XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
      Query Match      1.0%; Score 17.8; DB 1; Length 21;
      Best Local Similarity 90.5%; Pred. No. 3.2e+02;
      Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1734 ACACAAAAAATAAAAAAAAAA 1754
    ||| ||||| ||||| ||||| |||||
DB 21 ACGTAAAAAATAAAAAAAAAA 1

RESULT 639
AAQ75722/c
ID AAQ75722 standard; DNA; 21 BP.
XX AC AAQ75722;
XX
XX 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX DE Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A..
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1730 GTTTACAAAAAATAAAAAAAAAA 1750
    ||| ||||| ||||| ||||| |||||
DB 21 GCTTAAAAAATAAAAAAAAAA 1

RESULT 640
AAQ75760/c
ID AAQ75760 standard; DNA; 21 BP.
XX AC AAQ75760;
XX
XX 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.

```

```

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match      1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1733 TACAAAAAATAAAAAAAAAA 1753
    ||| ||||| ||||| ||||| |||||
DB 21 TATGAAAAAATAAAAAAAAAA 1

RESULT 641
AAQ75692/c
ID AAQ75692 standard; DNA; 21 BP.
XX AC AAQ75692;
XX
XX 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.

```

```
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1732 TTACAAAAA 1752
Db 21 TTGTA 1
RESULT 642
AAQ75705/C
ID AAQ75705 standard; DNA; 21 BP.
XX
AC AAQ75705;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1754
Db 21 ACCGAAAAA 1
RESULT 644
AAQ75756/C
ID AAQ75756 standard; DNA; 21 BP.
XX
AC AAQ75756;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
```

```
RESULT 643
AAQ75737/C
ID AAQ75737 standard; DNA; 21 BP.
XX
AC AAQ75737;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 1 C; 2 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1734 ACACAAAAA 1754
Db 21 ACCGAAAAA 1
RESULT 644
AAQ75756/C
ID AAQ75756 standard; DNA; 21 BP.
XX
AC AAQ75756;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
```

```
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX CC Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 3.2e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1731 TTTTACAAAAA 1751
DB 21 TTTGAAAAA 1
RESULT 645
AAQ75785/c
ID AAQ75785 standard; DNA; 21 BP.
XX AC AAQ75785;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 3.2e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1731 TTTTACAAAAA 1751
DB 21 TTTGAAAAA 1
RESULT 645
AAQ75785/c
ID AAQ75785 standard; DNA; 21 BP.
XX AC AAQ75785;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 3.2e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1731 TTTTACAAAAA 1751
DB 21 TTTGAAAAA 1
RESULT 647
AAQ75704/c
ID AAQ75704 standard; DNA; 21 BP.
XX AC AAQ75704;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
```

```
SQ Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 3.2e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1734 ACAA 1754
DB 21 ACGGAAAAA 1
RESULT 646
AAQ75685/c
ID AAQ75685 standard; DNA; 21 BP.
XX AC AAQ75685;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX CC Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17.8; DB 1; Length 21;
XX Best Local Similarity 90.5%; Pred. No. 3.2e+02;
XX Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1734 ACAA 1754
DB 21 AGATAAAAA 1
RESULT 647
AAQ75704/c
ID AAQ75704 standard; DNA; 21 BP.
XX AC AAQ75704;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX
```

KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.

PN JP06303997-A.

XX 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

DR WPI; 1995-018287/03.

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 3.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1753

Db 21 TCCTAAAAA 1

RESULT 648

AAQ75708/c

ID AAQ75708 standard; DNA; 21 BP.

XX AC AAQ75708;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 3.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1752

Db 21 TTCTAAAAA 1

RESULT 649

AAQ75759/c

ID AAQ75759 standard; DNA; 21 BP.

XX AC AAQ75759;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;

Best Local Similarity 90.5%; Pred. No. 3.2e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1755

Db 21 CATGAAAAA 1

```
RESULT 650
AAQ75734/c
ID AAQ75734 standard; DNA; 21 BP.
XX
AC AAQ75734;
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1730 GTTTACAAAAA 1750
DB 21 CGTTAAAAA 1
XX
RESULT 651
AAQ75683/c
ID AAQ75683 standard; DNA; 21 BP.
XX
AC AAQ75683;
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1730 GTTTACAAAAA 1750
DB 21 CGTTAAAAA 1
XX
RESULT 652
AAQ75696/c
ID AAQ75696 standard; DNA; 21 BP.
XX
AC AAQ75696;
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1735 CAAAAA 1755
DB 21 CGTAAAAA 1
XX
RESULT 652
AAQ75696/c
ID AAQ75696 standard; DNA; 21 BP.
XX
AC AAQ75696;
XX
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
```

```

Query Match      1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1753
DB 21 TAGTAAAAA 1

RESULT 653
AAQ75710/c
ID AAQ75710 standard; DNA; 21 BP.
XX
AC AAQ75710;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match      1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAA 1750
DB 21 GTCTAAAAA 1

RESULT 654
AAQ75721/c
ID AAQ75721 standard; DNA; 21 BP.
XX
AC AAQ75721;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;

```

```

KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
SQ A method for the analysis of cDNA comprises (a) preparing an aggregate of
double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
and using the aggregate of mRNAs as the template for each reverse
transcription primer; (b) digesting each of the prepared aggregates of
the double-stranded cDNAs with restriction enzyme and; (c)
electrophoresing the digested aggregate of cDNAs in separate lanes. The
method can be used to analyse gene expression rapidly and easily.
XX
SQ Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;

Query Match      1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 ACAA 1754
DB 21 ACTTAAAAA 1

RESULT 655
AAQ75792/c
ID AAQ75792 standard; DNA; 21 BP.
XX
AC AAQ75792;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
FN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX

```

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1733 TACAAAAAATAAAAAAAAAA 1753
DB 21 TAGAAAAAATAAAAAAAAAA 1

RESULT 656
AAZ26584
ID AAZ26584 standard; DNA; 21 BP.
XX
AC AAZ26584;
XX

DT 30-NOV-1999 (first entry)
XX
DE Human polymorphic region 773.
XX

KW Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
KW cell viability; loss of heterozygosity; precancerous condition; ASI;
KW allele specific inhibitor; somatic cell; diagnosis; prevention;
KW atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
KW dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
KW graft versus host disease; malignant cell removal; bone marrow; ss.
XX

OS Homo sapiens.
XX
PN WO9841648-A2.
XX

PD 24-SEP-1998.
XX

PF 19-MAR-1998; 98WO-US005419.
XX

PR 20-MAR-1997; 97US-0041057P.
XX

PA (VARI-) VARIAGENICS INC.
XX

PI Houseman D, Ledley FD, Stanton VP;
XX

DR WPI; 1998-521232/44.
XX

PT Identifying target genes for allele-specific drugs - used for diagnosis,
PT prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.
XX

PS Disclosure; Fig 7; 605pp; English.
XX

CC This invention describes a novel method for identifying an inhibitor
CC potentially useful for treatment of cancer, where the inhibitor is active
CC on a gene vital for cell growth or viability, and where the gene is
CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
CC used for preventing the development of cancer in a patient having a
CC precancerous condition, by administering to the patient a first allele
CC specific inhibitor (ASI) targeted to an allele of a first essential gene
CC present in cells of the precancerous condition, where the normal somatic
CC cells of the patient are heterozygous for the first gene, the inhibitor
CC is active on at least one but less than all allelic forms of the gene
CC present in a population and targets only one allelic form present in the
CC normal somatic cells, and the first gene. The products and methods can be
CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic

CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-226825 represent
CC human polymorphic sites described in the method of the invention
XX
XX Sequence 21 BP; 15 A; 0 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.8; DB 1; Length 21;
Best Local Similarity 90.5%; Pred. No. 3.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1730 GTTTACAAAAAATAAAAAAAAA 1750
DB 1 GTTTTAAAAAATAAAAAAAAAA 21

RESULT 657
AAQ75552/c
ID AAQ75552 standard; DNA; 19 BP.
XX
AC AAQ75552;
XX

DT 04-AUG-1995 (first entry)
XX

DE Reverse transcription primer used in cDNA analysis technique.
XX

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX

OS Synthetic.
XX

PN JP06303997-A.
XX

PD 01-NOV-1994.
XX

PF 16-APR-1993; 93JP-00112515.
XX

PR 16-APR-1993; 93JP-00112515.
XX

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX

DR WPI; 1995-018287/03.
XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX

PS Disclosure; Page 5; 11pp; Japanese.
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

XX Sequence 19 BP; 2 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAATAAAAAAAAA 1750
DB 19 TAAAAAATAAAAAAAAAA 1

RESULT 658
AAQ75553/c

ID AAQ75553 standard; DNA; 19 BP.
XX

AC AAQ75553;
XX


```

XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ATAAAAAAAAAAAAAAAAA 1

RESULT 659
AAQ75551/c
ID AAQ75551 standard; DNA; 19 BP.
XX
AC AAQ75551;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 1 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ATAAAAAAAAAAAAAAAAA 1

RESULT 660
AAQ75555/c
ID AAQ75555 standard; DNA; 19 BP.
XX
AC AAQ75555;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 1 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CTAATAAAAAAAAAAAAAA 1

RESULT 660
AAQ75555/c
ID AAQ75555 standard; DNA; 19 BP.
XX
AC AAQ75555;
XX
XX 04-AUG-1995 (first entry)
DT Reverse transcription primer used in cDNA analysis technique.
DE Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 5; 11pp; Japanese.
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY 1735 CAAAAAAAAAAAAAAAAA 1753
DB 19 CGAAAAAAAAAAAAAAAAA 1

RESULT 661
AAQ75557/C
ID AAQ75557 standard; DNA; 19 BP.
XX
AC AAQ75557;
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.

PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 19 BP; 0 A; 1 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 94.7%; Pred. No. 3.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACACAAAAAAAAAAAAAAAAA 1752
DB 19 AGAAAAAAAAAAAAAAAAA 1

RESULT 662
ADE29541
ID ADE29541 standard; RNA; 19 BP.
XX
AC ADE29541;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:163.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;
KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;

KW psoriasis; inflammatory bowel disease; drug screening;
KW genetic engineering; pharmacogenomic; gene mapping; ss.
OS Synthetic.
PN WO2003072590-A1.
XX
PD 04-SEP-2003.
XX
PF 28-JAN-2003; 2003WO-US002510.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;
XX
XX WPI; 2003-689980/65.
DR
XX New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PT protein kinase genes.
XX
PS Example 3; SEQ ID NO 163; 164pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.

SQ Sequence 19 BP; 16 A; 1 C; 0 G; 0 T; 2 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 3.3e+02;
Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAAAAAAAAAAAAAA 1751
DB 1 UUCAAAAAAAAAAAAAAAAA 19

RESULT 663
ADE29704/C
ID ADE29704 standard; RNA; 19 BP.
XX
AC ADE29704;
XX
DT 29-JAN-2004 (first entry)
XX
DE Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:326.
XX
KW short interfering nucleic acid; siNA; downregulation; inhibition;

KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytosolic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antiproliferative; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.
 XX
 OS Synthetic.
 XX
 XX WO2003072590-A1.
 XX
 XX
 XX PD 04-SEP-2003.
 XX
 XX PF 28-JAN-2003; 2003WO-US002510.
 XX
 XX PR 20-FEB-2002; 2002US-0358580P.
 XX PR 11-MAR-2002; 2002US-0363124P.
 XX PR 06-JUN-2002; 2002US-0386782P.
 XX PR 29-AUG-2002; 2002US-0406784P.
 XX PR 05-SEP-2002; 2002US-0408378P.
 XX PR 09-SEP-2002; 2002US-0409293P.
 XX PR 15-JAN-2003; 2003US-0440129P.
 XX
 XX PA (STRN-) SIRNA THERAPEUTICS INC.
 XX
 XX PI Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowkira B;
 XX
 XX DR WPI; 2003-689980/65.
 XX
 XX PT New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.
 XX
 XX Example 3; SEQ ID NO 326; 164pp; English.
 XX
 XX CC The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes in cells,
 CC tissue explants or organisms, e.g. for treating obesity, diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.
 XX
 XX SQ Sequence 19 BP; 2 A; 0 C; 1 G; 0 T; 16 U; 0 Other;
 Query Match 1.0%; Score 17.4; DB 1; Length 19;
 Best Local Similarity 94.7%; Pred. No. 3.3e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1733 TACAAAAA
 Db 19 TTCAAAAAA
 RESULT 664
 AAQ49436/c
 ID AAQ49436 standard; cDNA; 20 BP.
 XX
 XX AC AAQ49436;
 XX

DT 25-MAR-2003 (revised)
 DT 27-APR-1994 (first entry)
 XX
 DE Cytochrome P450 sequence amplification PCR primer polyT.
 XX
 KW Transgenic plants; altered petal colour; polymerase chain reaction; ss.
 XX
 OS Synthetic.
 XX
 XX WO9320206-A1.
 XX
 XX PD 14-OCT-1993.
 XX
 XX PF 25-MAR-1993; 93WO-AU000127.
 XX
 XX PR 27-MAR-1992; 92AU-00001538.
 XX PR 07-JAN-1993; 93AU-00006698.
 XX
 XX PA (ITFL-) INT FLOWER DEV PTY LTD.
 XX
 XX PI Holton TA, Cornish EC, Tanaka Y;
 XX
 XX DR WPI; 1993-336914/42.
 XX
 XX PT Nucleic acid isolate encoding flavonoid-3'-hydroxylase - is used to
 PT create transgenic plants with altered petal colour.
 XX
 XX PS Disclosure; Page 25; 86pp; English.
 XX
 XX CC The sequence is that of a PCR primer which was used in polymerase chain
 CC reactions for the amplification of cloned cytochrome P450 sequences.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1735 CAAAAA
 Db 19 CTAAAAA
 RESULT 665
 AAQ75591/c
 ID AAQ75591 standard; DNA; 20 BP.
 XX
 XX AC AAQ75591;
 XX
 XX DT 04-AUG-1995 (first entry)
 XX
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 XX PN JF06303997-A.
 XX
 XX PD 01-NOV-1994.
 XX
 XX PF 16-APR-1993; 93JP-00112515.
 XX
 XX PR 16-APR-1993; 93JP-00112515.
 XX
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 XX DR WPI; 1995-018287/03.
 XX
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.


```

PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 ATAAAAAAAAAAAAAAAAAA 1
RESULT 669
AAQ75594/C
ID AAQ75594 standard; DNA; 20 BP.
XX
AC AAQ75594;
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX

```

```

XX
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CGAAAAAAAAAAAAAAAAAA 1
RESULT 670
AAQ75581/C
ID AAQ75581 standard; DNA; 20 BP.
XX
AC AAQ75581;
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 0 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1732 TTACAAAAAAAAAAAAAAAA 1750
Db 19 TTAATAAAAAAAAAAAAAAAAA 1
RESULT 671
AAQ75578/C
ID AAQ75578 standard; DNA; 20 BP.
XX
AC AAQ75578;
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX

```

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 1; Mismatches 0; Gaps 0;
OY 1735 CAAAAA... 1753
DB 19 CTA... 1

RESULT 672
AAQ75602/c
ID AAQ75602 standard; DNA; 20 BP.
XX
XX AAQ75602;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 1; Mismatches 0; Gaps 0;
OY 1735 CAAAAA... 1753
DB 19 CTA... 1

RESULT 672
AAQ75602/c
ID AAQ75602 standard; DNA; 20 BP.
XX
XX AAQ75602;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX

PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1734 AAAAAA... 1752
DB 19 AGAAAA... 1

RESULT 673
AAQ75582/c
ID AAQ75582 standard; DNA; 20 BP.
XX
XX AAQ75582;
AC
XX 04-AUG-1995 (first entry)
DT
XX Reverse transcription primer used in cDNA analysis technique.
DE
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
XX JP06303997-A.
PN
XX 01-NOV-1994.
PD
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1732 TTACAAAA... 1750
DB 19 TTA... 1

[illegible]

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1753
DB 2 CTAATAAAAAAAAAAAAAAAAA 20

RESULT 677
ABZ85534
ID ABZ85534 standard; DNA; 20 BP.
XX
AC ABZ85534;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 776; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1754
DB 1 AAAAAAAAAAAAAAAAAAAGAAAA 19

RESULT 678
ABZ89487
ID ABZ89487 standard; DNA; 20 BP.
XX
AC ABZ89487;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4729; 872pp; English.
XX

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 18 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
 ||| ||||| ||||| ||||| |||||
 Db 2 ACCAAAAAAAAAAAAAAAAA 20

RESULT 679
 ABZ88564
 ID ABZ88564 standard; DNA; 20 BP.
 XX
 AC ABZ88564;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 3806; 872pp; English.
 XX

CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
 Best Local Similarity 94.7%; Pred. No. 3.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAAAAAA 1752
 ||| ||||| ||||| ||||| |||||
 Db 2 ACAGAAAAAAAAAAAAAAAA 20

RESULT 680
 ABZ89703
 ID ABZ89703 standard; DNA; 20 BP.
 XX
 AC ABZ89703;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 4945; 872pp; English.
 XX

CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 16 A; 0 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 20;
Best Local Similarity 94.7%; Pred. No. 3.4e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA 1749
||| |||||
DB 2 TTTAAAAA 20

RESULT 681
AAQ75735/C
ID AAQ75735 standard; DNA; 21 BP.

XX AC AAQ75735;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 21 BP; 0 A; 1 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1753
||| |||||
DB 19 CAAAAA 1

RESULT 682
AAQ75738/C

ID AAQ75738 standard; DNA; 21 BP.

XX AC AAQ75738;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1753
||| |||||
DB 19 CAAAAA 1

RESULT 683
AAQ75719/C

ID AAQ75719 standard; DNA; 21 BP.

XX AC AAQ75719;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.

PN JP06303997-A.

PD 01-NOV-1994.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;

Best Local Similarity 94.7%; Pred. No. 3.6e+02;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1750

Db 19 TTA 1

RESULT 684

AAQ75739/c

ID AAQ75739 standard; DNA; 21 BP.

XX AAQ75739;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 21;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA 1753

Db 19 CGA 1

RESULT 685

AAQ75729/c

ID AAQ75729 standard; DNA; 21 BP.

XX AAQ75729;

XX 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;

XX aggregate; restriction enzyme; ss.

XX Synthetic.

XX JP06303997-A.

XX 01-NOV-1994.

XX 16-APR-1993; 93JP-00112515.

XX 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.

XX Disclosure; Page 8; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily

XX Sequence 21 BP; 2 A; 0 C; 0 G; 19 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 17.4; DB 1; Length 21;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1732 TTACAAAAA 1750

Db 19 TTA 1

```
RESULT 686
AAQ75732/c
ID AAQ75732 standard; DNA; 21 BP.
XX
AC AAQ75732;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1732 TTACAAAAA 1750
Db 19 TTAATAAAAAA 1
RESULT 687
AAQ75718/c
ID AAQ75718 standard; DNA; 21 BP.
XX
AC AAQ75718;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 3 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1732 TTACAAAAA 1750
Db 19 TTAATAAAAAA 1
```

```
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAA 1753
Db 19 CTAATAAAAAA 1
RESULT 688
AAQ75741/c
ID AAQ75741 standard; DNA; 21 BP.
XX
AC AAQ75741;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;
```

```

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CGAAAAAAAAAAAAAAAAA 1

RESULT 689
AAQ75742/c
ID AAQ75742 standard; DNA; 21 BP.
XX
AC AAQ75742;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CGAAAAAAAAAAAAAAAAA 1

RESULT 690
AAQ75747/c
ID AAQ75747 standard; DNA; 21 BP.
XX
AC AAQ75747;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;

```

```

KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;

Query Match          1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CGAAAAAAAAAAAAAAAAA 1

RESULT 691
AAQ75715/c
ID AAQ75715 standard; DNA; 21 BP.
XX
AC AAQ75715;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX

```

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 3.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAAAAAA 1753
 DB 19 CTAATAAAAAAAAAAAAA 1

RESULT 692
 AAQ75686/c
 ID AAQ75686 standard; DNA; 21 BP.
 XX
 AC AAQ75686;

DT 04-AUG-1995 (first entry)
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.

XX JP06303997-A.
 XX 01-NOV-1994.
 PF 16-APR-1993; 93JP-00112515.
 XX 16-APR-1993; 93JP-00112515.
 PR 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.
 XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 3.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAAATAAAAAAAAAA 1752
 DB 19 ATAAAAAATAAAAAAAAAA 1

RESULT 693

AAQ75703/c
 ID AAQ75703 standard; DNA; 21 BP.
 XX
 AC AAQ75703;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.

XX JP06303997-A.
 PD 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 PF 16-APR-1993; 93JP-00112515.
 PR 16-APR-1993; 93JP-00112515.
 XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 PA
 XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 7; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 1 A; 0 C; 3 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
 Best Local Similarity 94.7%; Pred. No. 3.6e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAAAAAA 1753
 DB 19 CTAATAAAAAAAAAAAAA 1

RESULT 694
 AAQ75706/c
 ID AAQ75706 standard; DNA; 21 BP.
 XX
 AC AAQ75706;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.

XX Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 OS Synthetic.

XX JP06303997-A.
 PD 01-NOV-1994.
 XX 16-APR-1993; 93JP-00112515.
 PF 16-APR-1993; 93JP-00112515.
 PR 16-APR-1993; 93JP-00112515.

```
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA WPI; 1995-018287/03.
DR
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1753
Db 19 CTA AAAAAAAAAA AAAAAA 1

RESULT 695
AAQ75717/c
ID AAQ75717 standard; DNA; 21 BP.
AC AAQ75717;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 1 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1753
Db 19 CTA AAAAAAAAAA AAAAAA 1

RESULT 696
AAQ75731/c
ID AAQ75731 standard; DNA; 21 BP.
AC AAQ75731;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 21;
Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTA AAAAAAAAAA AAAAAA 1750
Db 19 TTA AAAAAAAAAA AAAAAA 1

RESULT 697
AAQ75782/c
ID AAQ75782 standard; DNA; 21 BP.
AC AAQ75782;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
```

```
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 3 C; 0 G; 18 T; 0 U; 0 Other;
    Query Match 1.0%; Score 17.4; DB 1; Length 21;
    Best Local Similarity 94.7%; Pred. No. 3.6e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAAAAAA 1752
Db 19 AGAAAAAAAAAAAAAAAAA 1
RESULT 698
AAQ75707/c
ID AAQ75707 standard; DNA; 21 BP.
XX AC AAQ75707;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 7; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
```

```
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 2 A; 0 C; 2 G; 17 T; 0 U; 0 Other;
    Query Match 1.0%; Score 17.4; DB 1; Length 21;
    Best Local Similarity 94.7%; Pred. No. 3.6e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CTAAAAAAAAAAAAAAAAAA 1
RESULT 699
AAQ75750/c
ID AAQ75750 standard; DNA; 21 BP.
XX AC AAQ75750;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
XX PT by digestion with restriction enzymes.
XX PS Disclosure; Page 8; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX CC and using the aggregate of mRNAs as the template for each reverse
XX CC transcription primer; (b) digesting each of the prepared aggregates of
XX CC the double-stranded cDNAs with restriction enzyme and; (c)
XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
    Query Match 1.0%; Score 17.4; DB 1; Length 21;
    Best Local Similarity 94.7%; Pred. No. 3.6e+02;
    Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAAAAAA 1753
Db 19 CGAAAAAAAAAAAAAAAAA 1
RESULT 700
AAQ75749/c
```



```

ID  AAQ75749 standard; DNA; 21 BP.
AC
XX
XX  AAQ75749;
XX
DT  04-AUG-1995 (first entry)
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX
XX  16-APR-1993; 93JP-00112515.
PF
XX
XX  16-APR-1993; 93JP-00112515.
PR
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX  WPI; 1995-018287/03.
DR
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 8; 11pp; Japanese.
PS
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX  Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX  Best Local Similarity 94.7%; Pred. No. 3.6e+02;
XX  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1735 CAAAAA..... 1753
DB  19 CGAAAAA..... 1

RESULT 701
AAQ75709/C
ID  AAQ75709 standard; DNA; 21 BP.
XX
XX  AAQ75709;
XX
XX  04-AUG-1995 (first entry)
DT
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX
XX  16-APR-1993; 93JP-00112515.
PF
XX
XX  16-APR-1993; 93JP-00112515.
PR
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX  WPI; 1995-018287/03.
DR
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 8; 11pp; Japanese.
PS
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX  Sequence 21 BP; 0 A; 2 C; 1 G; 18 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX  Best Local Similarity 94.7%; Pred. No. 3.6e+02;
XX  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1735 CAAAAA..... 1753
DB  19 CGAAAAA..... 1

RESULT 701
AAQ75709/C
ID  AAQ75709 standard; DNA; 21 BP.
XX
XX  AAQ75709;
XX
XX  04-AUG-1995 (first entry)
DT
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX
XX  16-APR-1993; 93JP-00112515.
PF
XX
XX  16-APR-1993; 93JP-00112515.
PR
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX  WPI; 1995-018287/03.
DR
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 8; 11pp; Japanese.
PS
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX  Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.0%; Score 17.4; DB 1; Length 21;

```

```

1  PA  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX  WPI; 1995-018287/03.
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 7; 11pp; Japanese.
PS
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX  Sequence 21 BP; 2 A; 0 C; 1 G; 18 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.0%; Score 17.4; DB 1; Length 21;
XX  Best Local Similarity 94.7%; Pred. No. 3.6e+02;
XX  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  1735 CAAAAA..... 1753
DB  19 CTA..... 1

RESULT 702
AAQ75720/C
ID  AAQ75720 standard; DNA; 21 BP.
XX
XX  AAQ75720;
XX
XX  04-AUG-1995 (first entry)
DT
XX
XX  Reverse transcription primer used in cDNA analysis technique.
DE
XX
XX  Analysis; gene expression; reverse transcription; primer; cDNA;
KW  aggregate; restriction enzyme; ss.
XX
XX  Synthetic.
OS
XX  JP06303997-A.
XX
XX  01-NOV-1994.
PD
XX
XX  16-APR-1993; 93JP-00112515.
PF
XX
XX  16-APR-1993; 93JP-00112515.
PR
XX
XX  (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX
XX  WPI; 1995-018287/03.
DR
XX
XX  Analysis of cDNA and gene expression - by amplification of mRNA followed
PT  by digestion with restriction enzymes.
XX
XX  Disclosure; Page 8; 11pp; Japanese.
PS
XX
XX  A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC  double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC  labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC  and using the aggregate of mRNAs as the template for each reverse
CC  transcription primer; (b) digesting each of the prepared aggregates of
CC  the double-stranded cDNAs with restriction enzyme and; (c)
CC  electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC  method can be used to analyse gene expression rapidly and easily
XX
XX  Sequence 21 BP; 3 A; 0 C; 1 G; 17 T; 0 U; 0 Other;
SQ
XX
XX  Query Match 1.0%; Score 17.4; DB 1; Length 21;

```

```

Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA1750
Db 19 TTA1750

RESULT 703
ABQ96219
ID ABQ96219 standard; DNA; 23 BP.
XX
AC ABQ96219;
XX
DT 28-OCT-2002 (first entry)
XX
DE Tumour suppression-related oligonucleotide #1870.
XX
KW Tumour; cytostatic; antiviral; neuroprotective; neurotropic; neuroleptic;
KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;
KW viral infection; cell degeneration disease; neurodegeneration; ds;
KW Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.
XX
OS Homo sapiens.
XX
PN FR2819824-A1.
XX
PD 26-JUL-2002.
XX
PF 23-JAN-2001; 2001PR-00000899.
XX
PR 23-JAN-2001; 2001PR-00000899.
XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.
XX
PI Telerman A, Amson R, Tuijnder M, Susini L;
XX
DR WPI; 2002-610803/66.
XX
PT New nucleic acid implicated e.g. in tumor suppression, useful for
PT diagnosis of tumors, viral infection and cellular degeneration and for
PT drug screening.
XX
PS Claim 1; Page 512; 623pp; French.
XX
CC The present invention relates to novel human nucleic acid sequences (I).
CC The present sequence is one such nucleic acid sequence. Expression of (I)
CC are implicated in tumour suppression or reversion and apoptosis and viral
CC resistance. (I) are useful as probes or primers for detecting,
CC identifying, measuring and/or amplifying nucleic acid sequences, as
CC antisense reagents and for recombinant production of polypeptides. (I),
CC polypeptides (II) encoded by (I), vector containing (I), cells containing
CC these vectors and antibodies (Ab) against (II) are all useful for
CC treatment/prevention of viral, tumour and cell degeneration diseases
CC (especially neurodegeneration, such as Alzheimer's disease and
CC schizophrenia). Analysing the expression of (I) is also useful for
CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
CC (I) are used for studying the aetiology of these diseases (also immune
CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
CC in the specification
XX
SQ Sequence 23 BP; 15 A; 0 C; 3 G; 3 T; 0 U; 2 Other;

Query Match 1.0%; Score 17.4; DB 1; Length 23;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1731 TTTACAAAAA1751
Db 1 TTTNGAAAAA21

Best Local Similarity 94.7%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 704
AAT94431
ID AAT94431 standard; mRNA; 19 BP.
XX
AC AAT94431;
XX
DT 02-MAR-1998 (first entry)
XX
DE Template mRNA poly-A tail SEQ ID NO:1 from WO9729211.
XX
DE DE
XX
KW Primer; detection; characterisation; mRNA; restriction display PCR;
KW synthesis; cDNA; ss.
XX
XX Synthetic.
XX
OS Homo sapiens.
XX
PN WO9729211-A1.
XX
PD 14-AUG-1997.
XX
PF 07-FEB-1997; 97WO-US002009.
XX
PR 09-FEB-1996; 96US-0011379P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Weinstein JN, Boulamwini J;
XX
DR WPI; 1997-415362/38.
XX
PT Detection and characterisation of mRNA by restriction display PCR -
PT comprising synthesis of cDNA, digestion with a restriction endonuclease,
PT ligation to an adaptor DNA and PCR amplification.
XX
PS Disclosure; Page 24; 40pp; English.
XX
CC A method has been improved for detecting and characterising mRNA
CC molecules which includes synthesising a double stranded (ds) cDNA from
CC isolated mRNA, digesting the ds cDNA with a restriction endonuclease to
CC produce cDNA fragments in which at least one end of the cDNA fragments
CC has a sequence capable of hybridising to an adaptor DNA sequence. The
CC improvement comprises: (a) hybridising adaptor DNA sequences to at least
CC one end of the cDNA fragments; (b) ligating the adaptor DNA sequences to
CC the cDNA fragments; (c) amplifying the cDNA fragments having ligated
CC adaptor DNA sequences by a PCR using primers that hybridise to the ends
CC of the cDNA fragments, where the primers have at least one nucleotide at
CC the 3' end that specifically hybridises to a subset of cDNA molecules;
CC and (d) detecting the presence of the resulting amplified cDNA fragments;
CC The present sequence represent a template poly-A tail used in the present
CC specification. The method designate restriction display PCR can be used
CC for characterising cells based on their mRNA content, for representing
CC expressed genes, and for discovery of therapeutics that alter cellular
CC gene expression. The method is also useful for characterising cells of a
CC variety of types and under a variety of physiological conditions. The
CC method is also useful for identifying cells or tissue from particular
CC individuals or species based on the fingerprint obtained from the mRNA
CC content of isolated cells or tissue and comparing it to cells or tissue
CC from a known source
XX
SQ Sequence 19 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 2 Other;

Query Match 1.0%; Score 17.2; DB 1; Length 19;
Best Local Similarity 94.4%; Pred. No. 3.5e+02;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA1752
Db 2 BAAAAA19

RESULT 705
AAx18390/c
ID AAX18390 standard; DNA; 19 BP.

```

XX AAX18390;
 AC 11-MAY-1999 (first entry)
 DT RT-PCR primer of the invention SEQ ID 31.
 DE RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 KW Synthetic.
 OS
 XX JPI1032765-A.
 PN 09-FEB-1999.
 XX 18-JUL-1997; 97JP-00208312.
 XX 18-JUL-1997; 97JP-00208312.
 PR (TAKI) TAKARA SHUZO CO LTD.
 PA WPI; 1999-183822/16.
 DR Peptides having at least two new nucleotides - useful as primers in RT-PCR.
 XX Example 1; Page 12; 19pp; Japanese.
 XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
 Query Match 1.0%; Score 17.2; DB 1; Length 19;
 Best Local Similarity 94.4%; Pred. No. 3.5e+02;
 Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAA 1752
 Db 18 BAAAAAAAAAAAAAAAAA 1
 RESULT 706
 AAQ61998
 ID AAQ61998 standard; DNA; 22 BP.
 AC AAQ61998;
 XX 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX Guanine quartet containing oligomer, #9.
 DE Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..22
 FT /*tag= a

FT /note= "Phosphorothionate intersugar linkages"
 XX WO9408053-A1.
 PN 14-APR-1994.
 PD 29-SEP-1993; 93WO-US009297.
 PF 29-SEP-1992; 92US-00954185.
 PR (ISIS-) ISIS PHARM INC.
 PA Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX WPI; 1994-135613/16.
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length of chromosomes.
 PT Disclosure; Page 107; 144pp; English.
 XX The sequences given in AAQ61990-2001 are oligonucleotides which contain G4 or G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyper- proliferation, malignancy, cardiovascular disease and snake bite. Oligonucleotides such as these, may be used for inhibiting division of malignant cells by modulating telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17.2; DB 1; Length 22;
 Best Local Similarity 86.4%; Pred. No. 3.9e+02;
 Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1015 GTGGTTGGGATGGGCTGGGG 1036
 Db 1 GGGGTTGGGGTTGGGTTGGGG 22
 RESULT 707
 AAQ61991
 ID AAQ61991 standard; DNA; 22 BP.
 AC AAQ61991;
 XX 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX Guanine quartet containing oligomer, #2.
 DE Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..22
 FT /*tag= a
 FT /note= "Phosphorothionate intersugar linkages"
 XX WO9408053-A1.
 PN 14-APR-1994.
 PD 29-SEP-1993; 93WO-US009297.
 PF

PR 29-SEP-1992; 92US-00954185.
 XX (ISIS-) ISIS PHARM INC.
 XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 XX Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX WPI; 1994-135613/16.
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 XX of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 XX of chromosomes.
 XX Disclosure; Page 105; 144pp; English.
 XX The sequences given in AAQ61895-2001 are oligonucleotides which contain
 XX G4 or G3 stretches and which may be used for inhibiting replication of
 XX herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
 XX influenza virus, or for treating inflammatory and neurological disorders
 XX caused by phospholipase A2 activity in cases of hyper- proliferation,
 XX malignancy, cardiovascular disease and snake bite. Oligonucleotides such
 XX as these, may be used for inhibiting division of malignant cells by
 XX modulating telomere length, which may also retard aging. (Updated on 25-
 XX MAR-2003 to correct PN field.)
 XX Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
 XX Query Match 1.0%; Score 17.2; DB 1; Length 22;
 XX Best Local Similarity 86.4%; Pred. No. 3.9e+02;
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1015 GTGGTTGGGATGGGCTGGGG 1036
 DB 1 GGGGTTGGGTTGGGTTGGGG 22
 RESULT 708
 AAQ61895
 ID AAQ61895 standard; DNA; 22 BP.
 XX AAQ61895;
 XX 25-MAR-2003 (revised)
 XX 04-NOV-1994 (first entry)
 XX HSV replication inhibiting oligomer, ISIS no 5677.
 XX Inhibition; replication; herpes simplex virus; HIV; HIV;
 XX human cytomegalovirus; influenza virus; inflammation;
 XX neurological disorders; phospholipase A2 activity; hyperproliferation;
 XX malignancy; cardiovascular disease; snake bite; malignancy;
 XX telomere length; retard; aging; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX misc_feature 1..22
 XX /tag= a
 XX /note= "Phosphorothionate intersugar linkages"
 XX WO9408053-A1.
 XX 14-APR-1994.
 XX 29-SEP-1993; 93WO-US009297.
 XX 29-SEP-1992; 92US-00954185.
 XX (ISIS-) ISIS PHARM INC.
 XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 XX Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;

DR WPI; 1994-135613/16.
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 XX of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 XX of chromosomes.
 XX Claim 5; Page 19; 144pp; English.
 XX The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides
 XX which contain a G4 or two G3 stretches and which may be used for
 XX inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
 XX such as these may also be used for inhibiting activity of HIV, human
 XX cytomegalovirus or influenza virus, or for treating inflammatory and
 XX neurological disorders caused by phospholipase A2 activity in cases of
 XX hyperproliferation, malignancy, cardiovascular disease and snake bite.
 XX They may also be used for inhibiting division of malignant cells by
 XX modulating telomere length, which may also retard aging. (Updated on 25-
 XX MAR-2003 to correct PN field.)
 XX Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;
 XX Query Match 1.0%; Score 17.2; DB 1; Length 22;
 XX Best Local Similarity 86.4%; Pred. No. 3.9e+02;
 XX Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1015 GTGGTTGGGATGGGCTGGGG 1036
 DB 1 GGGGTTGGGTTGGGTTGGGG 22
 RESULT 709
 AAQ61903
 ID AAQ61903 standard; DNA; 22 BP.
 XX AAQ61903;
 XX 25-MAR-2003 (revised)
 XX 04-NOV-1994 (first entry)
 XX HSV replication inhibiting oligomer, ISIS no 5670.
 XX Inhibition; replication; herpes simplex virus; HIV; HIV;
 XX human cytomegalovirus; influenza virus; inflammation;
 XX neurological disorders; phospholipase A2 activity; hyperproliferation;
 XX malignancy; cardiovascular disease; snake bite; malignancy;
 XX telomere length; retard; aging; ss.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX misc_feature 1..22
 XX /tag= a
 XX /note= "Phosphorothionate intersugar linkages"
 XX WO9408053-A1.
 XX 14-APR-1994.
 XX 29-SEP-1993; 93WO-US009297.
 XX 29-SEP-1992; 92US-00954185.
 XX (ISIS-) ISIS PHARM INC.
 XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 XX Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX WPI; 1994-135613/16.
 XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 XX of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 XX of chromosomes.

PS Disclosure; Page 19; 144pp; English.

XX The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides which contain a G4 or two G3 stretches and which may be used for inhibiting replication of herpes simplex virus (HSV). Oligonucleotides such as these may also be used for inhibiting activity of HIV, human cytomegalovirus or influenza virus, or for treating inflammatory and neurological disorders caused by phospholipase A2 activity in cases of hyperproliferation, malignancy, cardiovascular disease and snake bite. They may also be used for inhibiting division of malignant cells by modulating telomere length, which may also retard aging. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGGCTGGGG 1036
| | | | | | | | | | | | | | | | | | | |
Db 1 GGGGTTGGGTTGGGTTGGGG 22

RESULT 710

AAQ97987
ID AAQ97987 standard; DNA; 22 BP.

AC AAQ97987;

XX

DT 25-MAR-2003 (revised)

DT 19-OCT-1995 (first entry)

XX

DE Peptide nucleic acid oligomer targeting HIV gene.

XX

XX Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;

KW antiviral; antisense; triple helix; ss.

XX

OS Synthetic.

XX

XX Key Location/Qualifiers

FT misc_feature 1..22

FT /tag= a

FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine peptide residues, the nucleobase being attached covalently to the acetyl group and the peptide linkage being formed by condensation of the glycine carboxy group of one residue with the amino group of the 2-aminoethyl moiety in the next residue"

XX

XX WO9504068-A1.

XX

XX 09-FEB-1995.

XX

XX 28-JUL-1994; 94WO-US008517.

XX

XX 29-JUL-1993; 93US-00099718.

XX

XX (ISIS-) ISIS PHARM INC.

XX

XX Ecker DJ;

XX

XX WPI; 1995-082179/11.

XX

XX Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid sub:unit - binds in complementary manner to DNA and RNA, and useful for modulating HIV viral activity, e.g. in treating AIDS.

XX

PS Claim 2; Page 176; 186pp; English.

XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist of naturally occurring nucleobases covalently bound to a polyamide

CC backbone and (b) hybridise to the translation initiation AUG region, 5' untranslated region (5' UTR), 3' untranslated region (3' UTR), splice junctions or coding sequence of a human immunodeficiency virus gene chosen from env, gag, pol, rev and tat. The PNAs can be used to target RNA and single stranded DNA (ssDNA) to produce antisense-type gene regulation moieties. They have utility as gene-targeted drugs for modulating HIV processes. Hence they can be used to treat AIDS and other viral infections. They are also useful in diagnostic applications and as research tools. PNA oligomers have high affinity for complementary single stranded DNA. They are also able to form triple helices in which a first PNA strand binds with RNA or ssDNA and a second PNA strand binds with the resulting double helix or with the first PNA strand. The PNAs possess no significant charge and are water soluble, which facilitates cellular uptake. Further, since they contain amides of non-biological amino acids, they are biostable and resistant to enzymatic degradation by proteases. The present sequence is a specifically claimed PNA sequence (represented by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 22 BP; 0 A; 0 C; 16 G; 6 T; 0 U; 0 Other;

Query Match 1.0%; Score 17.2; DB 1; Length 22;
Best Local Similarity 86.4%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1015 GTGGTTGGGATGGGCTGGGG 1036
| | | | | | | | | | | | | | | | | | | |
Db 1 GGGGTTGGGTTGGGTTGGGG 22

RESULT 711

AAF98936/c

ID AAF98936 standard; DNA; 22 BP.

XX

AC AAF98936;

XX

DT 12-JUN-2001 (first entry)

XX

DE Immunostimulatory nucleic acid #52.

XX

KW Vaccine; cytostatic; virucidal; bactericidal; fungicidal; anti-parasitic; immunostimulatory; tumour; viral infection; bacterial infection;

KW fungal infection; parasitic infection; cancer; asthma;

KW infectious disease; allergy; immune deficiency; phosphorothioate; ss.

XX

OS Synthetic.

XX

XX WO200122972-A2.

XX

XX 05-APR-2001.

XX

XX 25-SEP-2000; 2000WO-US026383.

XX

XX 25-SEP-1999; 99US-0156113P.

PR 27-SEP-1999; 99US-0156135P.

PR 23-AUG-2000; 2000US-0227436P.

XX

XX (IOWA) UNIV IOWA RES FOUND.

PA (COLE-) COLEY PHARM GMBH.

XX

XX Krieg AM, Schetter C, Vollmer J;

XX

XX WPI; 2001-273485/28.

XX

XX Vaccinating against tumore, infectious diseases, allergies and asthma using immunostimulatory Py-rich and TG nucleic acids.

PT

XX Disclosure; Page 39; 338pp; English.

XX

XX The present invention relates to a method for stimulating an immune response. The method comprises administering an immunostimulatory nucleic acid to a non-rodent subject in sufficient quantity to stimulate an immune response. The present sequence is one such immunostimulatory

The invention relates to inhibiting angiogenesis in a subject, comprising administering at least one antiangiogenic nucleic acid molecule. Also included is a kit comprising a first container housing the antiangiogenic nucleic acids, and instructions for administering them to a subject having a condition characterised by unwanted angiogenesis. The method is useful for inhibiting angiogenesis associated with solid tumour growth, tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, Oeler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiodioma.

[illegible]

```

PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 79; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CAAAAA...AAAAA 1751
DB 17 CAAAAA...AAAAA 1

RESULT 717
AAA25453/C
ID AAA25453 standard; DNA; 17 BP.
XX
XX AAA25453;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1951.
DE
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 19-APR-1999; 99WO-US008547.
PR
XX
XX 23-JUN-1998; 98US-00103636.
PR

```

```

PR 20-APR-1998; 98US-0082404P.
XX
XX 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 79; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorodithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1733 TAAAAA...AAAAA 1749
DB 17 TAAAAA...AAAAA 1

RESULT 718
AAA25452/C
ID AAA25452 standard; DNA; 17 BP.
XX
XX AAA25452;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1950.
DE
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR
XX
XX 23-JUN-1998; 98US-00103636.
PR

```


XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haeblerli P;

XX PI Matulic-Adamic J;

XX DR WPI; 2000-013248/01.

XX PT New nucleic acids that interact, and optionally cleave, target sequences, used to treat cancer.

XX PS Claim 77; Page 79; 148pp; English.

XX CC The present invention describes nucleic acids (A) that interact stably with a target sequence and contain at least one phosphorodi-thioate link, having endonuclease activity. (A), and more generally any catalytic nucleic acid (A') that modulates expression of the oestrogen receptor gene, are used to treat cancer (particularly of breast or endometrium), in vivo or by transforming cells ex vivo and implanting treated cells, or for other conditions associated with levels of oestrogen receptor. CC Because of the high selectivity for targeted RNA, (A) can also be used to correlate inhibition of gene expression with alterations in phenotype. CC particularly for identification of therapeutic targets, and as research reagents (for RNA, in the same way that restriction endonucleases are used with DNA). The combination of modifications in (A) improves CC resistance to nucleases; binding affinity and/or activity. AAA23503 to CC AAA24748 to AAA25992 represent their corresponding target sequences, and CC AAA24748 to AAA25992 represent their corresponding target sequences. CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme sequences, and AAA26107 to AAA26271 represent their corresponding target sequences. AAA26219 to AAA26271 represent other ribozyme sequences and CC antisense oligonucleotides used in the exemplification of the present invention

XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 ACACAAAAA 1750

Db 17 ACACAAAAA 1

RESULT 719

AAA98232/C

ID AAA98232 standard; DNA; 17 BP.

XX AC AAA98232;

XX DT 30-JAN-2001 (first entry)

XX DE Human retrovirus HERV LTR PCR primer #31.

XX KW Cell-specific expression; tissue-specific expression; Gene therapy; LTR; U3-R segment; long terminal repeat; retroviral expression vector; PCR primer; ss.

XX OS Human endogenous retrovirus.

XX FN WO200053789-A2.

XX PD 14-SEP-2000.

XX PF 09-MAR-2000; 2000WO-EP002064.

XX PR 10-MAR-1999; 99DE-01010650.

XX PA (GSFU-) GSF FORSCHUNGSZENTRUM UMWELT & GESUNDHEIT.

XX PI Leib-Moesch C, Schoen U, Baust C;

XX WPI; 2000-587442/55.

XX DR Retroviral expression vector, useful in gene therapy, contains a promoter from a human endogenous retrovirus to provide cell-specific expression.

XX PT Disclosure; Page 27; 67pp; German.

XX PS This invention describes a novel retroviral expression vector (A) containing DNA sequences (I) for packaging vector RNA and for cell-specific expression of proteins or peptides encoding by heterologous DNA (II). The sequences controlling cell-specific expression contain a cell-specifically regulatable promoter region (P) from a human endogenous retrovirus (HERV) DNA sequence. The invention also describes (a) mRNA and RNA of (A); (b) prokaryotic and eukaryotic cells containing (A); (c) eukaryotic cells containing (A) in integrated form; (d) virions containing a retroviral expression vector RNA derived from (A); (e) a method for producing the virions of (d); (f) a method for incorporating protein-encoding nucleic acid sequences into a eukaryotic cell by infection with the virions of (d); and (g) a retroviral vector system containing (A) and a packaging cell line, that contains at least one (recombinant) retrovirus construct that encodes for the packaging proteins of (A). (A) are used for cell- or tissue-specific expression of foreign genes for gene therapy and to produce virions for introducing (II) into the chromosomal DNA of eukaryotic cells, preferably mammalian and specifically human. (A) retain the advantages of usual retroviral promoters with all the signal structures required for transcription in a small region within the U3-R segment, but without their disadvantages (excessive strength and limited cell specificity). Since (A) are derived from endogenous (harmless) viral sequences, they do not introduce any new viral sequences into the genome and recombination will not create new types of retrovirus. The promoters provide cell or tissue specific expression, according to which HERV they are derived from

XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1752

Db 17 AAAAAA 1

RESULT 720

AAA50197/C

ID AAA50197 standard; DNA; 17 BP.

XX AC AAA50197;

XX DT 07-NOV-2000 (first entry)

XX DE 2'-Methoxyethoxy-modified phosphorothioate oligonucleotide.

XX KW Phosphorothioate oligonucleotide; H-phosphonate chemistry; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..19

FT /*tag= a

FT /note= "2'-methoxyethoxy modified thymidine"

FT modified_base 1..17

FT /*tag= b

FT /note= "phosphorothioate internucleoside linkages"

XX WO200047593-A1.

XX PD 17-AUG-2000.

XX PF 11-FEB-2000; 2000WO-US003543.

XX XX

```
PR 12-FEB-1999; 99US-00250075.
XX (ISIS-) ISIS PHARM INC.
XX Manoharan M, Maier MA;
XX WPI; 2000-558188/51.
DR Preparation of mixed backbone oligomeric compounds useful as e.g. primers
PT for diagnostic tests, involves oxidation of H-phosphonate internucleoside
PT linkages to phosphodiester internucleoside linkages.
XX
PS Example 12; Page 34; 49pp; English.
XX
CC The present sequence is that of a phosphorothioate oligonucleotide
CC containing 20 T nucleobases, each having a 2'-methoxyethoxy group on its
CC 5' ribosyl sugar moiety. It is an example of an oligomeric compound
CC produced according to the methods of the invention. The invention
CC provides compounds and methods for the preparation of mixed backbone
CC oligomeric, or chimeric, compounds having phosphodiester internucleoside
CC linkages in addition to phosphorothioate and/or phosphoramidate
CC internucleoside linkages. The methods also include incorporation of
CC boranophosphate internucleoside linkages. The methods utilize H-
CC phosphonate intermediates that are coupled together forming contiguous
CC regions of 1 or more H-phosphonate internucleoside linkages. Each
CC contiguous region is subsequently oxidized to phosphodiester,
CC phosphorothioate, phosphoramidate or boranophosphate internucleoside
CC linkages prior to further elongation. Mixed backbone oligomeric compounds
CC are prepared in this manner by oxidizing adjacent regions with different
CC reagents. Oligomeric compounds of the invention are prepared using novel
CC oxidation steps that oxidize a region of 1 or more H-phosphonate
CC internucleoside linkages without degrading existing linkages that have
CC been previously oxidized. The oligonucleotides obtained are useful as
CC primers in PCR, probes, linkers, gene fragments and for other diagnostic
CC tests on e.g. biological tissue, fluid, cells etc., as research reagents,
CC and as antiviral agents
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 721
ABT34613
ID ABT34613 standard; DNA; 17 BP.
XX
XX ABT34613;
AC
XX
XX 12-JUN-2003 (first entry)
DT
DE
DE Tumour suppression related human fukutin oligo SEQ ID No 250.
XX
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; protein chip; gene therapy; tumour suppression;
KW human fukutin; ds.
XX
XX Homo sapiens.
OS
XX WO2003025175-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 17-SEP-2002; 2002WO-IB004208.
PF
XX
XX 17-SEP-2001; 2001PR-00011978.
PR
XX
```

```
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-313353/30.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
XX Disclosure; Page 63; 720pp; French.
XX
XX The invention relates to a novel isolated 17 mer nucleic acid sequence,
CC given in the specification, a sequence containing at least 15 consecutive
CC nucleotides from the 17 mer sequence, a sequence with, after optimal
CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
CC hybridizes to them under highly stringent conditions, or the complement
CC of any of them, or the corresponding RNA. The novel isolated nucleic
CC acids of the invention are useful as probes and primers for detecting,
CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
CC component of a gene chip, in vitro as (anti)sense reagents, and for
CC production of recombinant polypeptides. Any of the nucleic acids,
CC polypeptides, vectors containing the nucleic acids, cells containing the
CC vector or antibodies directed against the polypeptides are useful for
CC preparation of pharmaceuticals for prevention and/or treatment of viral
CC diseases that are characterised by development of tumours or cell
CC degeneration, specifically cancer but also Alzheimer's disease and
CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
CC patient samples is useful for diagnosis and/or prognosis of these
CC diseases. The polypeptides can also be used to generate antibodies, and
CC both the polypeptide and antibodies are useful as components of protein
CC chips. The nucleic acid sequences of the invention can be used in gene
CC therapy. This polynucleotide sequence represents a tumour suppression
CC related human fukutin oligonucleotide of the invention
XX
SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1644 GATCACTCTCCCTGACA 1660
Db 1 GATCACTCTCCCTGACA 17
RESULT 722
ADB04272/C
ID ADB04272 standard; DNA; 17 BP.
XX
XX ADB04272;
AC
XX
XX 20-NOV-2003 (first entry)
DT
DE
DE Human MD27 scanning oligonucleotide SEQ ID 5258.
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
PF
XX
XX 02-AUG-2001; 2001US-00922181.
PR
XX
XX (ABOM-) ABOMICA INC.
PA
XX
```

PI Shannon M, Gu Y, Nguyen C;
 XX WPI; 2003-423107/40.
 XX
 XX New zinc finger-containing proteins and nucleic acids, useful in
 PT manufacturing a medicament for treating or preventing a disorder
 PT associated with decreased or increased expression or activity of MD23,
 PT MD24, MD27 or MD212, e.g. cancer.
 XX
 PS Example 8; SEQ ID NO 5258; 103pp; English.
 XX
 CC The present invention relates to novel human zinc finger-containing
 CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
 CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
 CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
 CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
 CC or in manufacturing a medicament for treating or preventing a disorder
 CC associated with decreased or increased expression or activity of MD23,
 CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
 CC acids and proteins are also useful for diagnosing or monitoring a disease
 CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
 CC acids can also be used as probes to detect and characterize gross
 CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
 CC useful in constructing microarrays for measuring gene expression. The
 CC proteins are useful as therapeutic agents for gene therapy or as
 CC vaccines. The present sequence was used to illustrate the invention.
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA1751
 DB 17 CAAAAA1751
 RESULT 723
 AAD56441/C
 ID AAD56441 standard; DNA; 17 BP.
 XX
 AC AAD56441;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE Antisense oligo #2, to elicit RNase H degradation of target RNA.
 XX
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..17
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT misc_feature 9..10
 FT /*tag= b
 FT /note= "Bases 9 and 10 are linked by a butanediol linker
 FT which is represented as B in page 49 and X in page 59,
 FT Fig 9 and 10 of the specification".
 XX
 PN WO2003037909-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
 XX WPI; 2003-421516/39.
 DR

XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 PS Example 2; Page 90; 104pp; English.
 XX
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a cellular
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAA1752
 DB 17 AAAAAA1752
 RESULT 724
 AAD56448/C
 ID AAD56448 standard; DNA; 17 BP.
 XX
 AC AAD56448;
 XX
 DT 07-AUG-2003 (first entry)
 XX
 DE 2'F-ANA antisense oligo #3, to elicit RNase H degradation of target RNA.
 XX
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX
 OS Unidentified.
 XX
 PH Key Location/Qualifiers
 FT modified_base 1..17
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT misc_feature 9..10
 FT /*tag= b
 FT /note= "Bases 9 and 10 are linked by a butanediol linker
 FT which is represented as B in page 49 and Fig 5 and as X
 FT in page 52, 55 and Fig 6 of the specification"
 XX
 PN WO2003037909-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Viarovkina E, Mangos MM, Parniak MA, Min K;
 XX WPI; 2003-421516/39.
 DR
 PT Novel acyclic linker-containing oligonucleotide useful for preventing or

PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 PS Example 2; Fig 5; 104pp; English.
 XX
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1752
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 725
 AAD56449/c
 ID AAD56449 standard; DNA; 17 BP.
 XX
 AC AAD56449;
 XX
 DT 07-AUG-2003 (first entry)
 DE 2'-F-ANA antisense oligo #4, to elicit RNase H degradation of target RNA.
 XX
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..17
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT misc_feature 12..13
 FT /tag= b
 FT /note= "Bases 12 and 13 are linked by a butanediol linker
 FT which is represented as B in page 49 and Fig 5 and as X
 FT in page 55 and Fig 6 of the specification"
 XX
 PN WO2003037909-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX
 DR WPI; 2003-421516/39.
 XX
 PT Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.

XX
 PS Example 2; Fig 5; 104pp; English.
 XX
 CC The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1752
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 726
 AAD56447/c
 ID AAD56447 standard; DNA; 17 BP.
 XX
 AC AAD56447;
 XX
 DT 07-AUG-2003 (first entry)
 DE 2'-F-ANA antisense oligo #2, to elicit RNase H degradation of target RNA.
 XX
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..17
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT misc_feature 4..5
 FT /tag= b
 FT /note= "Bases 4 and 5 are linked by a butanediol linker
 FT which is represented as B in page 49 and Fig 5 and as X
 FT in page 55 and Fig 6 of the specification"
 XX
 PN WO2003037909-A1.
 XX
 PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX
 DR WPI; 2003-421516/39.
 XX
 PT Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 PS Example 2; Fig 5; 104pp; English.

XX The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 SQ

Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 727
 AAD56450/C
 ID AAD56450 standard; DNA; 17 BP.
 AC AAD56450;
 XX
 DT 07-AUG-2003 (first entry)
 DE 2'-F-ANA antisense oligo #5, to elicit RNase H degradation of target RNA.
 XX
 KW Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
 KW antisense; ss.
 XX
 OS Unidentified.

Key Location/Qualifiers
 modified_base 1..17
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "2'-deoxy-2'-fluoroarabinothymidine"
 FT misc_feature 9..10
 FT /*tag= b
 FT /note= "Bases 9 and 10 are linked by a secouridine linker
 FT which is represented as S in page 49 and X in page 57 and
 FT Fig 1, 2, 7 and 8 of the specification"
 XX
 PN WO2003037909-A1.
 XX
 FD 08-MAY-2003.
 XX
 XX 29-OCT-2002; 2002WO-CA001628.
 XX
 XX 29-OCT-2001; 2001US-0330719P.
 XX
 XX (UWMC-) UNIV MCGILL.
 XX
 XX Damha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX WPI; 2003-421516/39.
 XX
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 XX decreasing translation, reverse transcription and/or replication of a
 XX target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 XX Example 2; Fig 7; 104pp; English.
 XX
 XX The invention relates to an acyclic linker-containing oligonucleotide

CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX

XX Sequence 17 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
 SQ

Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 728
 ADB41972
 ID ADB41972 standard; DNA; 17 BP.
 XX
 AC ADB41972;
 XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #2295.
 XX
 KW cytostatic; antiviral; neuroprotective; nontropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 XX WO2003040369-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004219.
 XX
 XX 17-SEP-2001; 2001FR-00011981.
 XX
 XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Telerman A, Amson R, Tuijnder M;
 XX WPI; 2003-441574/41.
 XX
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 XX useful e.g. for treatment of tumors and viral infection, also related
 XX polypeptide and antibodies.
 XX
 XX Disclosure; Page 300; 771pp; French.
 XX
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 XX fragments of at least 15 consecutive nucleotides of these nucleotides, a
 XX sequence having at least 80% identity, after optimal alignment, with the
 XX nucleotides, a sequence that hybridizes under stringent conditions with
 XX the nucleotides, or the complement, or corresponding RNA, of the
 XX nucleotides. The nucleotides are used as probes or primers for detecting,
 XX identifying, quantifying and/or amplifying nucleic acids, as in vitro
 XX sense and antisense sequences, of nucleotides involved in tumour
 XX suppression or reversion, apoptosis and or viral resistance, to produce
 XX recombinant polypeptides, and to prepare transgenic animals, as
 XX experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1644 GATCAGCTCTCCCTGACA 1660
 |||||
 DB 1 GATCAGCTCTCCCTGACA 17

RESULT 729
 AAN30173
 ID AAN30173 standard; DNA; 18 BP.
 XX
 AC AAN30173;

DT 05-APR-1992 (first entry)

XX Sequence derived from the L1 region of the bovine papillomavirus (BPV)
 DE type 1a genome.

XX Diagnostic reagent; vaccine; medicine; wart; tumour; ss.

KW Bovine papillomavirus.

OS
 XX Key Location/Qualifiers
 FH CDS 1..18
 FT /*tag= a
 FT
 XX

PN EP92456-A.

XX 26-OCT-1983.

XX 01-APR-1983; 83EP-00901081.

XX 05-APR-1982; 82PR-00005887.

XX (INSP) INST PASTEUR.

PA (DANO/) DANOS O.

XX Danos O, Katinka M, Yaniv M;

XX WPI; 1983-802979/44.

DR P-PSDB; AAP30313.

XX DNA fragment coding for Papillomavirus antigenic proteins - and derived
 PT immunogen, vaccine and antibody.
 XX

PS Claim 6; Page 16; 25pp; French.

XX The inventors claim DNA fragments capable of expressing, in a host, a
 CC prod. contg. at least one antigenic determinant of papillomavirus (PV),
 CC (see AAN30170-N30173). Also claimed are immunogens consisting of at least
 CC one peptide sequence coded for by the DNA fragments (see AAP30310-
 CC P30313), vaccines contg. the immunogens and antibodies raised from them.
 CC The vaccines are useful in human and veterinary medicine and the
 CC antibodies are useful as diagnostic reagents. The DNA fragments are most
 CC esp. derived from the L1 region of human PV type 1a

XX Sequence 18 BP; 16 A; 1 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAATAAAAAAAAAA 1751
 |||||
 DB 2 CAAAAAATAAAAAAAAAA 18

RESULT 730

AAT94667/C

ID AAT94667 standard; DNA; 18 BP.

XX

AC AAT94667;

DT 27-MAR-1998 (first entry)

XX Anchored poly(T) oligonucleotide polyT-AnchA.

XX Flavonoid 3' hydroxylase; pigmentation; flower colour; transgenic plant;
 KW snapdragon; primer; ss.

XX Synthetic.

XX WO9732023-A1.

XX 04-SEP-1997.

XX 28-FEB-1997; 97WO-AU000124.

XX 01-MAR-1996; 96AU-00008386.

XX (FLOR-) FLORIGENE LTD.

XX Bruggiera F, Holton TA, Michael MZ;

XX WPI; 1997-448691/41.

XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
 PT corresponding DNA, used in the manipulation of pigmentation in plants.

XX Example 15; Page 59; 234pp; English.

XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
 CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
 CC region of a polyadenylation sequence. They were used to prime cDNA
 CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
 CC were also utilised in the PCR amplification of plant cytochrome P450
 CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
 CC flavonoid 3' hydroxylase (see AAW35704) was isolated using a differential
 CC display approach. This can be used to manipulate the pigmentation of
 CC transgenic plants

XX Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAATAAAAAAAAAA 1752
 |||||
 DB 17 AAAAAAATAAAAAAAAAA 1

RESULT 731

AAT94668/C

ID AAT94668 standard; DNA; 18 BP.

XX

AC AAT94668;

DT 27-MAR-1998 (first entry)

XX Anchored poly(T) oligonucleotide polyT-AnchC.

KW Flavonoid 3'-hydroxylase; pigmentation; flower colour; transgenic plant;
 XX snapdragon; primer; ss.
 OS Synthetic.
 PN WO9732023-A1.
 XX
 PD 04-SEP-1997.
 XX
 PF 28-FEB-1997; 97WO-AU000124.
 XX
 XX 01-MAR-1996; 96AU-00008386.
 XX
 PA (FLOR-) FLORIGENE LTD.
 XX
 XX Brugliera F, Holton TA, Michael MZ;
 XX WPI; 1997-448691/41.
 DR
 XX Novel flavonoid 3'-hydroxylase(s) from flowering plants - and
 PT corresponding DNA, used in the manipulation of pigmentation in plants.
 PT
 XX Example 15; Page 59; 234pp; English.
 PS
 XX Anchored poly(T) oligonucleotides polyT-anchA (AAT94667), polyT-anchC
 CC (AAT94668) and polyT-anchG (AAT94669) are complementary to the upstream
 CC region of a polyadenylation sequence. They were used to prime cDNA
 CC synthesis from snapdragon (Antirrhinum majus) petal and leaf RNA, and
 CC were also utilised in the PCR amplification of plant cytochrome P450
 CC sequences (see also AAT94670-73). A cDNA clone (see AAT94657) encoding
 CC flavonoid 3'-hydroxylase (see AAT94670) was isolated using a differential
 CC display approach. This can be used to manipulate the pigmentation of
 CC transgenic plants
 CC
 XX Sequence 18 BP; 0 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1752
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 732
 AAV54168/C
 ID AAV54168 standard; cDNA; 18 BP.
 XX
 AC AAV54168;
 XX
 DT 21-DEC-1998 (first entry)
 XX
 DE Nucleotide sequence PCR primer 5.
 XX
 XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 KW immunohistological staining.
 KW
 OS Synthetic.
 XX
 PN WO9839437-A1.
 XX
 PD 11-SEP-1998.
 XX
 PF 05-MAR-1998; 98WO-JP000905.
 XX
 XX 05-MAR-1997; 97JP-00050302.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 PA
 XX Sakaki Y;
 PI
 XX WPI; 1998-495844/42.
 DR

XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 PT treating diseases associated with apoptosis.
 XX
 XX Example 1; Page 48; 70pp; Japanese.
 PS
 XX This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases
 CC
 XX Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;
 SQ
 Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1734 AAAAAAAAAAAAAAAAAA 1750
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 733
 AAV37712
 ID AAV37712 standard; cDNA; 18 BP.
 XX
 AC AAV37712;
 XX
 XX 25-MAR-2003 (revised)
 DT 07-SEP-1998 (first entry)
 XX
 DE Human protein AQ2_11 3'-portion and polyA tail.
 XX
 XX Human; secreted protein; murine adult spleen; human foetal kidney; ovary;
 KW bone marrow; thymus; AE648_11; AE693_11; AK438_11; AK603_11; AM1060_11;
 KW AQ2_11; K433_11; L256_11; prevent; treat; ameliorate; medical; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO9820130-A2.
 XX
 PD 14-MAY-1998.
 XX
 XX 31-OCT-1997; 97WO-US019857.
 PF
 XX 01-NOV-1996; 96US-00742973.
 PR
 XX 29-OCT-1997; 97US-00960024.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 PI
 XX WPI; 1998-286946/25.
 DR
 XX New secreted proteins and associated polynucleotides - obtained from
 PT murine adult spleen, human foetal kidney, human ovary, murine bone marrow
 PT and murine adult thymus.
 PT
 XX Disclosure; Page 58; 75pp; English.
 PS
 XX The present invention describes novel proteins isolated from cDNA clones:
 CC AE648_11; AE693_11; AK438_11; AK609_11; AM1060_11; AQ2_11; K433_11; or
 CC L256_11, deposited as ATCC 98237. The present sequence represents the 3'-
 CC portion of AQ2_11 isolated from a human ovary cDNA library. The proteins
 CC from the present invention may be administered in a composition to
 CC prevent, treat or ameliorate a medical condition. The proteins may
 CC exhibit biological activities such as nutritional activity, cytokine and
 CC cell proliferation/differentiation activity, immune stimulating or
 CC suppressing activity, haematopoiesis regulating activity, tissue growth
 CC activity, activin/inhibin activity, chemotactic/chemokinetic activity,

CC haemostatic and thrombotic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, CC tumour inhibition activity and other activities. (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1752
Db 2 AAAAAAAAAAAAAAA 18

RESULT 734
AAV07750
ID AAV07750 standard; DNA; 18 BP.
XX AAV07750;
XX
DT 02-DEC-1998 (first entry)
XX
DE Phosphorothioate oligodeoxynucleotide.
XX
KW phosphorothioate; electrospray ionisation-Fourier transform;
KW mass spectrometry; off-resonance excitation; ss.
XX
OS Synthetic.

XX Key Location/Qualifiers
FH misc_difference 1..18
FT /*tag a
FT /notes "phosphorothioate internucleotide linkages"

XX WO9840520-A1.
XX
PD 17-SEP-1998.
XX
PF 12-MAR-1998; 98WO-US004919.
XX
PR 14-MAR-1997; 97US-0040717P.
XX (HYBR-) HYBRIDON INC.
XX
PI Wang BH;
XX
DR WPI; 1998-520830/44.
XX
XX Determining the nucleotide sequence of a nucleic acid analyte - using electro-spray ionisation.
PT
XX Example 1; Fig 3A; 25pp; English.
PS

XX The invention relates to an analytical method for determining the nucleotide sequence of nucleic acid analytes, including chemically modified oligonucleotides. This new method utilises electrospray ionisation-Fourier transform mass spectrometry. The ions are excited by sustained off-resonance excitation with single shot excitation, and the target fragmented by collisionally activated dissociation by a neutral gas, e.g. carbon dioxide. Alternatively, the excitation and dissociation can be nozzle skimmer dissociation. The method is used in molecular biology and biomedical applications. The method, utilising electrospray ionisation-Fourier transform ion cyclotron resonance mass spectrometry, is extremely rapid and acts directly on the oligonucleotide. The method is effective for a variety of nucleic acid analytes, particularly chemically modified oligonucleotides which have not previously been successfully sequenced. The present sequence represents a phosphorothioate oligodeoxynucleotide

XX Sequence 18 BP; 17 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAA 17

RESULT 735
AAA40563
ID AAA40563 standard; cDNA; 18 BP.
XX
AC AAA40563;
XX
DT 16-NOV-2000 (first entry)
XX
DE Human adult ovary cDNA fragment AQ2_11 #2.

XX Secreted protein; cytostatic; immunostimulatory; antimicrobial;
KW antiviral; immunosuppressive; antiinflammatory; vulnery; cytokine;
KW cell proliferation; differentiation; regulator; treatment; tumor;
KW autoimmune disease; inflammatory disorder; wound; microbial infection;
KW viral disease; graft versus host reaction suppression; ss.

XX Homo sapiens.

XX WO200037630-A1.

XX 29-JUN-2000.

XX 22-DEC-1999; 99WO-US031005.

XX 23-DEC-1998; 98US-00220876.

XX (GEMY) GENETICS INST INC.

XX Jacobs K, McCoey JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR;

XX WPI; 2000-442661/38.

XX P-PSDB; AAB10274.

XX Secreted human proteins AS296-1i and AS34-1i, useful for treating tumors, PT autoimmune diseases, inflammatory disorders, wounds, microbial infections and viral diseases.

XX Disclosure; Page 269; 293pp; English.

XX This invention describes novel secreted human proteins (I) which have cytostatic, immunostimulatory, antimicrobial, antiviral, immunosuppressive, antiinflammatory and vulnery activity and which act as cytokine, cell proliferation or differentiation regulators. (I) is useful for treating tumors, autoimmune diseases, inflammatory disorders, wounds, microbial infections and viral diseases. (I) is also useful for suppressing graft versus host reaction. AAA40490-A40580 represent cDNA fragments that encode the secreted proteins AAB10226-B10288 described in the method of the invention

XX Sequence 18 BP; 17 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1752
Db 2 AAAAAAAAAAAAAAA 18

RESULT 736
AAZ90644/c
ID AAZ90644 standard; DNA; 18 BP.

XX AC AA290644;
XX DT 13-JUN-2000 (first entry)
XX DE Human adipose tissue gene amplifying primer #5.
XX KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
XX KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX OS Homo sapiens.
XX PN JP2000037190-A.
XX PD 08-FEB-2000.
XX PF 23-JUL-1998; 98JP-00225228.
XX PR 23-JUL-1998; 98JP-00225228.
XX PA (NITSB) JAPAN TOBACCO INC.
XX DR WPI; 2000-306578/27.
XX PT A physiologically active protein specifically derived from mammal tissue.
XX PS Example 2; Page 18; 50pp; Japanese.
XX CC The invention relates to identification of genes and proteins of adipose
XX CC tissue relating to obesity, particularly complications of visceral
XX CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
XX CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
XX CC proteins (AA290631-633) are used in the genetic diagnosis, prevention
XX CC and treatment of adipose tissue related diseases. Sequences AA290640-51
XX CC represent PCR primers amplifying the human adipose tissue genes
XX SQ Sequence 18 BP; 0 A; 0 C; 2 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAA 1750
Db 18 ACAAAAAAAAAAAAAA 2

RESULT 737
AAF75596/C
ID AAF75596 standard; DNA; 18 BP.
XX AC AAF75596;
XX DT 10-MAY-2001 (first entry)
XX DE Binary encoded sequence tag method anchored primer #1.
XX KW Binary encoded sequence tag; BEST; nucleic acid analysis;
XX KW gene expression; adaptor; PCR primer; ss.
XX OS Synthetic.
XX PN WO200112855-A2.
XX PD 22-FEB-2001.
XX PF 11-AUG-2000; 2000WO-US022164.
XX PR 13-AUG-1999; 99US-0148870P.
XX PR 06-APR-2000; 2000US-00544713.
XX PA (UYUA) UNIV YALE.
XX

Pi Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
XX DR WPI; 2001-202878/20.
XX PT Producing binary sequence tags, useful for analyzing nucleic acid
XX PT sequence tags, gene expression or gene-expression patterns, involves
XX PT generating nucleic acid fragments, which are mixed with offset adaptors
XX PT and adaptor-indexers.
XX PS Disclosure; Page 100; 101pp; English.
XX CC The present invention describes a method of producing binary sequence
XX CC tags from nucleic acid fragments in a sample, involving incubating the
XX CC sample with cleaving reagents, mixing offset adaptors with the sample,
XX CC incubating with more cleaving reagents and mixing the sample with adaptor
XX CC -indexers where the adaptors are coupled to binary sequence tags. The
XX CC method is useful in sequence analysis, including analysis and comparison
XX CC of gene expression, nucleic acid samples and genomes
XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1751
Db 17 CAAAAAAAAAAAAA 1

RESULT 738
AAD20091
ID AAD20091 standard; mRNA; 18 BP.
XX AC AAD20091;
XX DT 03-JAN-2002 (first entry)
XX DE mRNA fragment used in 3' end PCR/IVT method of the invention.
XX KW RNA polymerase; RNAP; RNA detection; IVT; in vitro transcription; ss.
XX OS Unidentified.
XX PN US6271002-B1.
XX PD 07-AUG-2001.
XX PF 04-OCT-1999; 99US-00411074.
XX PR 04-OCT-1999; 99US-00411074.
XX PA (ROSE-) ROSETTA INPHARMATICS INC.
XX PI Linsley PS, Schelter JM;
XX DR WPI; 2001-624273/72.
XX PT Amplifying and detecting RNA derived from a population of cells by
XX PT employing a primer that contains an RNA polymerase promoter in a
XX PT polymerase chain reaction.
XX PS Example 3; Fig 1; 29pp; English.
XX CC The invention relates to methods and kits for amplification of mRNA using
XX CC a primer in PCR that contains an RNA polymerase (RNAP) promoter. The
XX CC invention provides methods for amplification and detection of RNA derived
XX CC from a population of cells, preferably eukaryotic cells and most
XX CC preferably mammalian cells, which methods preserve fidelity with respect
XX CC to sequence and transcript representation and additionally enable
XX CC amplification of extremely small amounts of mRNA. The method and kit are
XX CC useful for amplifying and detecting RNA derived from a population of
XX CC cells, especially eukaryotic cells like mammals. The RNAs generated are

CC useful for profiling gene expression in different populations of cells.
 CC The present sequence is a mRNA fragment used in 3' end PCR/IVT (in vitro
 CC transcription) method of the invention

XX Sequence 18 BP; 17 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
 SQ Query Match 1.0%; Score 17; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAA 1752
 |||||
 DB 2 AAAAAAAAAAAAAA 18

RESULT 739
 AAQ75558/c
 ID AAQ75558 standard; DNA; 19 BP.

XX AC AAQ75558;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX FN JP06303997-A.

XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.
 XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 19 BP; 0 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
 SQ Query Match 1.0%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAA 1752
 |||||
 DB 17 AAAAAAAAAAAAAA 1

RESULT 740
 AAQ75556/c
 ID AAQ75556 standard; DNA; 19 BP.

XX AC AAQ75556;
 XX

DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.

XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX PT by digestion with restriction enzymes.
 XX PS Disclosure; Page 5; 11pp; Japanese.

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

XX Query Match 1.0%; Score 17; DB 1; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAA 1752
 |||||
 DB 17 AAAAAAAAAAAAAA 1

RESULT 741
 AAQ75554/c
 ID AAQ75554 standard; DNA; 19 BP.

XX AC AAQ75554;
 XX DT 04-AUG-1995 (first entry)
 XX DE Reverse transcription primer used in cDNA analysis technique.
 XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
 XX KW aggregate; restriction enzyme; ss.
 XX OS Synthetic.
 XX PN JP06303997-A.

XX PD 01-NOV-1994.
 XX PF 16-APR-1993; 93JP-00112515.
 XX PR 16-APR-1993; 93JP-00112515.
 XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.
 XX

PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 XX by digestion with restriction enzymes.
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 19 BP; 1 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 742
 AAQ75598/c
 ID AAQ75598 standard; DNA; 19 BP.
 XX
 AC AAQ75598;
 XX
 DT 20-FEB-1998 (first entry)
 XX
 DE Telomerase Oligo-dT-Primer P3.
 XX
 KW Telomerase; substrate; primer; detection; 5'-region; retrovirus;
 KW long terminal repeat 2; LTR-2; diagnosis; tumour; screening;
 KW effector compound; PCR; amplification; Oligo-dT-Primer; ss.
 XX
 OS Synthetic.
 XX
 PN DE19644302-A1.
 XX
 PD 05-JUN-1997.
 XX
 PF 24-OCT-1996; 96DE-01044302.
 XX
 PR 28-NOV-1995; 95DE-01044317.
 XX
 PA (BOE) BOEHRINGER MANNHEIM GMBH.
 XX
 PI Emrich T, Leying H, Hinzpeter M, Karl G;
 XX
 DR WPI; 1997-299542/28.
 XX
 PT Measuring telomerase activity, useful for tumour diagnosis and compound
 PT screening - by extending substrate primer, followed by amplification and
 PT immobilising product for detection.
 XX
 PS Example; Page 11; 21pp; German.
 XX
 CC The present sequence is a telomerase Oligo-dT-Primer, which can be used
 CC in a novel method for detecting telomerase activity. The method comprises
 CC adding to a test sample a 1st primer, that serves as telomerase
 CC substrate, and nucleoside triphosphate (dNTP) and incubating to allow
 CC primer extension by the telomerase, amplifying the extension product,
 CC immobilising the amplification product (AP) on a solid phase and
 CC qualitative and/or quantitative detection of AP, where the substrate
 CC primer is preferably from the 5'-region of the long terminal repeat 2
 CC (LTR-2) sequence of a retrovirus. The method can be used to diagnose
 CC tumours and screen compounds for effector activity. Immobilisation of AP
 CC provides a signal that is reproducibly representative of telomerase
 CC activity, eliminates the need for gel electrophoretic separation and

CC provides high sensitivity. Radioactive labels are not required and the
 CC method can be automated for routine use. Specific detection is achieved
 CC by proper choice of hybridisation conditions, without separation of the
 CC telomerase extension product. A specific signal is generated by 1-10 cell
 CC equivalents, but for tumour analysis 10-1000 ng of tissue is usually used
 XX
 SQ Sequence 19 BP; 0 A; 0 C; 0 G; 17 T; 0 U; 2 Other;
 Query Match 1.0%; Score 17; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 743
 AAQ75598/c
 ID AAQ75598 standard; DNA; 20 BP.
 XX
 AC AAQ75598;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; Gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 5; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
 Query Match 1.0%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 744
 AAQ75605/c
 ID AAQ75605 standard; DNA; 20 BP.
 XX

```

AC AAQ75605;
XX
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAA 1

RESULT 746
AAQ75589/c
ID AAQ75589 standard; DNA; 20 BP.
XX
XX AAQ75589;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAA 1

RESULT 745
AAQ75596/c
ID AAQ75596 standard; DNA; 20 BP.
XX
XX AAQ75596;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAA 1

RESULT 745
AAQ75596/c
ID AAQ75596 standard; DNA; 20 BP.
XX
XX AAQ75596;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

A method for the analysis of cDNA comprises (a) preparing an aggregate of double-stranded cDNAs by using an aggregate of mRNAs and a plural type of labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798) and using the aggregate of mRNAs as the template for each reverse

OS
yy
Synthetic.

CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAA 1752
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 750
 AAQ75590/c
 ID AAQ75590 standard; DNA; 20 BP.

XX AC AAQ75590;
 XX
 DT 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 KW Synthetic.

OS JP06303997-A.

PN 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAA 1752
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 751
 AAQ75595/c
 ID AAQ75595 standard; DNA; 20 BP.

XX AC AAQ75595;

XX 04-AUG-1995 (first entry)
 XX Reverse transcription primer used in cDNA analysis technique.
 DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 KW Synthetic.

OS JP06303997-A.

PN 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

PR 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

XX Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.

PS Disclosure; Page 5; 11pp; Japanese.

XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily

XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAA 1752

Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 752

AAQ75606/c

ID AAQ75606 standard; DNA; 20 BP.

XX AC AAQ75606;

DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.

DE Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.

OS Synthetic.

XX JP06303997-A.

PN 01-NOV-1994.

PD 16-APR-1993; 93JP-00112515.

PF 16-APR-1993; 93JP-00112515.

XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX WPI; 1995-018287/03.

```
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db |||||
17 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 753
AAQ75603/c
ID AAQ75603 standard; DNA; 20 BP.
XX
XX AAQ75603;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 0 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db |||||
17 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 754
AAQ75587/c
ID AAQ75587 standard; DNA; 20 BP.
XX
XX AAQ75587;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 20 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 3.9e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db |||||
17 AAAAAAAAAAAAAAAAAA 1
XX
RESULT 755
ABQ79871/c
ID ABQ79871 standard; DNA; 20 BP.
XX
XX ABQ79871;
XX
XX 23-DEC-2002 (first entry)
XX
XX Nucleotide sequence of a PCR primer #1.
XX
XX Polymerase chain reaction; thermal cycle; immobilisation;
XX genetic engineering; PCR; primer; ss.
XX
XX Synthetic.
XX
XX JP2002191369-A.
```

XX 09-JUL-2002.
XX
XX 27-DEC-2000; 2000JP-00399573.
XX
XX 27-DEC-2000; 2000JP-00399573.
XX
XX (TOJO) TOYO KOHAN CO LTD.
XX (TAKA/) TAKAHASHI K.
XX WPI; 2002-630904/68.
XX
XX Carrying out a thermal cycle of polymerase chain reaction (PCR) by using
XX a substrate on which a DNA is immobilized used in medical, biochemical,
XX molecular biological and gene engineering fields.
XX
XX Example; Page 9; 13pp; Japanese.
XX
XX The invention relates to performing a thermal cycle of PCR by using a
XX substrate on which a deoxyribonucleic acid (DNA) is immobilized. The
XX method is useful in the medical, biochemical, molecular biological and
XX genetic engineering fields. Sequences ABQ79871-881 represent PCR primers
XX used in the method of the invention
XX
XX Sequence 20 BP; 3 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 20 AAAAAAAAAAAAAAAAAA 4
RESULT 756
ABZ89896
ID ABZ89896 standard; DNA; 20 BP.
XX
XX AC ABZ89896;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX
XX DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.

XX Disclosure; SEQ ID NO 5138; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytosstatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
XX
Query Match 1.0%; Score 17; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 4 AAAAAAAAAAAAAAAAAA 20
RESULT 757
ABZ85532
ID ABZ85532 standard; DNA; 20 BP.
XX
XX AC ABZ85532;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX PD 31-OCT-2002.
XX
XX PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX PI Miller S, Tang L, Shahabuddin S;
XX
XX DR WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.

XX Claim 15; SEQ ID NO 774; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 17 A; 2 C; 1 G; 0 T; 0 U; 0 Other;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751

Db 4 CAAAAAAAAAAAAAAAAA 20

RESULT 758

ABZ89872

ID ABZ89872 standard; DNA; 20 BP.

AC ABZ89872;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

FN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PA Nyce JW, Li Y, Sandrasegra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX Disclosure; SEQ ID NO 5114; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a

CC first active agent comprising an oligonucleotide antisense to the

CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

CC junctions of genes encoding a polypeptide associated with lung and/or

CC nasal airway dysfunction and a second active agent comprising an

CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiasthmatic, antiallergic, hypotensive,

CC immunosuppressive, and cytostatic activity. The composition may have a

CC use in antisense gene therapy. The composition is useful for treating or

CC preventing a respiratory, lung or malignant disease or condition, also

CC for enhancing the prophylactic or therapeutic respiratory effect of an

CC antiinflammatory steroid in a subject, for reducing or depleting levels

CC of, or reducing sensitivity to adenosine, reducing levels of adenosine

CC receptor, producing bronchodilation, increasing levels of ubiquinone or

CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

CC lung inflammation, lung allergies, or a respiratory disease or condition.

CC Note: The sequence data for this patent is not represented in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 16 A; 2 C; 1 G; 1 T; 0 U; 0 Other;

Qy 1735 CAAAAAAAAAAAAAAAAA 1751

Db 3 CAAAAAAAAAAAAAAAAA 19

RESULT 759

ABZ89719/C

ID ABZ89719 standard; DNA; 20 BP.

AC ABZ89719;

DT 17-OCT-2003 (first entry)

DE Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;

KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;

KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;

KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.

OS Homo sapiens.

XX WO200285308-A2.

FN 31-OCT-2002.

PD 23-APR-2002; 2002WO-US013135.

PF 24-APR-2001; 2001US-0286137P.

XX (EPIG-) EPIGENESIS PHARM INC.

PA Nyce JW, Li Y, Sandrasegra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

XX WPI; 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired

PT respiration, has oligo(s) antisense to specific gene(s) or its

PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or

PT ubiquinone.

XX PS Disclosure; SEQ ID NO 4961; 872pp; English.

XX CC The invention relates to a novel pharmaceutical composition, which has a

XX CC first active agent comprising an oligonucleotide antisense to the

XX CC initiation codon, coding region, 5' or 3' end genomic flanking regions,

XX CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of

XX CC junctions of genes encoding a polypeptide associated with lung and/or

XX CC nasal airway dysfunction and a second active agent comprising an

XX CC antiinflammatory steroid and ubiquinone. A composition of the invention

XX CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,

XX CC immunosuppressive, and cytostatic activity. The composition may have a

XX CC use in antisense gene therapy. The composition is useful for treating or

XX CC preventing a respiratory, lung or malignant disease or condition, also

XX CC for enhancing the prophylactic or therapeutic respiratory effect of an

XX CC antiinflammatory steroid in a subject, for reducing or depleting levels

XX CC of, or reducing sensitivity to adenosine, for reducing levels of adenosine

XX CC receptor, producing bronchodilation, increasing levels of ubiquinone or

XX CC lung surfactant in a subject's tissue, or treating bronchoconstriction,

XX CC lung inflammation, lung allergies, or a respiratory disease or condition.

XX CC Note: The sequence data for this patent is not represented in the printed

XX CC specification, but was obtained in electronic format directly from WIPO

XX CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 2 A; 1 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752

DB 19 AAAAAAAAAAAAAAAAAA 3

RESULT 760

AAQ75702/c

ID AAQ75702 standard; DNA; 21 BP.

XX AC AAQ75702;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX PT by digestion with restriction enzymes.

XX PS Disclosure; Page 7; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

XX CC and using the aggregate of mRNAs as the template for each reverse

XX CC transcription primer; (b) digesting each of the prepared aggregates of

XX CC the double-stranded cDNAs with restriction enzyme and; (c)

XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 762

AAQ75762/c

ID AAQ75762 standard; DNA; 21 BP.

XX AC AAQ75762;

XX DT 04-AUG-1995 (first entry)

CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 761

AAQ75752/c

ID AAQ75752 standard; DNA; 21 BP.

XX AC AAQ75752;

XX DT 04-AUG-1995 (first entry)

XX DE Reverse transcription primer used in cDNA analysis technique.

XX KW Analysis; gene expression; reverse transcription; primer; cDNA;

XX KW aggregate; restriction enzyme; ss.

XX OS Synthetic.

XX PN JP06303997-A.

XX PD 01-NOV-1994.

XX PF 16-APR-1993; 93JP-00112515.

XX PR 16-APR-1993; 93JP-00112515.

XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.

XX DR WPI; 1995-018287/03.

XX PT Analysis of cDNA and gene expression - by amplification of mRNA followed

XX PT by digestion with restriction enzymes.

XX PS Disclosure; Page 8; 11pp; Japanese.

XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of

XX CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of

XX CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)

XX CC and using the aggregate of mRNAs as the template for each reverse

XX CC transcription primer; (b) digesting each of the prepared aggregates of

XX CC the double-stranded cDNAs with restriction enzyme and; (c)

XX CC electrophoresing the digested aggregate of cDNAs in separate lanes. The

XX CC method can be used to analyse gene expression rapidly and easily

XX SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 4e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752

DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 762

AAQ75762/c

ID AAQ75762 standard; DNA; 21 BP.

XX AC AAQ75762;

XX DT 04-AUG-1995 (first entry)

XX Reverse transcription primer used in cDNA analysis technique.
DE
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 763
AAQ75795/c
ID AAQ75795 standard; DNA; 21 BP.
AC AAQ75795;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
PF
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 764
AAQ75798/c
ID AAQ75798 standard; DNA; 21 BP.
AC AAQ75798;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
SQ Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;

*Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;

Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 764
AAQ75798/c
ID AAQ75798 standard; DNA; 21 BP.
AC AAQ75798;
XX
DT 04-AUG-1995 (first entry)
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; Gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
PR
XX 16-APR-1993; 93JP-00112515.
PR
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
PA
XX WPI; 1995-018287/03.
DR
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
PS
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
SQ Sequence 21 BP; 0 A; 4 C; 0 G; 17 T; 0 U; 0 Other;

*Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1


```
XX Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
  Query Match 1.0%; Score 17; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 771
AAQ75763/c
ID AAQ75763 standard; DNA; 21 BP.
XX
AC AAQ75763;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
PF 16-APR-1993; 93JP-00112515.
XX
PR 16-APR-1993; 93JP-00112515.
XX
PA (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
DR WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
  Query Match 1.0%; Score 17; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02; 0; Indels 0; Gaps 0;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 773
AAQ75700/c
ID AAQ75700 standard; DNA; 21 BP.
XX
AC AAQ75700;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX
PN JP06303997-A.
XX
PD 01-NOV-1994.
XX
```

```

PF 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 7; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1736 AAAAAAAAAAAAAAAAAA 1752
XX |||||||
XX 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 774
XX AAQ75786/c
XX ID AAQ75786 standard; DNA; 21 BP.
XX
XX AC AAQ75786;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1736 AAAAAAAAAAAAAAAAAA 1752
XX |||||||
XX 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 775
XX AAQ75764/c
XX ID AAQ75764 standard; DNA; 21 BP.
XX
XX AC AAQ75764;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1736 AAAAAAAAAAAAAAAAAA 1752
XX |||||||
XX 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 776
XX AAQ75796/c
XX ID AAQ75796 standard; DNA; 21 BP.
XX
XX AC AAQ75796;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX

```

```

XX
XX SQ Sequence 21 BP; 0 A; 3 C; 1 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1736 AAAAAAAAAAAAAAAAAA 1752
XX |||||||
XX 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 775
XX AAQ75764/c
XX ID AAQ75764 standard; DNA; 21 BP.
XX
XX AC AAQ75764;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
XX by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
XX double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
XX labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
XX and using the aggregate of mRNAs as the template for each reverse
XX transcription primer; (b) digesting each of the prepared aggregates of
XX the double-stranded cDNAs with restriction enzyme and; (c)
XX electrophoresing the digested aggregate of cDNAs in separate lanes. The
XX method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1736 AAAAAAAAAAAAAAAAAA 1752
XX |||||||
XX 17 AAAAAAAAAAAAAAAAAA 1
XX
XX RESULT 776
XX AAQ75796/c
XX ID AAQ75796 standard; DNA; 21 BP.
XX
XX AC AAQ75796;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX

```

```

XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 777
AAQ75797/c
ID AAQ75797 standard; DNA; 21 BP.
XX
XX AAQ75797;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 777
AAQ75797/c
ID AAQ75797 standard; DNA; 21 BP.
XX
XX AAQ75797;
XX 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
OS
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 2 A; 1 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1

```



```
RESULT 779
AAQ75790/C
ID AAQ75790 standard; DNA; 21 BP.
XX AC AAQ75790;
XX AC AAQ75790;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX XX Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAAAA 1752
XX DB 17 AAAAAAAAAAAAAAAA 1
XX RESULT 780
AAQ75697/C
ID AAQ75697 standard; DNA; 21 BP.
XX AC AAQ75697;
XX AC AAQ75697;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX XX Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAAAA 1752
XX DB 17 AAAAAAAAAAAAAAAA 1
XX RESULT 781
AAQ75784/C
ID AAQ75784 standard; DNA; 21 BP.
XX AC AAQ75784;
XX AC AAQ75784;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX XX Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAAAA 1752
XX DB 17 AAAAAAAAAAAAAAAA 1
XX RESULT 782
AAQ75784/C
ID AAQ75784 standard; DNA; 21 BP.
XX AC AAQ75784;
XX AC AAQ75784;
XX DT 04-AUG-1995 (first entry)
XX DE Reverse transcription primer used in cDNA analysis technique.
XX KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX KW aggregate; restriction enzyme; ss.
XX OS Synthetic.
XX PN JP06303997-A.
XX XX 01-NOV-1994.
XX PD 16-APR-1993; 93JP-00112515.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX XX Disclosure; Page 9; 11pp; Japanese.
XX CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX SQ Sequence 21 BP; 1 A; 1 C; 0 G; 19 T; 0 U; 0 Other;
XX Query Match 1.0%; Score 17; DB 1; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 4e+02;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAAAA 1752
XX DB 17 AAAAAAAAAAAAAAAA 1
```

```
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 782
AAQ75698/c
ID AAQ75698 standard; DNA; 21 BP.
XX
AC AAQ75698;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 7; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 784
AAQ75751/c
ID AAQ75751 standard; DNA; 21 BP.
XX
AC AAQ75751;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
KW Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX 01-NOV-1994.
XX 16-APR-1993; 93JP-00112515.
XX 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX WPI; 1995-018287/03.
XX
PT Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
PS Disclosure; Page 8; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-075798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1

RESULT 783
AAQ75699/c
ID AAQ75699 standard; DNA; 21 BP.
XX
AC AAQ75699;
XX
DT 04-AUG-1995 (first entry)
XX
DE Reverse transcription primer used in cDNA analysis technique.
XX
```

```
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 1 C; 2 G; 17 T; 0 U; 0 Other;
  Query Match 1.0%; Score 17; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1736 AAAAAAAAAAAAAAAAAA 1752
  DB 17 AAAAAAAAAAAAAAAAAA 1
  RESULT 785
  ID AAQ75691/c
  AC AAQ75691;
  XX 04-AUG-1995 (first entry)
  DT Reverse transcription primer used in cDNA analysis technique.
  DE Analysis; Gene expression; reverse transcription; primer; cDNA;
  KW aggregate; restriction enzyme; ss.
  XX Synthetic.
  OS JP06303997-A.
  PN 01-NOV-1994.
  XX 16-APR-1993; 93JP-00112515.
  PF 16-APR-1993; 93JP-00112515.
  PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
  PA WPI; 1995-018287/03.
  XX Analysis of cDNA and gene expression - by amplification of mRNA followed
  PT by digestion with restriction enzymes.
  DE Disclosure; Page 7; 11pp; Japanese.
  XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
  CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
  CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
  CC and using the aggregate of mRNAs as the template for each reverse
  CC transcription primer; (b) digesting each of the prepared aggregates of
  CC the double-stranded cDNAs with restriction enzyme and; (c)
  CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
  CC method can be used to analyse gene expression rapidly and easily
  XX
  SQ Sequence 21 BP; 1 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
  Query Match 1.0%; Score 17; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1736 AAAAAAAAAAAAAAAAAA 1752
  DB 17 AAAAAAAAAAAAAAAAAA 1
  RESULT 786
  ID AAQ75754/c
  AC AAQ75754;
  XX 04-AUG-1995 (first entry)
  DT Reverse transcription primer used in cDNA analysis technique.
  DE Analysis; Gene expression; reverse transcription; primer; cDNA;
  KW aggregate; restriction enzyme; ss.
  XX Synthetic.
  OS JP06303997-A.
  PN 01-NOV-1994.
  XX 16-APR-1993; 93JP-00112515.
  PF 16-APR-1993; 93JP-00112515.
  PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
  PA WPI; 1995-018287/03.
  XX Analysis of cDNA and gene expression - by amplification of mRNA followed
  PT by digestion with restriction enzymes.
  DE Disclosure; Page 8; 11pp; Japanese.
  XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
  CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
  CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
  CC and using the aggregate of mRNAs as the template for each reverse
  CC transcription primer; (b) digesting each of the prepared aggregates of
  CC the double-stranded cDNAs with restriction enzyme and; (c)
  CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
  CC method can be used to analyse gene expression rapidly and easily
  XX
  SQ Sequence 21 BP; 1 A; 2 C; 1 G; 17 T; 0 U; 0 Other;
  Query Match 1.0%; Score 17; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1736 AAAAAAAAAAAAAAAAAA 1752
  DB 17 AAAAAAAAAAAAAAAAAA 1
  RESULT 787
  ID AAQ75755/c
  AC AAQ75755;
  XX 04-AUG-1995 (first entry)
  DT Reverse transcription primer used in cDNA analysis technique.
  DE Analysis; Gene expression; reverse transcription; primer; cDNA;
  KW aggregate; restriction enzyme; ss.
  XX Synthetic.
  OS JP06303997-A.
  PN 01-NOV-1994.
  XX 16-APR-1993; 93JP-00112515.
  PF 16-APR-1993; 93JP-00112515.
  PR (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
  PA WPI; 1995-018287/03.
  XX Analysis of cDNA and gene expression - by amplification of mRNA followed
  PT by digestion with restriction enzymes.
  DE Disclosure; Page 7; 11pp; Japanese.
  XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
  CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
  CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
  CC and using the aggregate of mRNAs as the template for each reverse
  CC transcription primer; (b) digesting each of the prepared aggregates of
  CC the double-stranded cDNAs with restriction enzyme and; (c)
  CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
  CC method can be used to analyse gene expression rapidly and easily
  XX
  SQ Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
  Query Match 1.0%; Score 17; DB 1; Length 21;
  Best Local Similarity 100.0%; Pred. No. 4e+02;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1736 AAAAAAAAAAAAAAAAAA 1752
  DB 17 AAAAAAAAAAAAAAAAAA 1
```

```
PR 16-APR-1993; 93JP-00112515.
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 8; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 2 A; 1 C; 1 G; 17 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 788
AAQ75761/c
ID AAQ75761 standard; DNA; 21 BP.
XX
XX AAQ75761;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
XX aggregate; restriction enzyme; ss.
XX Synthetic.
XX
XX JP06303997-A.
XX
XX 01-NOV-1994.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX 16-APR-1993; 93JP-00112515.
XX
XX (NITE ) NIPPON TELEGRAPH & TELEPHONE CORP.
XX
XX WPI; 1995-018287/03.
XX
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX
XX Disclosure; Page 9; 11pp; Japanese.
XX
XX A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
XX Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1
RESULT 790
AAQ75789/c
ID AAQ75789 standard; DNA; 21 BP.
XX
XX AAQ75789;
XX
XX 04-AUG-1995 (first entry)
XX
XX Reverse transcription primer used in cDNA analysis technique.
XX
XX Analysis; gene expression; reverse transcription; primer; cDNA;
```

KW aggregate; restriction enzyme; ss.
OS Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 791
AAQ75701/c
ID AAQ75701 standard; DNA; 21 BP.
XX AC AAQ75701;
XX DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 7; 11pp; Japanese.
XX

CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 2 C; 0 G; 18 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 792
AAQ75766/c
ID AAQ75766 standard; DNA; 21 BP.
XX AC AAQ75766;
XX DT 04-AUG-1995 (first entry)
XX Reverse transcription primer used in cDNA analysis technique.
XX Analysis; gene expression; reverse transcription; primer; cDNA;
KW aggregate; restriction enzyme; ss.
XX Synthetic.
XX JP06303997-A.
XX PD 01-NOV-1994.
XX PF 16-APR-1993; 93JP-00112515.
XX PR 16-APR-1993; 93JP-00112515.
XX PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
XX DR WPI; 1995-018287/03.
XX Analysis of cDNA and gene expression - by amplification of mRNA followed
PT by digestion with restriction enzymes.
XX Disclosure; Page 9; 11pp; Japanese.
XX
CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
CC and using the aggregate of mRNAs as the template for each reverse
CC transcription primer; (b) digesting each of the prepared aggregates of
CC the double-stranded cDNAs with restriction enzyme and; (c)
CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
CC method can be used to analyse gene expression rapidly and easily
XX
SQ Sequence 21 BP; 1 A; 3 C; 0 G; 17 T; 0 U; 0 Other;
Query Match 1.0%; Score 17; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 17 AAAAAAAAAAAAAAAAAA 1
RESULT 793

AAQ75783/c
 ID AAQ75783 standard; DNA; 21 BP.
 AC AAQ75783;
 XX
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE Reverse transcription primer used in cDNA analysis technique.
 XX
 KW Analysis; gene expression; reverse transcription; primer; cDNA;
 KW aggregate; restriction enzyme; ss.
 XX
 OS Synthetic.
 XX
 PN JP06303997-A.
 XX
 PD 01-NOV-1994.
 XX
 PF 16-APR-1993; 93JP-00112515.
 XX
 PR 16-APR-1993; 93JP-00112515.
 XX
 PA (NITE) NIPPON TELEGRAPH & TELEPHONE CORP.
 XX
 DR WPI; 1995-018287/03.
 XX
 PT Analysis of cDNA and gene expression - by amplification of mRNA followed
 PT by digestion with restriction enzymes.
 XX
 PS Disclosure; Page 9; 11pp; Japanese.
 XX
 CC A method for the analysis of cDNA comprises (a) preparing an aggregate of
 CC double-stranded cDNAs by using an aggregate of mRNAs and a plural type of
 CC labelled reverse transcription primers (GENESEQ files AAQ75547-Q75798)
 CC and using the aggregate of mRNAs as the template for each reverse
 CC transcription primer; (b) digesting each of the prepared aggregates of
 CC the double-stranded cDNAs with restriction enzyme and; (c)
 CC electrophoresing the digested aggregate of cDNAs in separate lanes. The
 CC method can be used to analyse gene expression rapidly and easily
 XX
 SQ Sequence 21 BP; 0 A; 2 C; 2 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 1.0%; Score 17; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAAAAAA 1752
 DB 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 794
 AAA98276/c
 ID AAA98276 standard; DNA; 22 BP.
 AC AAA98276;
 XX
 DT 02-FEB-2001 (first entry)
 XX
 DE Human mismatch repair gene hMSH6 intron 9 DNA fragment.
 XX
 KW Human mismatch repair gene; hMSH6; disease predisposition; genotype;
 KW mutation; carcinoma; colorectal; endometrial; ovarian; leukemia;
 KW neoplastic disease; drug development; ss.
 XX
 OS Homo sapiens.
 XX
 PN DE19909878-A1.
 XX
 PD 07-SEP-2000.
 XX
 PF 06-MAR-1999; 99DE-01009878.
 XX

PR 06-MAR-1999; 99DE-01009878.
 XX
 PA (UYDR) UNIV DRESDEN TECH.
 XX
 PI Plasmid J, Kruppa C, Schackert H;
 XX
 DR WPI; 2000-588378/56.
 XX
 PT Novel variants of the human mismatch repair gene, MSH6, useful e.g. for
 PT determining predisposition to cancer and for development of drugs.
 XX
 PS Claim 1; Page 4; 14pp; German.
 XX
 CC This invention describes a novel method of determining a predisposition
 CC to disease by genotyping a subject's DNA sequence (A) of the human
 CC mismatch repair gene, MSH6 at specified positions and comparing with
 CC reference DNA sequences, optionally taking into account all possible
 CC combinations of variations of the individual mutations, including any
 CC chosen absolute number of variations. (A), and analysis of their
 CC sequences, are useful for the following: (i) determining a predisposition
 CC to disease, especially colorectal, endometrial and ovarian carcinoma and
 CC leukemia; (ii) determining an increased mutation rate (frequency of base
 CC substitutions, insertions and/or deletions) in eukaryotic cells; (iii)
 CC predicting the progression, severity and survival time of patients with
 CC neoplastic disease; (iv) the development of therapeutic and 'life-style'
 CC drugs; (v) predicting individual differences in response to known
 CC chemotherapeutic agents (e.g. cis-platin) or drugs developed from (iv);
 CC (vi) optimizing individual treatments and interventions against neoplasia
 CC ; (vii) controlling the mutation rate in eukaryotic cells, in vitro or in
 CC vivo; (viii) constructing genes and vectors, particularly for development
 CC of pharmaceuticals; (ix) developing diagnostic kits and other systems for
 CC genotyping; and (x) developing in vivo and in vitro test systems for
 CC expressing individual forms of the MSH6 gene, e.g. for studying
 CC pathophysiology of disease or processes in which MSH6 is involved, and
 CC for drug development and testing
 XX
 SQ Sequence 22 BP; 4 A; 1 C; 0 G; 17 T; 0 U; 0 Other;
 XX
 Query Match 1.0%; Score 17; DB 1; Length 22;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAAAAAA 1752
 DB 22 AAAAAAAAAAAAAAAAAA 6
 RESULT 795
 AAQ73379
 ID AAQ73379 standard; DNA; 20 BP.
 XX
 AC AAQ73379;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAY-1995 (first entry)
 XX
 DE Anti-HSV-1 G4 oligo #5652.
 XX
 KW Hybridise; herpes simplex virus; HSV; open reading frame;
 KW translation initiation site; coding region; 5' UTR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9419945-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 07-MAR-1994; 94WO-US002471.
 XX
 PR 12-MAR-1993; 93US-00031147.
 XX
 PF (ISIS-) ISIS PHARM INC.
 XX

PI Draper KG, Crooke ST, Mirabelli CK, Ecker DJ, Hanecak R;
 PI Anderson KP, Brown-Driver VL, Wyatt JR;
 XX WPI; 1994-302552/37.

XX New oligonucleotide(s) hybridising with DNA or RNA of herpesvirus gene -
 PT are used in the treatment and diagnosis of herpes simplex virus,
 PT cytomegalovirus, Epstein Barr virus and varicella zoster infections.

XX Claim 12; Page 36; 72pp; English.

XX The sequences given in AAQ73325-81 represent oligonucleotides which
 CC hybridise specifically with DNA or RNA from a herpes virus gene
 CC corresponding to one of the open reading frames UL5, -8, -9, -20, -27-
 CC 29, -30, -42, -52 or IE175 of herpes simplex virus type 1 (HSV-1). These
 CC oligos pref. hybridise with a translation initiation site, a coding
 CC region or a 5' untranslated region. These oligos may be used in
 CC compositions for the treatment and diagnosis of herpes viral infection,
 CC by contacting the virus or the animal, or its cells, tissues or body
 CC fluids with the oligo. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred.No. 4.1e+02; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 2;

Qy 1019 TTGGGGATGGGCTGGGGTT 1038

Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 796

AAQ61999
 ID AAQ61999 standard; DNA; 20 BP.

XX AAQ61999;

XX 25-MAR-2003 (revised)

DT 04-NOV-1994 (first entry)

XX Guanine quartet containing oligomer, #10.

XX Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1..20
 FT /+tag= a
 FT /note= "Phosphorothionate intersugar linkages"

XX WO9408053-A1.

XX 14-APR-1994.

XX 29-SEP-1993; 93WO-US009297.

XX 29-SEP-1992; 92US-00954185.

XX (ISIS-) ISIS PHARM INC.

XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;

PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;

XX WPI; 1994-135613/16.

XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 PT of chromosomes.

XX Disclosure; Page 107; 144pp; English.

XX The sequences given in AAQ61990-2001 are oligonucleotides which contain
 CC G4 or G3 stretches and which may be used for inhibiting replication of
 CC herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
 CC influenza virus, or for treating inflammatory and neurological disorders
 CC caused by phospholipase A2 activity in cases of hyper-proliferation,
 CC malignancy, cardiovascular disease and snake bite. Oligonucleotides such
 CC as these, may be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred.No. 4.1e+02;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGGATGGGCTGGGGTT 1038

Db 1 TTGGGGTTGGGGTTGGGGTT 20

RESULT 797

AAQ61896
 ID AAQ61896 standard; DNA; 20 BP.

XX AAQ61896;

XX 25-MAR-2003 (revised)

DT 04-NOV-1994 (first entry)

XX HSV replication inhibiting oligomer, ISIS no 5652.

XX Inhibition; replication; herpes simplex virus; HSV; HIV;

KW human cytomegalovirus; influenza virus; inflammation;

KW neurological disorders; phospholipase A2 activity; hyperproliferation;

KW malignancy; cardiovascular disease; snake bite; malignancy;

KW telomere length; retard; aging; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_feature 1..20
 FT /+tag= a
 FT /note= "Phosphorothionate intersugar linkages"

XX WO9408053-A1.

XX 14-APR-1994.

XX 29-SEP-1993; 93WO-US009297.

XX 29-SEP-1992; 92US-00954185.

XX (ISIS-) ISIS PHARM INC.

XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;

PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;

XX WPI; 1994-135613/16.

XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 PT of chromosomes.

XX Claim 5; Page 19; 144pp; English.

XX The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides
 CC which contain a G4 or two G3 stretches and which may be used for
 CC inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
 CC such as these may also be used for inhibiting activity of HIV, human

CC cytomegalovirus or influenza virus, or for treating inflammatory and
 CC neurological disorders caused by phospholipase A2 activity in cases of
 CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
 CC They may also be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 4.1e+02; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGGTT 1038

||||| ||||| ||||| ||||| |||||
 Db 1 TTGGGGTTGGGTTGGGTT 20

RESULT 798

AAQ61995

ID AAQ61995 standard; DNA; 20 BP.

XX AAQ61995;

XX 25-MAR-2003 (revised)

DT 04-NOV-1994 (first entry)

DE Guanine quartet containing oligomer, #6.

XX Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.

OS Synthetic.

XX Key

Location/Qualifiers

FT misc_feature

1..20

FT /*tag= a

FT /note= "Phosphorothionate intersugar linkages"

XX WO9408053-A1.

XX 14-APR-1994.

XX 29-SEP-1993; 93WO-US009297.

XX 29-SEP-1992; 92US-00954185.

XX (ISIS-) ISIS PHARM INC.

XX Hancak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;

PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;

XX WPI; 1994-135613/16.

XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 of chromosomes.

XX Disclosure; Page 106; 144pp; English.

XX The sequences given in AAQ61990-2001 are oligonucleotides which contain
 CC G4 or G3 stretches and which may be used for inhibiting replication of
 CC herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
 CC influenza virus, or for treating inflammatory and neurological disorders
 CC caused by phospholipase A2 activity in cases of hyper- proliferation,
 CC malignancy, cardiovascular disease and snake bite. Oligonucleotides such
 CC as these, may be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGGTT 1038

||||| ||||| ||||| ||||| |||||
 Db 1 TTGGGGTTGGGTTGGGTT 20

RESULT 799

AAQ61904

ID AAQ61904 standard; DNA; 20 BP.

XX AAQ61904;

XX 25-MAR-2003 (revised)

DT 04-NOV-1994 (first entry)

DE HSV replication inhibiting oligomer, ISIS no 5650.

XX Inhibition; replication; herpes simplex virus; HSV; HIV;

KW human cytomegalovirus; influenza virus; inflammation;

KW neurological disorders; phospholipase A2 activity; hyperproliferation;

KW malignancy; cardiovascular disease; snake bite; malignancy;

KW telomere length; retard; aging; ss.

OS Synthetic.

XX Key

Location/Qualifiers

FT misc_feature

1..20

FT /*tag= a

FT /note= "Phosphorothionate intersugar linkages"

XX WO9408053-A1.

XX 14-APR-1994.

XX 29-SEP-1993; 93WO-US009297.

XX 29-SEP-1992; 92US-00954185.

XX (ISIS-) ISIS PHARM INC.

XX Hancak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;

PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;

XX WPI; 1994-135613/16.

XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
 of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 of chromosomes.

XX Disclosure; Page 19; 144pp; English.

XX The sequences given in AAQ61825-50 and AAQ61886-906 are oligonucleotides
 CC which contain a G4 or two G3 stretches and which may be used for
 CC inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
 CC such as these may also be used for inhibiting activity of HIV, human
 CC cytomegalovirus or influenza virus, or for treating inflammatory and
 CC neurological disorders caused by phospholipase A2 activity in cases of
 CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
 CC They may also be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1019 TTGGGATGGGCTGGGTT 1038

Db 1 TTTGGGTTGGGCTGGGGTT 20

RESULT 800

AAQ97982

ID AAQ97982 standard; DNA; 20 BP.

XX AC AAQ97982;

XX 25-MAR-2003 (revised)

DT 19-OCT-1995 (first entry)

XX Peptide nucleic acid oligomer targetting HIV gene.

DE Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;

XX Antiviral; antisense; triple helix; ss.

KW Synthetic.

OS

XX Key Location/Qualifiers

FT misc_feature 1..20

FT /tag= a

FT /note= "at least one (and preferably all) of the backbone

FT subunits are composed of N-acetyl N-(2-aminoethyl)glycine

FT peptide residues, the nucleobase being attached

FT covalently to the acetyl group and the peptide linkage

FT being formed by condensation of the glycine carboxy group

FT of one residue with the amino group of the 2-aminoethyl

FT moiety in the next residue"

XX

XX WO9504068-A1.

XX 09-FEB-1995.

XX 28-JUL-1994; 94WO-US008517.

XX 29-JUL-1993; 93US-00099718.

XX (ISIS-) ISIS PHARM INC.

XX Ecker DJ;

XX WPI; 1995-082179/11.

XX Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid

PT subunit - binds in complementary manner to DNA and RNA, and useful for

PT modulating HIV viral activity, e.g. in treating AIDS.

XX Claim 2; Page 176; 186pp; English.

XX New peptide nucleic acid (PNA) oligomers are provided which (a) consist

CC of naturally occurring nucleobases covalently bound to a polyamide

CC backbone and (b) hybridise to the translation initiation AUG region, 5'

CC untranslated region (5' UTR), 3' untranslated region (3' UTR), splice

CC junctions or coding sequence of a human immunodeficiency virus gene

CC chosen from env, gag, pol, rev and tat. The PNAs can be used to target

CC RNA and single stranded DNA (ssDNA) to produce antisense-type gene

CC regulation moieties. They have utility as gene-targetted drugs for

CC modulating HIV processes. Hence they can be used to treat AIDS and other

CC viral infections. They are also useful in diagnostic applications and as

CC research tools. PNA oligomers have high affinity for complementary single

CC stranded DNA. They are also able to form triple helices in which a first

CC PNA strand binds with RNA or ssDNA and a second PNA strand binds with the

CC resulting double helix or with the first PNA strand. The PNAs possess no

CC significant charge and are water soluble, which facilitates cellular

CC uptake. Further, since they contain amides of non-biological amino acids,

CC they are biostable and resistant to enzymatic degradation by proteases.

CC The present sequence is a specifically claimed PNA sequence (represented

CC by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-

CC 2003 to correct PN field.)

XX Sequence 20 BP; 0 A; 0 C; 12 G; 8 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1019 TTGGGGATGGGCTGGGGTT 1038

DB 1 TTGGGGTTGGGTTGGGGTT 20

RESULT 801

AAZ09195

ID AAZ09195 standard; DNA; 20 BP.

XX AC AAZ09195;

XX 19-OCT-1999 (first entry)

DE Oligonucleotide 7 for DNA analysis.

XX Primer; DNA analysis; amplification; hybridisation; ss.

XX Synthetic.

XX JP11196874-A.

XX 27-JUL-1999.

XX 14-JAN-1998; 98JP-00005399.

XX 14-JAN-1998; 98JP-00005399.

XX (HITA) HITACHI LTD.

XX WPI; 1999-496652/42.

XX Analysis of DNA fragment - comprises addition of known common

PT oligonucleotide, amplification of resultant DNA fragment and analysis and

PT labelling of amplified DNA.

XX Example 1; Page 12; 17pp; Japanese.

XX This invention describes a novel method for the analysis of a DNA fragment

CC which comprises: (i) addition of a known common oligonucleotide sequence

CC to at least one terminal of each DNA fragment, (ii) amplification of the

CC resultant DNA fragment as a primer using a first common primer containing

CC a complementary nucleotide sequence to the above mentioned known common

CC oligonucleotide sequence, a second common primer containing a

CC complementary nucleotide sequence to the prepared known common

CC oligonucleotide sequence optionally having been introduced with

CC complementary nucleotide sequence at a terminal, and a specific primer

CC capable of hybridisation with a DNA fragment containing whole or part of

CC the gene having known sequence, to give amplified DNA, (iii) analysis of

CC the amplified DNA to find the information of the DNA fragment, in which

CC the specific primer is designed to prepare fragments of the common first

CC and second primers and to give short fragment of amplified DNA and (iv)

CC labelling them to make their differentiation. Differentiation of

CC informations of known and unknown genes readily provides information of

CC unknown gene and simultaneous monitoring of signals derived from minor

CC genes. Furthermore, labelling of DNAs according to functions of known

CC genes can be performed. AAZ09189-Z09201 represent oligonucleotide primers

XX used to illustrate the method of the invention

XX Sequence 20 BP; 15 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;

Best Local Similarity 90.0%; Pred. No. 4.1e+02;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1731 TTTACAAAAA 1750

DB 1 TCTCAAAAAA 20

RESULT 802
AAA91207/C
ID AAA91207 standard; DNA; 20 BP.
XX
XX
AC AAA91207;
XX
XX 08-MAY-2001 (first entry)
XX
XX Antisense IGFBP-5 inhibitor #13.
XX
XX Insulin-like growth factor binding protein-5; IGFBP-5; human;
KW Antisense oligonucleotide; hormone-regulated cancer; prostatic cancer;
KW breast cancer; therapy; ss.
XX
XX Homo sapiens.
OS
XX WO200105435-A2.
XX
XX 25-JAN-2001.
XX
XX 19-JUL-2000; 2000WO-CA000853.
XX
XX 19-JUL-1999; 99US-0144495P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
PA (MIYA/) MIYAKE H.
XX
XX Gleave M;
PI
XX WPI; 2001-168448/17.
XX
XX Composition for treating hormone-regulated cancer, e.g. breast and
PT prostatic tumors, comprising an antisense oligonucleotide that inhibits
PT expression of insulin like growth factor binding protein-5 by hormone-
XX regulated tumor cells.
XX
XX Disclosure; Page 34; 45pp; English.
XX
XX This sequence represents an antisense oligonucleotide targeted against
CC human insulin-like growth factor binding protein-5 (IGFBP-5). The
CC invention relates to a composition for treatment of hormone-regulated
CC cancer, comprising an antisense oligonucleotide (such as this sequence)
CC which inhibits expression of IGFBP-5 by hormone-regulated tumour cells.
CC The compositions is useful for delaying progression of hormone-regulated
CC tumour cells such as prostatic cancer cells or breast cancer cells, to an
CC androgen-independent state, by treating hormone sensitive tumour cells
CC with the antisense sequence which inhibits expression of IGFBP-5 by the
CC tumour cells. The composition can also be used for treating a hormone-
CC responsive cancer in an individual, and administering the composition to
CC the individual after initiation of hormone-withdrawal to induce apoptotic
CC cell death of hormone-responsive tumour cells, and therefore delaying the
CC progression of hormone-responsive cancer cells to a hormone-independent
CC state in the individual. It can also be used for inhibiting or delaying
CC metastatic bone progression of an IGF-1 sensitive tumour in a mammal, by
CC administering the composition to inhibit the expression of IGFBP-5 by the
CC hormone-responsive cancer cells, and therefore inhibiting or delaying
CC metastatic bone progression of the tumour
XX
XX Sequence 20 BP; 3 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1731 TTTACAAAAA AAAAAAAAAA 1750
DB 20 TTTGAAAAA AAAAAAAAAA 1
XX
XX
RESULT 803
AAF72967/C
ID AAF72967 standard; DNA; 20 BP.
XX
XX
AC AAF72967;
XX
XX 24-APR-2001 (first entry)
XX
XX Human daxx inhibitory antisense phosphorothioate oligonucleotide SEQ:68.
XX
XX Antisense oligonucleotide; daxx; inhibition; phosphorothioate;
KW Fas binding protein; CENP-C binding protein; dap6; EAP; cytostatic;
KW antiinflammatory; death associated protein 6; Ets-1 associated protein;
KW infection; inflammation; tumour formation; ss.
XX
XX Homo sapiens.
OS
XX US6180353-B1.
XX
XX 30-JAN-2001.
XX
XX 24-JAN-2000; 2000US-00490692.
XX
XX 24-JAN-2000; 2000US-00490692.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Dean NM, Cowser LM;
PI
XX WPI; 2001-217744/22.
XX
XX Novel antisense compounds capable of modulating expression of daxx useful
PT for diagnosis, prophylaxis and treatment of diseases associated with
PT expression of daxx.
XX
XX Claim 1; Col 43; 59pp; English.
XX
XX The present invention describes an antisense compound (I) up to 30
CC nucleobases in length, where (I) inhibits expression of daxx (also known
CC as Fas binding protein, CENP-C binding protein, dap6 for death associated
CC protein 6 and EAP for Ets-1 associated protein). (I) has cytostatic and
CC antiinflammatory activity, and can be used in antisense therapy and as a
CC modulator of daxx. (I) is useful for inhibiting the expression of daxx in
CC cells or tissues in vitro. (I) can be utilised for diagnostics,
CC therapeutics for the treatment of diseases associated with the expression
CC of daxx, prophylaxis e.g. to prevent or delay infection, inflammation or
CC tumour formation and as research reagent. The present sequence represents
CC an inhibitory human daxx antisense phosphorothioate oligonucleotide which
CC is used in the exemplification of the present invention
XX
XX Sequence 20 BP; 0 A; 11 C; 0 G; 9 T; 0 U; 0 Other;
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 859 GCAGGAAGAGGAGGAGGAGG 878
DB 20 GCAGGAAGAGGAGGAGGAGG 1
XX
XX
RESULT 804
AAS05713/C
ID AAS05713 standard; DNA; 20 BP.
XX
XX AAS05713;
AC
XX
XX 07-SEP-2001 (first entry)
XX
XX Polypyrimidine Crick strand oligonucleotide.
DE
XX reverse phase triplex forming oligonucleotide; RP-TFO;
KW protected nucleic acid sequence; PNAS; single nucleotide polymorphism;
KW SNP; short tandem repeat; cancer; Factor V Leiden SNP; ss.
XX
XX Synthetic.

PD	31-OCT-2002.	
XX		
XX	23-APR-2002; 2002WO-US013135.	
XX		
XX	24-APR-2003; 2001US-0286137P.	
XX		
XX	(EPIC-) EPIGENESIS PHARM INC.	
PA		
XX	Nyce JW, Li Y, Sandraeagra A, Katz E, Pabalan J, Aguilar D;	
PI	Miller S, Tang L, Shahabuddin S;	
PI	WPI; 2003-229219/22.	
DR		
XX		
XX	Pharmaceutical composition for treating ailments associated with impaired	
PT	respiration, has oligo(s) antisense to specific gene(s) or its	
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or	
PT	ubiquinone.	
PT		
XX		
XX	Claim 15; SEQ ID NO 678; 872pp; English.	
PS		
XX		
CC	The invention relates to a novel pharmaceutical composition, which has a	
CC	first active agent comprising an oligonucleotide antisense to the	
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,	
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of	
CC	junctions of genes encoding a polypeptide associated with lung and/or	
CC	nasal airway dysfunction and a second active agent comprising an	
CC	antiinflammatory steroid and ubiquinone. A composition of the invention	
CC	has antiinflammatory, antiallergic, antiasthmatic, hypotensive,	
CC	immunosuppressive, and cytostatic activity. The composition may have a	
CC	use in antisense gene therapy. The composition is useful for treating or	
CC	preventing a respiratory, lung or malignant disease or condition, also	
CC	for enhancing the prophylactic or therapeutic respiratory effect of an	
CC	antiinflammatory steroid in a subject, for reducing or depleting levels	
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine	
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or	
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,	
CC	lung inflammation, lung allergies, or a respiratory disease or condition.	
CC	Note: The sequence data for this patent is not represented in the printed	
CC	specification, but was obtained in electronic format directly from WIPO	
CC	at ftp.wipo.int/pub/published_pct_sequences	
XX		
XX	Sequence 20 BP; 3 A; 2 C; 1 G; 14 T; 0 U; 0 Other;	
XX		
XX	Query Match 1.0%; Score 16.8; DB 1; Length 20;	
XX	Best Local Similarity 90.0%; Pred. No. 4.1e+02;	
XX	Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0	
QY	1730 GTTTACAAAAA AAAAAAAAA 1749	
DB		
DB	20 GGTTCCTCAAAAAA AAAAAAAAA 1	
XX		
XX	RESULT 807	
XX	ABZ92865	
ID	ABZ92865 standard; DNA; 20 BP.	
AC		
XX	ABZ92865;	
XX		
DT	17-OCT-2003 (first entry)	
XX		
DE	Human oligonucleotide sequence.	
XX		
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;	
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;	
KW	antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;	
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;	
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;	
KW	lung inflammation; respiratory disease; ds.	
XX		
XX	Homo sapiens.	
OS		
XX		
PN	WO200285308-A2.	
XX		

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(BFIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
Miller S, Tang L, Shahabuddin S;

WPT; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.

Disclosure; SEQ ID NO 8107; 872bp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiaesthetic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pt_sequences

Sequence 20 BP; 18 A; 0 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
||| |||||||
Db 1 AAGTAAAAAAAAAAAAAAAAAAAAA 20

RESULT 808
ABZ85669/c
ID ABZ85669 standard; DNA; 20 BP.
XX AC ABZ85669;
DT
DT 17-OCT-2003 (first entry)
DE DE
DE Human oligonucleotide sequence.
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiaesthetic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
OS Homo sapiens.
XX XX
PN WO200285308-A2.
XX

PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 911; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 0 A; 2 C; 0 G; 18 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACACAAAAAAGAAAAA 1753
Db 20 AGAAAAAAGAAAAA 1

RESULT 809
ABZ86569/C
ID ABZ86569 standard; DNA; 20 BP.
XX
AC ABZ86569;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX

PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
DR
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Claim 15; SEQ ID NO 1811; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 1 A; 6 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 177 GCTGCCCCCGAAGCAGCCGG 196
Db 20 GCTGCCACCAAGCAGCCGG 1

RESULT 810
ABZ88813
ID ABZ88813 standard; DNA; 20 BP.
XX
AC ABZ88813;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX

```
PD 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 4055; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 16 A; 0 C; 1 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1728 GAGTTTACAAAAA 1747
DB 1 GAATTTAAAAA 20
RESULT 811
ABZ85535
ID ABZ85535 standard; DNA; 20 BP.
XX
XX ABZ85535;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
```

```
PD 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIC-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Claim 15; SEQ ID NO 777; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 18 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1736 AAAAAA 1755
DB 1 AAAAAAAGAAAGAAAAA 20
RESULT 812
ABZ89014
ID ABZ89014 standard; DNA; 20 BP.
XX
XX ABZ89014;
XX
XX 17-OCT-2003 (first entry)
XX
XX Human oligonucleotide sequence.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200285308-A2.
PN
XX
```

```
PD 31-OCT-2002.
XX
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
XX Disclosure; SEQ ID NO 4256; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16.8; DB 1; Length 20;
Best Local Similarity 90.0%; Pred. NO. 4.1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1733 TACAAAAA 1752
Db 1 TACCTAAAAA 20
RESULT 813
AAF95712
ID AAF95712 standard; DNA; 21 BP.
XX
XX AAF95712;
XX
XX 06-JUN-2001 (first entry)
DT
XX Human gene single nucleotide polymorphism #473.
DE
XX Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
XX polymorphism; vascular disease; coronary artery disease; forensics;
KW myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW pulmonary embolism; paternity test; ds.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
PH replace(11,T)
FT /*tag= a
FT /standard_name= "single nucleotide polymorphism"
```

```
XX
XX WO200118250-A2.
XX
XX 15-MAR-2001.
XX
XX 07-SEP-2000; 2000WO-US024503.
XX
XX 10-SEP-1999; 99US-0153357P.
XX
XX 26-JUL-2000; 2000US-0220947P.
XX
XX 16-AUG-2000; 2000US-0225724P.
XX
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Lander ES, Gargill M, Ireland JS, Bolk S, Daley GQ, Mccarthy JJ;
XX WPI; 2001-226749/23.
XX
XX Nucleic acids comprising single nucleotide polymorphisms, useful in
PT applications such as forensics, paternity testing, medicine, genetic
PT analysis and phenotype correlations to diseases such as diabetes and
PT atherosclerosis.
XX
XX Example; Page 81; 242pp; English.
XX
XX The present invention provides a method of diagnosing a vascular disease
CC in an individual, involving determining the sequence at various
CC polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC genes. The sequences at a number of polymorphic sites are also provided
CC in the specification. In particular, the method can be used in the
CC diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC useful in forensics, paternity testing, genetic analysis and phenotype
CC correlations to diseases. The present sequence is an example of one of
CC the human gene SNPs shown in the specification
XX
XX Sequence 21 BP; 5 A; 3 C; 10 G; 3 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. NO. 4.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 831 AGAGGAAGCTGCTGGGTCT 850
Db 2 AGAGGAAGCTGCTGGGTCT 21
RESULT 814
ABS97317/C
ID ABS97317 standard; DNA; 21 BP.
XX
XX ABS97317;
XX
XX 23-DEC-2002 (first entry)
DT
XX Aryl hydrocarbon nuclear translocation receptor sequencing primer #6.
DE
XX Human; ss; primer; cytochrome P450 A1; CYP450A1; UGT2B4; MDR1; PCR;
KW cytochrome P450 A2; CYP450A2; cytochrome P450 02E; CYP45002E1; LTF;
KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR112;
KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;
KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;
KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;
KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;
KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;
KW NADPH quinone oxidoreductase 2; NQO2; sulfoltransferase thermolabile; STM;
KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;
KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;
KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;
KW multidrug resistance associated protein 3; cancer; prostate;
KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;
KW altered drug metabolism; cardiovascular function; colorectal tumour;
```

central nervous system; pulmonary; immunological.

Homo sapiens.

WO200257410-A2.

25-JUL-2002.

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389.

(DNAS-) DNA SCI LAB INC.

Guida M, Hall J;

WPI; 2002-698522/75.

Isolated nucleic acid molecules having polymorphisms in known human genes e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Example 6; Page 109; 714pp; English.

This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome p450 A1 (CYP450A1), cytochrome p450 A2 (CYP450A2), cytochrome p450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADRB1), aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNT), cathepsin S (CTSS), cyclooxygenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydrolase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), kallikrein 2) KLK2, nicotinamide-N-methyl transferase (NNMT), NADPH quinone oxidoreductase 2 (NQO2), sulfoltransferase thermolabile (STM), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B7 (UGT2B7), UDP-glucuronosyl transferase (UGT2B15), urokinase receptor (UPA), multidrug resistance 1 (MDR1), lactotransferrin (LTF), multidrug resistance associated protein 3 (MRP3), orphan nuclear receptor (NR1I2), or acetylcholine muscarinic receptor 1, 2, 3, 4, or 5 (CHMR1, CHMR2, CHMR3, CHMR4 or CHMR5) sequence. The polymorphisms in the human genes cited in the invention are useful as genetic linkage markers for locating and characterizing the genes that are responsible for specific traits within the genome and eventually identifying the genes responsible for a variety of disorder-related traits as a result of their e.g., overexpression, constitutive expression, mutation or underexpression, which may be used in diagnosing and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP450A1, CYP450A2, CYP4502E1, ARNT, EPHX2, GST12, NNMT, NQO2, NR1I2, STM, UGT2B4, UGT2B7, UGT2B15, AHR, MDR1 and/or MDR3 are useful for screening individuals for altered drug metabolism. The polymorphic sequences contained in CYP450A1, CYP450A2, AHR, MDR1 and/or MDR3 may also be used to screen individuals for susceptibility to cancer. Polymorphic sequences in ADRB1 or CHMR2 are used to screen for altered cardiovascular function, in COX2 for altered susceptibility to colorectal tumours, in DBI or CHMR1 for altered central nervous system function, in FLAP and HNMT for altered pulmonary immunological or haematological function, in KLK2 for altered serine protease activity in the prostate, in LTF for altered immunological or haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and peripheral nervous system function. The present sequence represents a PCR primer used to amplify the sequences of the invention

Sequence 21 BP; 3 A; 4 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 1.0%; Score 16.8; DB 1; Length 21;
Best Local Similarity 90.0%; Pred. No. 4.3e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1728 GAGTTTACAAAAA 1747

DB 20 GAGTTTGA 1

RESULT 815

ADD05293

ID ADD05293 standard; DNA; 21 BP.

XX

AC ADD05293;

XX

DT 01-JAN-2004 (first entry)

XX

DE Primer of the invention #6.

XX

KW female sex hormone; primer; ss.

XX

OS Synthetic.

XX

PN WO2003074704-A1.

XX

PD 12-SEP-2003.

XX

PF 28-FEB-2003; 2003WO-JP002311.

XX

PR 01-MAR-2002; 2002JP-00055669.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Katagiri M, Fujimoto S, Goda Y;

XX

DR WPI; 2003-731681/69.

XX

PT Novel proteins for binding, identifying and concentrating female sex hormones.

PT

PS Example 8; SEQ ID NO 31; 101pp; Japanese.

XX

CC The present invention relates to proteins that bind to female sex hormones. The method is useful for binding, identifying and concentrating female sex hormones. The present invention represents a primer of the invention.

XX

SQ Sequence 21 BP; 5 A; 2 C; 10 G; 4 T; 0 U; 0 Other;

Query Match

Best Local Similarity 1.0%; Score 16.8; DB 1; Length 21;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAGATTGT 1415

DB 2 GAGGAGACTGTGAGAGTGGT 21

RESULT 816

ADD05286/c

ID ADD05286 standard; DNA; 22 BP.

XX

AC ADD05286;

XX

DT 01-JAN-2004 (first entry)

XX

DE Primer of the invention #2.

XX

KW female sex hormone; primer; ss.

XX

OS Synthetic.

XX

PN WO2003074704-A1.

XX

PD 12-SEP-2003.

XX

PF 28-FEB-2003; 2003WO-JP002311.

XX

PR 01-MAR-2002; 2002JP-00055669.

XX

PA (TAKE) TAKEDA CHEM IND LTD.


```
XX Katagiri M, Fujimoto S, Goda Y;
PI WPI; 2003-731681/69.
DR Novel proteins for binding, identifying and concentrating female sex
XX hormones.
PT Example 3; SEQ ID NO 24; 101pp; Japanese.
XX
XX The present invention relates to proteins that bind to female sex
CC hormones. The method is useful for binding, identifying and concentrating
CC female sex hormones. The present invention represents a primer of the
CC invention.
XX
XX Sequence 22 BP; 4 A; 10 C; 3 G; 5 T; 0 U; 0 Other;
SQ
Query Match 1.0%; Score 16.8; DB 1; Length 22;
Best Local Similarity 90.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1396 GAGGAGACTGTGAGAAATTGT 1415
DB |||||||||||
20 GAGGAGACTGTGAGAGTGT 1
RESULT 817
AAAX18373/c
ID AAX18373 standard; DNA; 18 BP.
XX
AC AAX18373;
XX
XX 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 14.
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
XX
XX JPI1032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
XX PCR.
XX
XX Disclosure; Page 11; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates
XX to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
XX -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
XX a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
XX natural number indicating the repetition of alpha; beta, delta = V or N;
XX V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
XX thymine; gamma = thymine; k = natural number of 3 or over indicating the
XX repetition of gamma, in which thymine expressed by gamma is composed of
XX 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
XX useful as primers for RT-PCR and determination of base sequences. The new
XX sequences allow for reproductive and highly efficient analysis of gene
XX sequences
XX
XX Sequence 18 BP; 1 A; 0 C; 0 G; 17 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 90.0%; Pred. No. 4.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1732 TTACAAAAA 1749
DB |||||||
18 TAAAAA 1
RESULT 819
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
XX
AC ABK13935;
XX
XX 21-MAY-2002 (first entry)
XX
XX 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
```

```
XX Best Local Similarity 94.4%; Pred. No. 4.3e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1734 ACAAAAAA 1751
DB |||||||
18 ATAAAAA 1
RESULT 818
AAAX18372/c
ID AAX18372 standard; DNA; 18 BP.
XX
AC AAX18372;
XX
XX 11-MAY-1999 (first entry)
XX
XX RT-PCR primer of the invention SEQ ID 13.
XX
XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX Synthetic.
XX
XX JPI1032765-A.
XX
XX 09-FEB-1999.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
XX
XX (TAKI ) TAKARA SHUZO CO LTD.
XX
XX WPI; 1999-183822/16.
XX
XX Peptides having at least two new nucleotides - useful as primers in RT-
XX PCR.
XX
XX Disclosure; Page 11; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates
XX to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
XX -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
XX a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
XX natural number indicating the repetition of alpha; beta, delta = V or N;
XX V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
XX thymine; gamma = thymine; k = natural number of 3 or over indicating the
XX repetition of gamma, in which thymine expressed by gamma is composed of
XX 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
XX useful as primers for RT-PCR and determination of base sequences. The new
XX sequences allow for reproductive and highly efficient analysis of gene
XX sequences
XX
XX Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1732 TTACAAAAA 1749
DB |||||||
18 TAAAAA 1
RESULT 819
ABK13935/c
ID ABK13935 standard; DNA; 18 BP.
XX
AC ABK13935;
XX
XX 21-MAY-2002 (first entry)
XX
XX 5'-PCR primer used to produce single pattern characteristic by HaeII.
XX
```

KW Identification of transcribed gene; mRNA profile; gene expression;
KW cellular process; fingerprinting; susceptibility to external factor;
KW development; disease; PCR; primer; ss.
OS Synthetic.
XX
XX WO200208461-A2.
XX
XX 31-JAN-2002.
XX
XX 23-JUL-2001; 2001WO-IB001539.
XX
XX 21-JUL-2000; 2000GB-00018016.
XX
XX 21-JUL-2000; 2000US-0219925P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX Linnarsson S, Ernfors P, Bauren G;
PI
XX WPI; 2002-217065/27.
XX
XX Providing mRNA profile, by generating two independent patterns
PT Characteristic of sample mRNA population, analyzing patterns, comparing
PT gene expression by cell types under varied conditions, and identifying
PT genes.
XX
XX Disclosure; Fig 1; 67pp; English.
XX
XX The present invention relates to a method for providing a profile of mRNA
CC molecules present in a sample. The method comprises generating two
CC independent patterns characteristic of the population of mRNA molecules
CC expressed in the sample and analysing the patterns using a combinatorial
CC algorithm, comparing gene expression by different or same cell types
CC under different conditions, and identifying genes having a role in
CC various cellular processes. The method is useful for the analysis and
CC identification of transcribed genes, and fingerprinting. The method can
CC be used to identify genes which play a role in determining various
CC cellular processes, including susceptibility to external factors,
CC development, and disease. The present sequence for a PCR primer is used
CC in the production of a single pattern characteristic of a sample,
CC employing a Type II restriction enzyme (i.e. HaeII) in the methods of the
CC present invention
XX
XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1752
DB 18 CGAAAAA AAAAAAAAAA 1
RESULT 820
ACF36339/c
ID ACF36339 standard; DNA; 18 BP.
XX
XX ACF36339;
AC ACF36339;
DT
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA fragment.
XX
KW Gene variant identification; restriction enzyme; HaeII; ds.
XX
OS Synthetic.
XX
XX WO2003064689-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-IB000255.
PF

XX
PR 29-JAN-2002; 2002US-0352245P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX Lonnberg P, Oldin M, Linnarsson S, Ernfors P;
PI
XX WPI; 2003-627619/59.
XX
XX Determining polyadenylation sites within transcribed gene sequences
PT present in a sample comprises assigning to gene fragments gene candidates
PT within a database by comparing signals in the dataset with the database.
XX
XX Example; Fig 2; 81pp; English.
XX
XX The invention relates to determining the presence of and/or identifying a
CC polyadenylation site within a sequence of a transcribed gene or variants
CC present in a sample. The method involves assigning to gene fragments gene
CC candidates within a database by comparing signals in the dataset with the
CC database, the database comprising data representing mRNAs with known
CC polyA sites and/or 'virtual genes' representing a possible
CC polyadenylation site within an actual gene. The method is useful for
CC determining the presence of and/or identifying a polyadenylation site or
CC alternative polyadenylation sites within a sequence of a transcribed gene
CC or sequences of transcribed gene variants present or potentially present
CC in a sample, in identifying gene features, particularly in identifying
CC differences between sequence variants that occur in a population of
CC nucleic acid molecules, especially in identifying or discovering polyA
CC site usage or determining polyA site usage in a nucleic acid sample, and
CC gene variants arising from alternative polyA sites. The present sequence
CC represents a double stranded product DNA fragment
XX
XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16.4; DB 1; Length 18;
Best Local Similarity 94.4%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1752
DB 18 CGAAAAA AAAAAAAAAA 1
RESULT 821
ACF36364/c
ID ACF36364 standard; DNA; 18 BP.
XX
XX ACF36364;
AC ACF36364;
DT
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW electrophoresis; type II restriction enzyme; HaeII; ds.
XX
OS Synthetic.
XX
XX WO2003064691-A2.
XX
XX 07-AUG-2003.
XX
XX 28-JAN-2003; 2003WO-IB000843.
XX
XX 29-JAN-2002; 2002US-0352215P.
XX
XX (GLOB-) GLOBAL GENOMICS AB.
XX
XX Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
PI Montellius A;
XX
XX WPI; 2003-618365/58.
XX

PT Producing a population of double-stranded product DNA molecules, useful
 PT for mRNA profiling, comprises amplification by nested polymerase chain
 PT reaction.

XX Example; Fig 1; 105pp; English.

XX The invention relates to producing a population of double-stranded
 CC product DNA molecules comprising amplification by a nested PCR method.
 CC The method is useful in profiling mRNA transcribed in a system under
 CC investigation. The oligonucleotides are used as size standards in
 CC electrophoresis, and as internal controls allowing for calculation of a
 CC relative amounts of material present. The present sequence represents a
 CC double stranded product DNA, which aids in outlining an approach to
 CC production of a single pattern characteristic of a sample, employing a
 CC type II restriction enzyme (HaeII)

XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 18;
 Best Local Similarity 94.4%; Pred. No. 4.3e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAATAAAAAAAAAA 1752

Db 18 CAAAAAATAAAAAAAAAA 1

RESULT 822

ADE29811/c
 ID ADE29811 standard; RNA; 19 BP.

XX ADE29811;

XX 29-JAN-2004 (first entry)

XX Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:433.

XX short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytosstatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.

XX Synthetic.

XX WO2003072590-A1.

XX 04-SEP-2003.

XX 28-JAN-2003; 2003WO-US002510.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;

XX WPI; 2003-689980/65.

XX New short interfering nucleic acid, useful e.g. for treatment and
 PT diagnosis of cancer, downregulates expression of mitogen-activated
 PT protein kinase genes.

XX Example 3; SEQ ID NO 433; 164pp; English.

XX The present invention describes a short interfering nucleic acid (siNA)
 CC that downregulates expression of a mitogen-activated protein kinase
 CC (MAPK) genes by RNA interference. Also described: (1) a method for
 CC modulating expression of MAPK genes in cells, tissue explants or
 CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
 CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
 CC vectors that express siNA and cells containing these vectors. MAPK siNAs
 CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
 CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
 CC antiarthritic, antipsoriatic and gastrointestinal activities. The MAPK
 CC siNAs can be used to modulate the expression of MAPK genes in cells,
 CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
 CC and II; a wide range of tumours, and inflammatory diseases (asthma,
 CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
 CC disease). They can also be used for drug screening; diagnosis; target
 CC identification and validation; genetic engineering; pharmacogenomics;
 CC studying gene function and gene mapping (e.g. of single-nucleotide
 CC polymorphisms). The present sequence represents a MAPK siNA which is used
 CC in the exemplification of the present invention.

XX Sequence 19 BP; 1 A; 12 C; 4 G; 0 T; 2 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 19;

Best Local Similarity 94.4%; Pred. No. 4.4e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1119 CGCGTCGGAGGAGGGC 1136

Db 19 CGCGTCGGAGGAGGGC 2

RESULT 823

ADE29706

ID ADE29706 standard; RNA; 19 BP.

XX ADE29706;

XX 29-JAN-2004 (first entry)

XX Mitogen activated protein kinase siNA oligonucleotide SEQ ID NO:328.

XX short interfering nucleic acid; siNA; downregulation; inhibition;
 KW mitogen-activated protein kinase; MAP kinase; MAPK; RNA interference;
 KW cytosstatic; anorectic; antidiabetic; antiinflammatory; antiasthmatic;
 KW immunosuppressive; antibacterial; antirheumatic; antiarthritic;
 KW antipsoriatic; gastrointestinal; obesity; diabetes; tumour;
 KW inflammatory disease; asthma; septic shock; rheumatoid arthritis;
 KW psoriasis; inflammatory bowel disease; drug screening;
 KW genetic engineering; pharmacogenomic; gene mapping; ss.

XX Synthetic.

XX WO2003072590-A1.

XX 04-SEP-2003.

XX 28-JAN-2003; 2003WO-US002510.

XX 20-FEB-2002; 2002US-0358580P.

XX 11-MAR-2002; 2002US-0363124P.

XX 06-JUN-2002; 2002US-0386782P.

XX 29-AUG-2002; 2002US-0406784P.

XX 05-SEP-2002; 2002US-0408378P.

XX 09-SEP-2002; 2002US-0409293P.

XX 15-JAN-2003; 2003US-0440129P.

XX (SIRN-) SIRNA THERAPEUTICS INC.

XX Mcswiggen J, Beigelman L, Usman N, Haerberli P, Chowrira B;

XX WPI; 2003-689980/65.

PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer, downregulates expression of mitogen-activated
PS protein kinase genes.
XX Example 3; SEQ ID NO 328; 164pp; English.

CC The present invention describes a short interfering nucleic acid (siNA)
CC that downregulates expression of a mitogen-activated protein kinase
CC (MAPK) genes by RNA interference. Also described: (1) a method for
CC modulating expression of MAPK genes in cells, tissue explants or
CC organisms by introduction of siNA; (2) kits for in vitro or in vivo
CC delivery of siNA; (3) conjugates and/or complexes of siNA; and (4)
CC vectors that express siNA and cells containing these vectors. MAPK siNAs
CC have cytostatic, anorectic, antidiabetic, antiinflammatory,
CC antiasthmatic, immunosuppressive, antibacterial, antirheumatic,
CC antiarthritic, antiproliferative and gastrointestinal activities. The MAPK
CC siNAs can be used to modulate the expression of MAPK genes, in cells,
CC tissue explants or organisms, e.g. for treating obesity; diabetes types I
CC and II; a wide range of tumours, and inflammatory diseases (asthma,
CC septic shock, rheumatoid arthritis, psoriasis and inflammatory bowel
CC disease). They can also be used for drug screening; diagnosis; target
CC identification and validation; genetic engineering; pharmacogenomics;
CC studying gene function and gene mapping (e.g. of single-nucleotide
CC polymorphisms). The present sequence represents a MAPK siNA which is used
CC in the exemplification of the present invention.

XX
SQ Sequence 19 BP; 2 A; 4 C; 12 G; 0 T; 1 U; 0 Other;
Query Match 0.9%; Score 16.4; DB 1; Length 19;
Best Local Similarity 88.9%; Pred. No. 4.4e+02;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1119 CGCCGUGGGAGAGGGC 1136
DB 1 CGCCGUGGGAGAGGGC 18

RESULT 824
AAV12302
ID AAV12302 standard; DNA; 20 BP.
XX
AC AAV12302;
XX
DT 17-JUN-1998 (first entry)
XX
DE Ribonucleotide reductase R1 3'UTR fragment SEQ ID NO:46.
XX
KW Ribonucleotide reductase R1; 3'-untranslated region; 3'UTR; tumour;
KW housekeeping gene; identification; modulator; metastasis; neoplastic;
KW papilloma; atherosclerosis; angiogenesis; viral infection; ss.
XX
OS Homo sapiens.
XX
PN WO9800532-A2.
XX
PD 08-JAN-1998.
XX
PF 30-JUN-1997; 97WO-CA000454.
XX
PR 01-JUL-1996; 96US-0021152P.
XX
PA (WRIGHT) WRIGHT J A.
PA (YOUNG) YOUNG A H.
XX
PI Wright JA, Young AH;
PI
DR WPI; 1998-086958/08.
XX
PS New oligo-nucleotide(s) complementary to untranslated regions of
PT housekeeping genes - are useful in, e.g. identifying modulators of tumour
PT growth/metastasis and inhibiting growth of neoplastic cells.
XX
PS Claim 4; Page 29; 64pp; English.

XX
CC The present sequence represents a 3'-untranslated region (3'UTR) fragment
CC of ribonucleotide reductase R1. The present invention describes: (i)
CC oligonucleotides (ON) comprising at least 7 consecutive nucleotides (nt)
CC or their analogues of a 3'UTR of a housekeeping gene; (2) antisense ON
CC (AON) complementary to ON; (3) ribozymes (Rb) complementary or homologous
CC to ON, and able to cleave it; (4) DNA sequence encoding ON, AON and Rb;
CC (5) an antibody (Ab) that binds to ON, AON and Rb; (6) a nt probe ntP
CC that hybridise to ON, AON and Rb. ON, AON, Rb and Ab are used to modulate
CC (especially inhibit) growth of tumour cells (especially neoplastic cells)
CC and to reduce their capacity for metastasis. The above may also be used
CC to treat benign proliferative disorders e.g. papillomas, atherosclerosis,
CC angiogenesis and viral infections, e.g. human immunodeficiency virus,
CC hepatitis or herpes. ON may further be used: (i) to identify modulators
CC of tumour growth/metastasis; (ii) to identify compounds (especially
CC potential antitumour agents) that inhibit or enhance interaction between
CC ON and its binding substances; (iii) as probes for detecting related
CC sequences, and (iv) to generate Ab, used for detection and quantification
CC of UTR especially for monitoring progress of cancer therapy. SON inhibit
CC tumorigenicity of neoplastic cells, particularly where these are
CC resistant to hydroxyurea
XX
SQ Sequence 20 BP; 17 A; 1 C; 2 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 16.4; DB 1; Length 20;
Best Local Similarity 94.4%; Pred. No. 4.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753
DB 1 AAAAAAAAAAAAAAAAAA 18

RESULT 825
AAAX92839/c
ID AAAX92839 standard; DNA; 20 BP.
XX
AC AAAX92839;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydia pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.
XX
PS Page 1543; Disclosure; 1912pp; English.
XX
CC AAAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in

CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
 CC nodosum or pharyngitis. The polypeptides encoded by the open reading
 CC frames of the C. pneumoniae genome (see AAY34584-AAY35879) can be used
 CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
 CC nucleotide sequences can also be used as immunogenic compositions,
 CC especially where the vector directs the expression of a neutralising
 CC epitope of C. pneumoniae

XX Sequence 20 BP; 8 A; 3 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 137 TCTGGAGTCCCTTTC 154
 Db 18 TCTGGAGTCCCTTTC 1

RESULT 826

AAF99943
 ID AAF99943 standard; DNA; 20 BP.

AC AAF99943;

XX 12-JUL-2001 (first entry)

XX Synthetic oligonucleotide #9.

XX Oligonucleotide purification; liquid chromatography;

XX hydrophobic protective group; deprotection; ds.

XX Synthetic.

XX JP2000342265-A.

XX 12-DEC-2000.

XX 02-JUN-1999; 99JP-00154974.

XX 02-JUN-1999; 99JP-00154974.

XX (TOAG) TOA GOSHI CHEM IND LTD.

XX WPI; 2001-268251/28.

XX A process for purification of oligonucleotides using liquid
 PT chromatography.

XX Example 1; Page 4; 13pp; Japanese.

XX The present sequence is an oligonucleotide provided in a specification
 CC relating to the simplified purification of oligonucleotides by liquid
 CC chromatography. The process comprises: (a) pouring oligonucleotides
 CC protected with a hydrophobic group and oligonucleotide with no protective
 CC group into a liquid chromatography column packed with an acid and alkali
 CC resistant packing agent, such as polystyrene resin; (b) pouring a mixed
 CC developing solvent composed of a buffer made from a volatile salt and a
 CC water soluble organic solvent at a suitable concentration gradient into
 CC the column; (c) pouring an acid, particularly 6-16 v/v% acetic acid, into
 CC the column to deprotect the oligonucleotides protected with the
 CC hydrophobic group; (d) pouring a mixed developing solvent composed of a
 CC buffer made from a volatile salt, particularly 0.05-0.5 N aqueous
 CC ammonium hydrogencarbonate solution adjusted at pH 8-10, and a water
 CC soluble organic solvent at a suitable concentration gradient to elute the
 CC deprotected oligonucleotides; and (e) removal of the solvent and the salt
 CC from the eluted oligonucleotides

XX Sequence 20 BP; 17 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1753
 Db 2 AAAAAAAAAAGAAAAAAAAA 19

RESULT 827

ABA05916/C
 ID ABA05916 standard; DNA; 20 BP.

XX ABA05916;

XX 05-MAR-2002 (first entry)

XX Hepatitis B virus diagnostic PCR primer SEQ ID NO 6.

XX Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;

XX PCR primer; ss.

XX Hepatitis B virus.

XX EPI152063-A1.

XX 07-NOV-2001.

XX 03-MAY-2000; 2000EP-00109436.

XX 03-MAY-2000; 2000EP-00109436.

XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Schroeder KH, Koike K;

XX WPI; 2002-068256/10.

XX Diagnosing hepatitis B virus (HBV) infection stages and determining the
 PT risk for hepatocellular carcinoma, comprises identifying full length HBV
 PT transcripts and truncated HBV transcripts in a serum sample.

XX Example 1; Page 6; 25pp; English.

XX The invention relates to diagnosis of hepatitis B virus (HBV) infection
 CC stages comprising identification of full length HBV transcripts (I) and
 CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
 CC is indicative of a particular infection stage. The method is useful for
 CC diagnosing HBV infection stages and determining the risk for developing
 CC hepatocellular carcinoma. The present sequence is that of a HBV
 CC diagnostic PCR primer, useful for the invention

XX Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1733 TACAAAAAAAAAAAAAAAAA 1750
 Db 18 TTCAAAAAAAAAAAAAAAAAA 1

RESULT 828

ABZ88617
 ID ABZ88617 standard; DNA; 20 BP.

XX ABZ88617;

XX 17-OCT-2003 (first entry)

XX Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 3859; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiasthmatic, antiallergic, antialsthmatic, hypotensive,
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 13 A; 2 C; 0 G; 5 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1731 TTTTCAAAAAAAAAAAAAA 1748
 |||||
 DB 3 TTTTCAAAAAAAAAAAAAA 20
 RESULT 829
 AB291658
 ID AB291658 standard; DNA; 20 BP.
 XX
 AC AB291658;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.
 XX
 PS Disclosure; SEQ ID NO 6900; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention
 CC has antiinflammatory, antiallergic, antialsthmatic, hypotensive,
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 15 A; 1 C; 0 G; 4 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1731 TTTTCAAAAAAAAAAAAAA 1748
 |||||
 DB 3 TTTTCAAAAAAAAAAAAAA 20
 RESULT 830
 AB299187/c
 ID AB299187 standard; DNA; 20 BP.
 XX
 AC AB299187;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human PDE4C oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

antisease gene therapy; respiratory; lung; adenosine sensitivity;
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 Miller S, Tang L, Shahabuddin S;
 WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
 respiration, has oligo(s) antisense to specific gene(s) or its
 corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 ubiquinone.

Disclosure; SEQ ID NO 14429; 872bp; English.

The invention relates to a novel pharmaceutical composition, which has a
 first active agent comprising an oligonucleotide antisense to the
 initiation codon, coding region, 5' or 3' end genomic flanking regions,
 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 junctions of genes encoding a polypeptide associated with lung and/or
 nasal airway dysfunction and a second active agent comprising an
 antiinflammatory steroid and ubiquinone. A composition of the invention
 has antiinflammatory, antiasthmatic, antiallergic, hypotensive, or
 immunosuppressive, and cytostatic activity. The composition may have a
 use in antisense gene therapy. The composition is useful for treating or
 preventing a respiratory, lung or malignant disease or condition, also
 for enhancing the prophylactic or therapeutic respiratory effect of an
 antiinflammatory steroid in a subject, for reducing or depleting levels
 of, or reducing sensitivity to adenosine, reducing levels of adenosine
 receptor, producing bronchodilation, increasing levels of ubiquinone or
 lung surfactant in a subject's tissue, or treating bronchoconstriction,
 lung inflammation, lung allergies, or a respiratory disease or condition.
 Note: The sequence data for this patent is not represented in the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 1 A; 11 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 861 AGGAAGAGGAGGAGG 878
 |||||
 Db 18 AGGAAGAGGATGAGGAGG 1

RESULT 831
 AB287759/C
 ID AB287759 standard; DNA; 20 BP.

XX AC AB287759;
 XX
 DT 17-OCT-2003 (first entry)
 XX Human oligonucleotide sequence.
 XX
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;

antisease gene therapy; respiratory; lung; adenosine sensitivity;
 adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 lung inflammation; respiratory disease; ds.

Homo sapiens.

WO200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 Miller S, Tang L, Shahabuddin S;
 WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
 respiration, has oligo(s) antisense to specific gene(s) or its
 corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 ubiquinone.

Disclosure; SEQ ID NO 3001; 872bp; English.

The invention relates to a novel pharmaceutical composition, which has a
 first active agent comprising an oligonucleotide antisense to the
 initiation codon, coding region, 5' or 3' end genomic flanking regions,
 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 junctions of genes encoding a polypeptide associated with lung and/or
 nasal airway dysfunction and a second active agent comprising an
 antiinflammatory steroid and ubiquinone. A composition of the invention
 has antiinflammatory, antiallergic, antiasthmatic, hypotensive, or
 immunosuppressive, and cytostatic activity. The composition may have a
 use in antisense gene therapy. The composition is useful for treating or
 preventing a respiratory, lung or malignant disease or condition, also
 for enhancing the prophylactic or therapeutic respiratory effect of an
 antiinflammatory steroid in a subject, for reducing or depleting levels
 of, or reducing sensitivity to adenosine, reducing levels of adenosine
 receptor, producing bronchodilation, increasing levels of ubiquinone or
 lung surfactant in a subject's tissue, or treating bronchoconstriction,
 lung inflammation, lung allergies, or a respiratory disease or condition.
 Note: The sequence data for this patent is not represented in the printed
 specification, but was obtained in electronic format directly from WIPO
 at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 2 A; 3 C; 13 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 20;
 Best Local Similarity 94.4%; Pred. No. 4.6e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 168 GCCCACCCTGCTGCCCC 185
 |||||
 Db 19 GCCCACCCTGCTGCCCC 2

RESULT 832
 AAQ41813
 ID AAQ41813 standard; DNA; 21 BP.

XX AC AAQ41813;
 XX
 DT 25-MAR-2003 (revised)
 DT 03-SEP-1993 (first entry)
 XX Baculovirus C2 complex binding site #10.
 XX
 KW Myc; c-myc; mammalian; E box; cancer; therapy; C1; C2; complex;
 KW homo-oligomer; hetero-oligomer; myogenin; Max; oncoprotein; primer;

KW probe; electrophoretic mobility shift assay; EMSA; ss.

XX Synthetic.

XX Key Location/Qualifiers

PH protein_bind 12..17

FT /tag= a

FT /note= "C2 complex binding site"

XX W09308701-A1.

XX PD 13-MAY-1993.

XX PF 09-OCT-1992; 92WO-US008603.

XX PR 30-OCT-1991; 91US-00785567.

XX PA (GEHO) GEN HOSPITAL CORP.

XX PI Kingston RE, Papoulas O;

XX DR WPI; 1993-167291/20.

XX Prodn. of c-Myc protein from mammalian cells - and detection of c Myc

PT inhibitors for use in cancer therapy.

XX PS Disclosure; Fig 7a; 101pp; English.

CC The sequences given in AAQ41767-825 represent sequences which are bound
in an electrophoretic mobility shift assay (EMSA) by Myc. The isolated
sequences contain the central E box core of CACGTG which binds very
weakly with Myc homo-oligomers (C1 complex), but more tightly with Myc
hetero-oligomers (C2 complex). The C2 complex requires a 26-29 kD factor
in addition to Myc. The additional factor copurifies with Myc and
resembles Max protein. A second copurifying 40-50 kD factor has been
identified (forming C2' complex). Sites selected by the C2' complex
contain the core CAGTGTG which bears remarkable homology to a myogenin
binding site (see AAQ41763). Oligonucleotides containing the E box can be
used in the purification of Myc from a mammalian source. See also
CC AAQ41761-861. The isolated target sequences may be used in a method to
inhibit c-Myc oncoprotein activity. (Updated on 25-MAR-2003 to correct PN
field.)

XX Sequence 21 BP; 6 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 21;

Best Local Similarity 94.4%; Pred. No. 4.8e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1171 AAATGTGCCACGTGCTCC 1188

DB 4 AAATGTACCACGTGCTCC 21

RESULT 833

AAZ26142

ID AAZ26142 standard; DNA; 21 BP.

XX AC AAZ26142;

XX DT 30-NOV-1999 (first entry)

XX DE Human polymorphic region 331.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
cell viability; loss of heterozygosity; precancerous condition; ASI;
allele specific inhibitor; somatic cell; diagnosis; prevention;
atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
graft versus host disease; malignant cell removal; bone marrow; ss.

XX Homo sapiens.

XX

PN W09841648-A2.

XX PD 24-SEP-1998.

XX PF 19-MAR-1998; 98WO-US005419.

XX PR 20-MAR-1997; 97US-0041057P.

XX PA (VARI-) VARIAGENICS INC.

XX PI Housman D, Ledley PD, Stanton VP;

XX DR WPI; 1998-521232/44.

XX Identifying target genes for allele-specific drugs - used for diagnosis,
prevention and treatment of, e.g. cancers, atherosclerotic plaque,
PT dysplastic lesions, endometriosis or graft versus host disease.

XX PS Disclosure; Fig 7; 605pp; English.

XX This invention describes a novel method for identifying an inhibitor
potentially useful for treatment of cancer, where the inhibitor is active
on a gene vital for cell growth or viability, and where the gene is
subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is
used for preventing the development of cancer in a patient having a
precancerous condition, by administering to the patient a first allele
specific inhibitor (ASI) targeted to an allele of a first essential gene
present in cells of the precancerous condition, where the normal somatic
cells of the patient are heterozygous for the first gene, the inhibitor
is active on at least one but less than all allelic forms of the gene
present in a population and targets only one allelic form present in the
normal somatic cells, and the first gene. The products and methods can be
used in the diagnosis, prevention and treatment of LOH disorders, e.g.
cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
lesions, benign tumours, endometriosis, polycystic kidney disease, and
graft versus host disease. The method can also be used to remove
malignant cells from bone marrow transplants. AAZ25812-236825 represent
human polymorphic sites described in the method of the invention

XX Sequence 21 BP; 17 A; 3 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 21;

Best Local Similarity 94.4%; Pred. No. 4.8e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1753

DB 1 AAATAAAAAAAAAAAAAAAAAA 18

RESULT 834

AAZ26500

ID AAZ26500 standard; DNA; 21 BP.

XX AC AAZ26500;

XX DT 30-NOV-1999 (first entry)

XX DE Human polymorphic region 689.

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;
cell viability; loss of heterozygosity; precancerous condition; ASI;
allele specific inhibitor; somatic cell; diagnosis; prevention;
atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;
dysplastic lesion; benign tumour; polycystic kidney disease; transplant;
graft versus host disease; malignant cell removal; bone marrow; ss.

XX Homo sapiens.

XX PN W09841648-A2.

XX PD 24-SEP-1998.

XX

XX PS Disclosure; Page 5; 49pp; French.

CC The specification describes nucleic acid sequences from genes (or related regions) that encode proteins involved in controlling resistance or susceptibility to development of tumours (e.g. Marek disease tumours) in chickens. The nucleic acid sequences include sequences from gene of systems B or Rfp-Y of the poultry major histocompatibility complex (MHC), other than genes of class II B-L and genes 17.5, 12.3 or B-FIV of class I. The nucleic acid sequences are used to genotype poultry, particularly to select (for breeding) birds resistant to virus-induced tumours. PCR primers AAX60267-68 were used in the course of the invention

XX SQ Sequence 21 BP; 1 A; 8 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.4; DB 1; Length 21;
Best Local Similarity 94.4%; Pred. No. 4.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 231 CCGCGGCACCCCGGGGCC 248
DB 18 CCGCGGCATCCCGGGGCC 1

RESULT 837
AAX18389/c
ID AAX18389 standard; DNA; 18 BP.
XX AAX18389;
AC AAX18389;
XX
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 30.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX Synthetic.
XX JP11032765-A.
XX
XX PD 09-FEB-1999.
XX
XX PF 18-JUL-1997; 97JP-00208312.
XX
XX PR 18-JUL-1997; 97JP-00208312.
XX
XX PA (TAKI) TAKARA SHUZO CO LTD.
XX
XX DR WPI; 1999-183822/16.
XX
XX PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
XX PS Example 1; Page 12; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

XX SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.9%; Score 16.2; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 4.5e+02;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1735 CAAAAA 1751
DB 17 BAAAAA 1

RESULT 838
AAV48674
ID AAV48674 standard; DNA; 21 BP.
XX AAV48674;
AC AAV48674;
XX
DT 15-OCT-1998 (first entry)
XX
DE junB gene antisense oligonucleotide JunB-T-3.
XX
KW junB; junD; antisense oligonucleotide; modulate; gene expression; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX EP956579-A1.
XX
XX PD 05-AUG-1998.
XX
XX PF 31-JAN-1997; 97EP-00101531.
XX
XX PR 31-JAN-1997; 97EP-00101531.
XX
XX PA (BIOG-) BIOGNOSTIK GES BIOMOLEKULARE DIAGNOSTIK.
XX
XX PI Schlingensiepen K, Brysch W;
XX
XX DR WPI; 1998-400910/35.
XX
XX PT Preparation of antisense oligonucleotide(s) which lack long runs of consecutive guanosine or inosine - and have specific ratio of residues able to form two or three hydrogen bonds, have greater activity and reduced toxicity, used therapeutically or to modulate growth of cells in culture.
XX
XX PS Example 3; Fig 5c; 286pp; English.

CC AAV48564-708 represent antisense oligonucleotides directed against the junB and junD genes. Of these, only oligonucleotides AAV48565-614 resulted in effective downregulation of negative growth control by JunB or JunD, while AAV48615-708 had little effect. The oligonucleotides exemplify the invention. The specification describes oligonucleotides that contain 8-30 nucleotides, which contain at most 8 nucleotides that can each form three hydrogen bonds to cytosine; do not contain four consecutive nucleotides able to form three H-bonds each to four consecutive cytosines; do not contain two sequences of three consecutive nucleotides each able to form three H-bonds to three consecutive cytosines, and the ratio between residues able to form two H-bonds each (2R) or three such bonds (3R) is given by 2R/3R = 0.33-0.72. The oligonucleotides are used to modulate expression of genes, particularly the genes for p53, Erbb-2, junB, junD, TGF-beta 1 or beta 2 to control proliferation of primary cell cultures (e.g. bone marrow stem, liver or kidney cells, osteoclasts, osteoblasts and/or keratinocytes). The oligonucleotides can also be used to analyse function of proteins (by altering their expression or activity) and therapeutically, e.g. in cases of cancer or (targeting TGF) for stimulating the immune system

XX SQ Sequence 21 BP; 0 A; 5 C; 14 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16.2; DB 1; Length 21;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 348 TCGGGGGCGCGGTGGTGGG 368
DB 1 TCGGGGGCGTGGCGGGCGGG 21

XX The sequence is that of the 3' end of a sequence encoding a secreted
CC protein from a human fetal kidney clone AK296. Such a sequence is
CC predicted to have biological activities which would make them suitable
CC for treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, cytokine and cell
CC proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, haematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumour
CC invasion suppressor activity, and tumour inhibition activity. It is also
CC stated to be useful for gene therapy

XX SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAA 16

RESULT 842
AAC66068
ID AAC66068 standard; DNA; 16 BP.
XX
AC AAC66068;
XX
DT 22-FEB-2001 (first entry)
DE DNA chip primer #4.
XX
KW DNA chip; primer; nucleoside derivative; photolabile protecting group;
KW photolithographic nucleic acid chip; ss.
XX
OS Synthetic.
XX
PN WO200061594-A2.
XX
PD 19-OCT-2000.
PF 07-APR-2000; 2000WO-DE001148.
XX
PR 08-APR-1999; 99DE-01015867.
PR 28-JAN-2000; 2000DE-01003631.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Beier M, Hoheisel J;
XX
DR WPI; 2000-679457/66.
XX
PT New nucleoside derivatives with photolabile protecting groups, useful in
PT oligonucleotide synthesis, particularly on solid phases, e.g. for
PT hybridization testing.
XX
PS Disclosure; Fig 9; 48pp; German.
XX
CC This invention describes nucleoside derivatives (I) with photolabile
CC protecting groups. (I) are used to synthesize oligonucleotides using the
CC photolithographic nucleic acid chip method, particularly where these are
CC intended for performing enzymatic reactions initiated from a free 3'-
CC hydroxy (especially solid-phase polymerase reactions or ligase reactions,
CC but also reverse transcription, cDNA synthesis etc.), also for
CC hybridization testing, sequencing and in DNA computing. (I) are produced
CC with high selectivity by reaction with a mild acylating agent that has
CC high specificity for the 3'-position, without significant side-reactions
CC (cf. more reactive acylating agents such as chloroformates)

SQ Sequence 16 BP; 16 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 1 AAAAAAAAAAAAAA 16

RESULT 843
ABA04585/c
ID ABA04585 standard; DNA; 16 BP.
XX
AC ABA04585;
XX
DT 15-FEB-2002 (first entry)
DE Oligonucleotide #5.
XX
KW Analytical support; genomic sequencing; mutation detection;
KW pharmaceutical development; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = F1(CH2)6-PO-thymine, where F1 is flavine
FT and PO is a phosphate group"
XX
PN FR2805348-A1.
XX
PD 24-AUG-2001.
XX
PF 23-FEB-2000; 2000FR-00002236.
XX
PR 23-FEB-2000; 2000FR-00002236.
XX
PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX
PI Cuzin M, Peltie P, Fontecave M, Decout JL, Dueymes C;
XX
DR WPI; 2001-628265/73.
XX
PT Support for hybridization analysis of nucleic acids for sequencing
PT techniques, comprises an array of oligonucleotides having a label where
PT the fluorescence changes follow hybridization.
XX
PS Example 1; Page 12; 33pp; French.
XX
CC The present invention relates to an analytical support, to which a number
CC of oligonucleotides are fixed. The oligonucleotides are labelled with a
CC fluorescent compound, the fluorescence of which varies when the
CC oligonucleotide hybridises to its complement. The analytical support is
CC useful in hybridisation testing for identification of specific nucleic
CC acids, such as genomic sequencing, detecting mutations or pharmaceutical
CC development. The present oligonucleotide was used to illustrate the
CC invention

XX SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1

```

RESULT 844
AAF30895/C
ID AAF30895 standard; DNA; 16 BP.
XX
XX
AC AAF30895;
XX
XX 09-JUL-2001 (first entry)
DT
XX Oligonucleotide-minor groove binder complex.
XX
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1
FT /tag= a
FT /note= "thymine modified by a minor groove binder (2-
FT dimethylaminonaphthalene-6- sulfonamide"
XX
XX WO200131063-A1.
XX
XX 03-MAY-2001.
PD
XX 26-OCT-2000; 2000WO-US029786.
PF
XX 26-OCT-1999; 99US-00428236.
PR
XX (EPOC-) EPOCH BIOSCIENCES INC.
PA
XX Dempsy RO, Afonina IA, Vermeulen NMJ;
PI
XX WPI; 2001-328656/34.
DR
XX
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.
XX
XX Disclosure; Page 101; 105pp; English.
XX
XX The present sequence is that of an oligonucleotide (ODN)-minor groove
XX binder (MGB) complex. MGBs bind in a non-intercalating manner to the
XX minor groove of non-single-stranded DNA, RNA or their hybrids. ODN-MGB-LF
XX conjugates of the invention also comprise a latent fluorophore (LF),
XX which binds similarly to the MGB but in an intercalating manner, or lies
XX in the minor groove, or is oriented in some other way to the DNA molecule
XX by MGB, such that it becomes fluorescent (or its fluorescent properties
XX change detectably). The conjugates are used as hybridisation probes and
XX amplification primers for fluorescent detection of specifically
XX hybridising sequences, for analysis or diagnosis, especially (real-time)
XX PCR, for single-nucleotide mismatch discrimination, target or signal
XX amplification, array-based assays and sequencing, including detection of
XX double-stranded DNA by triplex formation
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1736 AAAAAAAAAAAAAA 1751
XX |
XX 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 845
XX AAF30880/C
XX
XX ID AAF30880 standard; DNA; 16 BP.
XX
XX AC AAF30880;
XX
XX 09-JUL-2001 (first entry)
DT

```

```

XX Oligonucleotide portion of ODN-MGB-LF conjugate.
DE
XX ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;
XX hybridisation; detection; fluorescence; probe; ss.
XX
XX Synthetic.
OS
XX WO200131063-A1.
XX
XX 03-MAY-2001.
PD
XX 26-OCT-2000; 2000WO-US029786.
PF
XX 26-OCT-1999; 99US-00428236.
PR
XX (EPOC-) EPOCH BIOSCIENCES INC.
PA
XX Dempsy RO, Afonina IA, Vermeulen NMJ;
PI
XX WPI; 2001-328656/34.
DR
XX
XX Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX mismatch discrimination.
XX
XX Disclosure; Page 58; 105pp; English.
XX
XX The present sequence is that of the oligonucleotide (ODN) component of an
XX ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
XX invention. MGBs bind in a non-intercalating manner to the minor groove of
XX non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
XX but in an intercalating manner, or lies in the minor groove, or is
XX oriented in some other way to the DNA molecule by MGB, such that it
XX becomes fluorescent (or its fluorescent properties change detectably).
XX The conjugates are used as hybridisation probes and amplification primers
XX for fluorescent detection of specifically hybridising sequences, for
XX analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
XX mismatch discrimination, target or signal amplification, array-based
XX assays and sequencing, including detection of double-stranded DNA by
XX triplex formation. Many different targets can be detected a single
XX reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
XX hybridisation-triggered fluorescence. Upon hybridisation to the
XX complementary target sequence there was an increase in fluorescence
XX yield, measured as the ratio of the fluorescence emitted by the hybrid
XX between the ODN-MGB-LF conjugate and its target sequence to the
XX fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
XX of 8.3
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1736 AAAAAAAAAAAAAA 1751
XX |
XX 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 846
XX AAF42481/C
XX
XX ID AAF42481 standard; DNA; 16 BP.
XX
XX AC AAF42481;
XX
XX 01-OCT-2001 (first entry)
DT
XX
XX Oligonucleotide used to produce branched chain compounds.
XX
XX Branched chain compound; nucleic acid synthesis; primer extension;
XX reverse transcription; nucleic acid hybridization;
XX nucleic acid amplification; ss.

```

```

OS Synthetic.
XX Key Location/Qualifiers
FH modified_base 1 /*tag= a
FT /note= "COOH attached"
FT 2. .3
FT /*tag= c
FT /note= "branch present"
FT modified_base 2 /*tag= b
FT /note= "COOH attached"
XX EP1111068-A1.
XX 27-JUN-2001.
XX 21-DEC-1999; 99EP-00125484.
XX 21-DEC-1999; 99EP-00125484.
XX (LION-) LION BIOSCIENCE AG.
XX (VBCG-) VBC GENOMICS GMBH.
XX Schmidt W, Hiller R, Huber M, Mueller M;
XX WPI; 2001-466959/51.
XX
XX Branched compounds useful in e.g. nucleic acid synthesis reaction
XX comprises nucleic acid moieties optionally extended by a polymerase.
XX Example 1; Page 10; 31pp; English.
XX
XX The specification describes branched compounds containing nucleic acid
XX moieties optionally extended by a polymerase. The branched chain
XX compounds of the invention are used in nucleic acid synthesis reaction,
XX primer extension reaction, reverse transcription reaction of RNA into
XX DNA, nucleic acid hybridization experiment (for identifying sequence of a
XX nucleic acid), and nucleic acid amplification experiment (for analysing
XX the expression pattern of genes). The compounds are also used in solid-
XX phase enzymatic reactions. The present sequence was used in the course of
XX the invention to produce branched chain compounds
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAA 1751
XX Db 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 847
XX ABA97402/c
XX ID ABA97402 standard; DNA; 16 BP.
XX AC ABA97402;
XX
XX 18-JUN-2002 (first entry)
XX
XX DE Nucleotide sequence of oligomer # 1 used to test thermal stability.
XX
XX Protein nucleic acid molecule; PNA; ds.
XX
XX Synthetic.
XX
XX WO200168673-A1.
XX
XX 20-SEP-2001.
XX

```

```

PF 13-MAR-2001; 2001WO-US008111.
XX
XX 14-MAR-2000; 2000US-0189190P.
XX 30-NOV-2000; 2000US-0250334P.
XX
XX (ACTI-) ACTIVE MOTIF.
XX
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
XX Chakhmakhechev O, Buryakova A, Choob M, Hondorp K;
XX WPI; 2002-041177/05.
XX
XX Oligonucleotides analogs useful in detection, separation and purification
XX of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
XX Example 17; Page 118; 197pp; English.
XX
XX This invention relates to oligonucleotide analogues comprising a protein
XX nucleic acid molecule (PNA) monomer. They are used in the detection and
XX separation of nucleic acid molecules and as probes, primers, linkers,
XX adapters and antisense agents on solid supports. Modifications enhance
XX their use as capture and detection probes e.g. by the incorporation of
XX biotin, digoxigenin, radioisotopes, fluorescent labels such as
XX fluorescein and reporter molecules such as alkaline phosphatase. They are
XX also used for enhancing or inhibiting the activity of an enzyme or
XX cellular activity. The compounds are stable to nucleases and proteases,
XX have high affinity, binding specificity and solubility. The polyamide
XX backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
XX nucleic acid molecules with greater affinity than DNA or RNA
XX concentration. The compounds are relatively simple to synthesize and are
XX used in a wide variety of applications. This sequence represents a DNA
XX oligomer which is used to represent the thermal stability of the
XX oligomers of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 16; DB 1; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 4.4e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAA 1751
XX Db 16 AAAAAAAAAAAAAA 1
XX
XX RESULT 848
XX AAD56451/c
XX ID AAD56451 standard; DNA; 16 BP.
XX AC AAD56451;
XX
XX 07-AUG-2003 (first entry)
XX
XX DE 2'P-ANA antisense oligo #6, to elicit RNase H degradation of target RNA.
XX
XX Acyclic linker; gene expression; gene therapy; ribonuclease; RNase H;
XX antisense; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1. .16
XX /*tag= a
XX /mod_base= OTHER
XX /note= "2'-deoxy-2'-fluoroarabinothymidine"
XX misc_feature 8. .9
XX /*tag= b
XX /note= "Bases 8 and 9 are linked by two secouridine
XX linkers which is represented as S in page 49 and X in
XX page 57 and Fig 7 and 8 of the specification"
XX
XX WO20003037909-A1.
XX

```

PD 08-MAY-2003.
 XX
 PF 29-OCT-2002; 2002WO-CA001628.
 XX
 PR 29-OCT-2001; 2001US-0330719P.
 XX
 PA (UYMC-) UNIV MCGILL.
 XX
 PI Danha MJ, Viazovkina E, Mangos MM, Parniak MA, Min K;
 XX
 DR WPI; 2003-421516/39.
 XX
 XX Novel acyclic linker-containing oligonucleotide useful for preventing or
 PT decreasing translation, reverse transcription and/or replication of a
 PT target RNA in a system, comprises a modified deoxyribonucleotide.
 XX
 XX Example 2; Fig 7; 104pp; English.
 PS
 XX The invention relates to an acyclic linker-containing oligonucleotide
 CC comprising at least one modified deoxyribonucleotide. Oligonucleotides of
 CC the invention are useful for preventing or decreasing translation,
 CC reverse transcription and/or replication of a target RNA in a system.
 CC They are useful for selectively preventing gene expression in a sequence-
 CC specific manner, for hybridising to complementary RNA such as cellular
 CC mRNA or viral RNA, to hybridise to and induce cleavage of complementary
 CC RNA. They are also useful therapeutically in formulations or medicaments
 CC to prevent or treat a disease characterised by the expression of a
 CC particular target RNA. The invention is used in gene therapy. The present
 CC sequence is an antisense oligo used to elicit human RNase (ribonuclease)
 CC H degradation of target RNA. This sequence is used in the exemplification
 CC of the invention
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1751
 Db 16 AAAAAAAAAAAAAAAAAA 1
 RESULT 849
 AAL54078/C
 ID AAL54078 standard; DNA; 16 BP.
 XX
 AC AAL54078;
 XX
 DT 06-MAR-2003 (first entry)
 XX
 DE Oligo-homodeoxyribonucleotide sequence, oligo dT.
 XX
 KW Detection; single-stranded sensor; detectable fluorescence emission;
 KW forensic testing; paternity testing; tissue typing; hereditary disorder;
 KW human population genetics; human evolutionary history; cystic fibrosis;
 KW human haplotype diversity; Tay-Sachs; sickle-cell anaemia; ss.
 XX
 OS Unidentified.
 XX
 XX WO200284271-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 16-APR-2002; 2002WO-US012176.
 PF
 XX 16-APR-2001; 2001US-00836579.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA (CHAJ/) CHA J N.
 XX
 PI Cha JN, Morse DE, Stucky GD;
 XX

DR WPI; 2003-103378/09.
 XX
 PT Detecting polynucleotides, for pharmacogenetic testing, comprises
 PT contacting a target polynucleotide with a complementary single-stranded
 PT sensor polynucleotide and an agent that allows the sensor to fluoresce
 PT upon excitation.
 XX
 XX Example 1; Page 25; 41pp; English.
 PS
 XX The invention relates to a novel assay for detecting a polynucleotide in
 CC a sample, which comprises: contacting a sample suspected of containing a
 CC target polynucleotide with a predetermined single-stranded sensor
 CC polynucleotide complementary to the target polynucleotide, in a solution
 CC comprising an agent that is a nonaqueous solvent that allows the sensor
 CC polynucleotide to produce a detectable fluorescence emission; exciting
 CC the sensor polynucleotide; and determining fluorescence emission. The
 CC assay is useful for detecting a single or double-stranded target
 CC polynucleotide, such as, DNA or RNA in a sample. The assay finds use in a
 CC wide variety of different applications including pharmacogenetic testing,
 CC forensic testing to identify the species or individual which was the
 CC source of a forensic specimen, in anthropological setting, paternity
 CC testing, testing for compatibility between prospective tissue or blood
 CC donors and patients and in screening for hereditary disorders. The method
 CC is also useful to study alterations of gene expression in response to a
 CC stimulus, disease, drug or medication, and other applications include
 CC human population genetics, analyses of human evolutionary history and
 CC characterisation of human haplotype diversity. The method is useful for
 CC detecting polynucleotide sequences from contaminants or pathogens
 CC including bacteria, yeast, and viruses to detect single nucleotide
 CC polymorphisms, which may be associated with particular alleles or subsets
 CC of alleles. The method is useful for detection of mutations and to detect
 CC nucleotide sequences associated with increased risk of diseases or
 CC disorders including cystic fibrosis, Tay-Sachs, and sickle-cell anaemia.
 CC This polynucleotide sequence represents an oligonucleotide sequence used
 CC in a fluorescence technique of the invention
 XX
 SQ Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.4e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1751
 Db 16 AAAAAAAAAAAAAAAAAA 1
 RESULT 850
 ADB68519/C
 ID ADB68519 standard; DNA; 16 BP.
 XX
 AC ADB68519;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE DNA hybridisation oligomer SEQ ID 9.
 XX
 KW hydroxyproline nucleic acid; HyPNA; PNA; peptide nucleic acid;
 KW gene expression; respiration; secretion; signalling;
 KW ion-channel activity; cell motility; developmental phenotype;
 KW tumour regression; hybridisation; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT misc_difference 1
 FT /*tag= a
 FT /note= "Optional N-terminal acetyl"
 XX
 XX WO2003068798-A2.
 XX
 XX 21-AUG-2003.
 XX

```
PF 07-FEB-2003; 2003WO-US003904.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PR 09-FEB-2002; 2002US-00072975.
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efinov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX
XX WPI; 2003-689653/65.
DR
XX
XX Method of inhibiting expression of genes or RNA transcripts, useful for
PT therapy and determining effects of genes, by administering oligomers
PT containing hydroxyproline nucleic acid.
XX
XX Example 17; Page 233; 240pp; English.
PS
XX
XX The invention relates to a novel method of inhibiting the expression of
CC one or more genes or RNA transcripts by administering at least one
CC oligonucleotide analogue that includes at least one hydroxyproline
CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. Thr
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the DNA hybridisation oligomer SEQ ID 9 of the invention. This
CC sequence may also comprise a peptide nucleic acid (PNA).
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1751
DB 16 AAAAAAAAAAAAAA 1
RESULT 851
AAAG9800/c
ID AAG9800 standard; RNA; 17 BP.
XX
XX
XX AAG9800;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1095.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
PF
XX
XX 26-OCT-1995; 95US-0005974P.
PR
XX
XX 11-JAN-1996; 96US-00584040.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX (CHIR ) CHIRON CORP.
PA
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI
XX
XX WPI; 1997-259017/23.
DR
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
PS
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
SQ
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1751
DB 17 AAAAAAAAAAAAAA 2
RESULT 852
AAAG9801/c
ID AAG9801 standard; RNA; 17 BP.
XX
XX
XX AAG9801;
XX
XX 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1096.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9715662-A2.
PN
XX
XX 01-MAY-1997.
PD
XX
XX 25-OCT-1996; 96WO-US017480.
PF
XX
XX 26-OCT-1995; 95US-0005974P.
PR
XX
XX 11-JAN-1996; 96US-00584040.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX (CHIR ) CHIRON CORP.
PA
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
PI
XX
XX WPI; 1997-259017/23.
DR
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
PS
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
```


CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX7275 to AAX7572 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1751
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 853
 AAA30181/c
 ID AAA30181 standard; DNA; 17 BP.
 XX
 AC AAA30181;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE PCR primer GRI5G used in pollenosis associated gene identification.
 XX
 KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
 KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200020575-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-JP005506.
 XX
 PR 06-OCT-1998; 98JP-00284610.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Lu N, Ogawa K;
 XX
 DR WPI; 2000-317712/27.
 XX
 PT Gene highly expressed in patients with high cedar pollen-specific IGE
 PT levels, useful for diagnosing pollenosis, and screening candidate
 PT compounds for pollenosis treatment.
 XX
 PS Example 6; Page 38; 44pp; Japanese.
 CC
 CC This sequence represents a PCR primer used in the identification of a
 CC human pollenosis associated gene. The gene is highly expressed in
 CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
 CC invention relates to the nucleotide sequence encoding the pollenosis
 CC associated protein, diagnosing pollenosis and screening candidate
 CC compounds for treating pollenosis. The gene can be used in diagnosing
 CC pollenosis, particularly cedar pollenosis, and screening candidate
 CC compounds for pollenosis treatment
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAA 1750
 DB 17 CAAAAAAAAAAAAA 2

CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX7275 to AAX7572 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 0 G; 0 T; 16 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1751
 DB 16 AAAAAAAAAAAAAA 1
 RESULT 853
 AAA30181/c
 ID AAA30181 standard; DNA; 17 BP.
 XX
 AC AAA30181;
 XX
 DT 16-AUG-2000 (first entry)
 XX
 DE PCR primer GRI5G used in pollenosis associated gene identification.
 XX
 KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
 KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200020575-A1.
 XX
 PD 13-APR-2000.
 XX
 PF 06-OCT-1999; 99WO-JP005506.
 XX
 PR 06-OCT-1998; 98JP-00284610.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Lu N, Ogawa K;
 XX
 DR WPI; 2000-317712/27.
 XX
 PT Gene highly expressed in patients with high cedar pollen-specific IGE
 PT levels, useful for diagnosing pollenosis, and screening candidate
 PT compounds for pollenosis treatment.
 XX
 PS Example 6; Page 38; 44pp; Japanese.
 CC
 CC This sequence represents a PCR primer used in the identification of a
 CC human pollenosis associated gene. The gene is highly expressed in
 CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
 CC invention relates to the nucleotide sequence encoding the pollenosis
 CC associated protein, diagnosing pollenosis and screening candidate
 CC compounds for treating pollenosis. The gene can be used in diagnosing
 CC pollenosis, particularly cedar pollenosis, and screening candidate
 CC compounds for pollenosis treatment
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAA 1750
 DB 17 CAAAAAAAAAAAAA 2

RESULT 854
 AAZ35714/c
 ID AAZ35714 standard; DNA; 17 BP.
 XX
 AC AAZ35714;
 XX
 DT 31-JAN-2000 (first entry)
 XX
 DE Murine gene anchor PCR primer SEQ ID NO:3.
 XX
 KW Rare expressed gene; analysis; expression; nucleic acid sample;
 KW PCR primer; ss.
 XX
 OS Synthetic.
 OS Mus sp.
 XX
 PN EP959141-A2.
 XX
 PD 24-NOV-1999.
 XX
 PF 18-MAY-1999; 99EP-00109795.
 XX
 PR 20-MAY-1998; 98JP-00153651.
 XX
 PA (HITA) HITACHI LTD.
 XX
 PI Muramatsu T, Fujita T, Kiyama M, Irie T, Okano K;
 XX
 DR WPI; 2000-001284/01.
 XX
 PT Preparation of nucleic acid sample, useful for analysis of rare expressed
 PT genes.
 XX
 PS Disclosure; Page 11; 22pp; English.
 XX
 CC The present invention describes a process for the preparation of a
 CC nucleic acid sample comprising: (a) providing a nucleic acid sample
 CC having a plurality of species of sequences, and providing one or a
 CC plurality of kinds of probes having a known sequence substantially
 CC complementary to a portion of sequence of the nucleic acid sample; (b)
 CC mixing and hybridizing the nucleic acid sample with probes; (c)
 CC subsequently recovering nucleic acid molecules; or (i) providing a
 CC nucleic acid sample having a plurality of species of sequences, and
 CC providing one or a plurality of kinds of probes having a known sequence
 CC substantially complementary to a portion of sequence of the nucleic acid
 CC sample; (iii) mixing and hybridizing the nucleic acid sample with the
 CC probes; (iii) treating the product of (ii) with nuclease activity of an
 CC enzyme or the probe itself; and (iv) subsequently recovering the nucleic
 CC acid molecules not digested by the nuclease activity in (iii); or (i)
 CC providing a nucleic acid sample having a plurality of species of
 CC sequences and oligonucleotides primer having predetermined sequences for
 CC synthesizing DNA strands; (ii) providing one or a plurality of kinds of
 CC probes having a known sequence substantially complementary to a portion
 CC of a sequence of the nucleic acid sample having such a structure to
 CC prevent a polymerase reaction from its 3' end and a nuclease reaction
 CC from its 5' end; (iii) mixing and hybridizing the nucleic acid sample
 CC with the primers and probes; (iv) executing polymerase chain reaction for
 CC the samples prepared in (iii); and (v) subsequently recovering nucleic
 CC acid molecules synthesized in (iv). The method is useful for the
 CC preparation of a nucleic acid sample for the analysis of rare expressed
 CC genes. The present sequence represents a PCR primer used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAA 1750
 DB 17 CAAAAAAAAAAAAA 2

```
Db      17 CAAAAAAAAAAAAA 2
RESULT 855
AAZ82721/c
ID      AAZ82721 standard; DNA; 17 BP.
XX
AC      AAX82721;
XX
DT      10-NOV-2000 (first entry)
XX
DE      Human IgA nephropathy-associated cDNA primer #62.
XX
KW      IgA nephropathy-associated protein; diagnosis; treatment; antisense;
KW      human; primer; ss.
XX
OS      Homo sapiens.
XX
FN      WO9963085-A1.
XX
PD      09-DEC-1999.
XX
PF      28-MAY-1999; 99WO-JP002855.
XX
PR      02-JUN-1998; 98JP-00152603.
XX
PA      (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI      Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
PI      Sawada S, Takei M, Shibata K, Furuya A;
XX
DR      WPI; 2000-097328/08.
XX
PT      DNA sequences preferentially expressed in IgA nephropathy patients,
PT      proteins encoded by them, and antibodies to those proteins.
XX
PS      Claim 3; Page 170; 180pp; Japanese.
XX
CC      This invention describes novel DNA sequences preferentially expressed in
CC      IgA nephropathy patients, and DNA sequences stringently hybridizing to
CC      them. Independent claims cover diagnostic reagents for IgA nephropathy
CC      incorporating the antisense sequences; the treatment of IgA nephropathy
CC      using the antisense sequences for mRNA inhibition; proteins associated
CC      with IgA nephropathy, containing sequences encoded by the DNA sequences;
CC      antibodies recognizing these proteins; the production of the proteins by
CC      culture of host cells transformed with DNA encoding them; diagnostic
CC      reagents for IgA nephropathy containing the antibodies; and compositions
CC      for the treatment of IgA nephropathy which contain the antibodies. The
CC      products of the invention can be used for the diagnosis and treatment of
CC      IgA nephropathy. This sequence represents a primer used in the isolation
CC      and identification of the human IgA nephropathy-associated proteins
CC      described in the method of the invention
XX
SQ      Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAA 1750
      |||
Db      17 CAAAAAAAAAAAAA 2

RESULT 856
AAZ36740/c
ID      AAZ36740 standard; DNA; 17 BP.
XX
AC      AAZ36740;
XX
DT      13-MAR-2000 (first entry)
XX
DE      Anchored oligo(dT) primer GT15G used for modified differential display.
```

```
XX
KW      Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW      differentially expressed nucleic acid; disease state; cancer;
KW      autoimmune disease; infectious disease; aging; developmental disorder;
KW      proliferative disorder; neurological disorder; toxicity; primer;
KW      treatment resistance; differential expression; drug discovery;
KW      growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
OS      Synthetic.
XX
FN      WO9955913-A2.
XX
PD      04-NOV-1999.
XX
PF      27-APR-1999; 99WO-US009119.
XX
PR      27-APR-1998; 98US-0083331P.
PR      27-AUG-1998; 98US-0098070P.
PR      04-FEB-1999; 99US-0118624P.
XX
PA      (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI      McClelland M, Welsh J, Trenkle T;
XX
DR      WPI; 2000-086388/07.
XX
PT      Measuring expression of low abundance reduced complexity target nucleic
PT      acid molecules.
XX
PS      Example 3; Page 91; 187pp; English.
XX
CC      AAZ36739-41 represent oligo(dT) primers used for modified differential
CC      display, in the method of the invention. The specification describes a
CC      method for measuring the level of two or more nucleic acid molecules in a
CC      target. The method comprises contacting a probe with an arbitrarily or
CC      statistically sampled target and detecting the amount of specific binding
CC      of the target to the probe. The methods can be used to identify
CC      differentially expressed nucleic acid molecules associated with disease
CC      states, such as cancer, autoimmune disease, infectious disease, aging,
CC      developmental disorder, proliferative disorder or neurological disorder.
CC      Alternatively the methods can be used to assess the efficacy or toxicity
CC      of or a resistance to a treatment. Also the methods can be used to
CC      determine differential expression of nucleic acid molecules in response
CC      to a stimulus, e.g. a chemical, drug or growth factor (especially
CC      epidermal growth factor), radiation, stress or a pathogen. The methods
CC      can also be used to determine co-regulated genes that can be potential
CC      targets for drug discovery
XX
SQ      Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1735 CAAAAAAAAAAAAA 1750
      |||
Db      17 CAAAAAAAAAAAAA 2

RESULT 857
AAZ25449/c
ID      AAZ25449 standard; DNA; 17 BP.
XX
AC      AAZ25449;
XX
DT      19-JUL-2000 (first entry)
XX
DE      Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1947.
XX
KW      Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW      hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW      gene expression modification; cancer; phosphorothioate; endonuclease;
KW      anticancer; breast cancer; endometrium cancer; ss.
```

```

XX OS Homo sapiens.
XX PN WO9954459-A2.
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-US008547.
XX PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX PI Matulic-Adamic J;
XX DR WPI; 2000-013248/01.
XX PT New nucleic acids that interact, and optionally cleave, target sequences,
XX PT used to treat cancer.
XX PS Claim 77; Page 79; 148pp; English.
XX CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium), or
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications and/or activity. AAA23503 to
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24748 to AAA25992 represent their corresponding target sequences, and
CC AAA25993 to AAA26105 represent their corresponding target sequences.
CC AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX SQ Sequence 17 BP; 0 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1751
DB 17 AAAAAAAAAAAAAA 2
RESULT 858
AAA25454/c
ID AAA25454 standard; DNA; 17 BP.
XX AC AAA25454;
XX DT 19-JUL-2000 (first entry)
XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1952.
XX KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
XX KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX KW gene expression modification; cancer; phosphorothioate; endonuclease;
XX KW anticancer; breast cancer; endometrium cancer; ss.
XX OS Homo sapiens.

```

```

XX WO9954459-A2.
XX PD 28-OCT-1999.
XX PF 19-APR-1999; 99WO-US008547.
XX PR 20-APR-1998; 98US-0082404P.
XX PR 23-JUN-1998; 98US-00103636.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
XX PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX PI Matulic-Adamic J;
XX DR WPI; 2000-013248/01.
XX PT New nucleic acids that interact, and optionally cleave, target sequences,
XX PT used to treat cancer.
XX PS Claim 77; Page 79; 148pp; English.
XX CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(di)thioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium), or
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications and/or activity. AAA23503 to
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24748 to AAA25992 represent their corresponding target sequences, and
CC AAA25993 to AAA26105 represent their corresponding target sequences.
CC AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1748
DB 16 TACAAAAA 1
RESULT 859
AAC64204/c
ID AAC64204 standard; DNA; 17 BP.
XX AC AAC64204;
XX DT 21-FEB-2001 (first entry)
XX DE PCR anchor primer, SEQ ID NO:5, used in human gene 373 isolation.
XX KW Human; polliosis-associated gene 373; IgE; immunoglobulin E;
XX KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX KW drug screening; allergic disease; PCR primer; ss.
XX OS Synthetic.
XX PN WO200065046-A1.
XX XX

```

PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JF002730.
PR
XX 27-APR-1999; 99JP-00120489.
PI (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX WPI; 2000-687339/67.
XX
PT Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 70; 80pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis gene 373; expression constructs and
CC host cells comprising pollinosis-associated gene 373 nucleic acids;
CC pollinosis-associated gene 373 primers and probes; antibodies against the
CC protein encoded by the gene; methods of detection of pollinosis-
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC diseases via the detection of pollinosis-associated gene 373 nucleic
CC acids. The invention additionally encompasses methods of screening drug
CC candidates for the treatment of allergic disease by measuring the
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC T-cells in the presence of a test compound relative to a control.
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC diseases and in the screening of drug candidates for the treatment of
CC such diseases. The present sequence represents a PCR primer used in the
CC isolation of human pollinosis-associated gene 373 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1750
DB 17 CAAAAA AAAAAAAAAA 2

RESULT 860
AAC64183/c
ID AAC64183 standard; DNA; 17 BP.
XX
XX AAC64183;
AC
XX
XX 21-FEB-2001 (first entry)
DT
DE PCR anchor primer, SEQ ID NO:4, used in human gene 419 isolation.
XX
XX Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IgE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200065045-A1.
PN
XX 02-NOV-2000.
PD
XX 26-APR-2000; 2000WO-JF002729.
PF
XX

PR 27-APR-1999; 99JP-00120490.
XX (GENO-) GENOX RES INC.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
XX WPI; 2000-687338/67.
XX
PT Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Example 6; Page 50; 77pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression also
CC constructs and host cells comprising pollinosis-associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1750
DB 17 CAAAAA AAAAAAAAAA 2

RESULT 861
AAC64173/c
ID AAC64173 standard; DNA; 17 BP.
XX
XX AAC64173;
AC
XX
XX 21-FEB-2001 (first entry)
DT
DE PCR anchor primer, SEQ ID NO:4, used in human gene 513 isolation.
XX
XX Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO200065049-A1.
PN
XX 02-NOV-2000.
PD
XX 26-APR-2000; 2000WO-JP002733.
PF
XX 27-APR-1999; 99JP-00120491.
PR
XX (GENO-) GENOX RES INC.
XX

Example 6; Page 40; 69pp; Japanese.

CC The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA

XX

SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAAAAAA 1750
|||
Db 17 CAAAAAAAAAAAAAAAAA 2

RESULT	863	
AAC64215/c		
ID	AAC64215	standard; DNA; 17 BP.
XX		
XX	AAC64215;	
XX		
XX	21-FEB-2001	(first entry)
XX		
DE	PCR anchor primer,	SEQ ID NO:4, used in human gene 627 isolation.
XX		
XX	Human;	pollinosis-associated gene 627; IgE; immunoglobulin E;
KW	cedar pollen allergy;	T-cell; reduced expression; detection; diagnosis;
KW	drug screening;	allergic disease; PCR primer; ss.
XX		
XX	Synthetic.	
XX		
PN	WO200065051-A1.	
XX		
PD	02-NOV-2000.	
XX		
PF	26-APR-2000;	2000WO-JP002735.
XX		
PR	27-APR-1999;	99JP-00120493.
XX		
PA	(GENO-)	GENOX RES INC.
XX		
PI	Nagasu T, Sugita Y,	Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI	Obayashi I, Imai Y,	Ogawa K, Matsui K;
XX		
DR	WPI:	2000-687344/67.

XX Pollinosis-associated gene 627 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX;
PS Example 6; Page 42; Sipp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 627 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene

CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC diagnosis of pollinosis-associated gene 627 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 627 nucleic acids; and a method of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 627
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 627 cDNA

XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1750
|||||
Db 17 CAAAAA AAAAAAAAAA 2

RESULT 864
AAC64232/c
ID AAC64232 standard; DNA; 17 BP.
XX
AC AAC64232;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:4, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.

XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;

XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.

XX
PS Page 46; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection

CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA

XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAAAAAA 1750
|||||
Db 17 CAAAAA AAAAAAAAAA 2

RESULT 865
AAC92294/c
ID AAC92294 standard; DNA; 17 BP.
XX
AC AAC92294;
XX
DT 22-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:4.
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.

XX
OS Homo sapiens.
XX
PN WO200073439-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003191.
XX
PR 27-MAY-1999; 99JP-00148784.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;

XX
DR WPI; 2001-061528/07.
XX
PT Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.

XX
PS Example 6; Page 44; 61pp; Japanese.
XX
CC The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention

XX
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1750
 | | | | | | | | | | | | | | | | | | | |
 Db 17 CAAAAA AAAAAAAAAA 2

RESULT 866
 AAC82876/c
 ID AAC91721 standard; DNA; 17 BP.
 XX
 AC AAC82876;
 XX
 DT 20-MAR-2001 (first entry)
 XX
 DE Human pollinosis-associated gene 441 primer #3.
 XX
 KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
 KW pollen scattering; antigen; primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073435-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003190.
 XX
 PR 27-MAY-1999; 99JP-00148783.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 DR WPI; 2001-061526/07.
 XX
 PT Pollinosis-associated gene 441 which undergoes lower expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 36; 42pp; Japanese.
 XX

CC This invention describes a novel nucleic acid molecule comprising a
 CC sequence (I) which undergoes significantly low expression in subjects
 CC after pollen scattering, and is useful in diagnosis of allergic diseases
 CC and screening candidate compounds for remedies capable of regulating the
 CC response of T cells to the stimulus by an antigen
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1750
 | | | | | | | | | | | | | | | | | | | |
 Db 17 CAAAAA AAAAAAAAAA 2

RESULT 868
 AAH47128/c
 ID AAH47128 standard; DNA; 17 BP.
 XX
 AC AAH47128;
 XX
 DT 30-NOV-2001 (first entry)
 XX
 DE Nucleotide sequence of primer GT15G.
 XX
 KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
 KW PCR primer; ss.
 XX

Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAAAAAA 1750
 | | | | | | | | | | | | | | | | | | | |
 Db 17 CAAAAA AAAAAAAAAA 2

RESULT 866
 AAC91721/c
 ID AAC91721 standard; DNA; 17 BP.
 XX
 AC AAC91721;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 787 isolation.
 XX
 KW Human; pollinosis-associated gene 787; pollen allergy; T-cell;
 KW reduced expression; detection; diagnosis; drug screening;
 KW allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200073440-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 18-MAY-2000; 2000WO-JP003192.
 XX
 PR 27-MAY-1999; 99JP-00148785.
 XX
 PA (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E,
 PI Yokoi A;
 XX
 DR WPI; 2001-032159/04.
 XX

CC The invention relates to the human pollinosis-associated gene 787 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC after the pollen-scattering season, relative to expression levels in T-
 CC cells before the pollen-scattering season. The gene was isolated from T-
 CC cells from individuals allergic to pollen using the differential display
 CC method. The invention also relates to pollinosis-associated gene 787
 CC primers and probes; methods of detection of pollinosis-associated gene
 CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
 CC detection of pollinosis-associated gene 787 nucleic acids. The invention
 CC additionally encompasses a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 787
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 787 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OS Homo sapiens.
 PN WO200165259-A1.
 PD 07-SEP-2001.
 XX 23-FEB-2001; 2001WO-JP001372.
 XX 02-MAR-2000; 2000JP-00061832.
 PR (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
 PI WPI; 2001-557789/62.
 DR Diagnosis of allergies including atopic dermatitis.
 PT Example 6; Page 66; 83pp; Japanese.
 XX The invention provides a method of diagnosis of allergies that involves:
 CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
 CC in i-cells; and comparing them with the level of expression in healthy i-
 CC cells. The method is useful for diagnosing allergies, particularly atopic
 CC dermatitis. The present sequence represents a PCR primer used for
 CC analysis of the expression of the above genes
 XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 SQ

Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAA 1750
 |||||
 DB 17 CAAAAA AAAAAAAAAA 2

RESULT 869
 ABK13941/c
 ID ABK13941 standard; DNA; 17 BP.
 XX AC ABK13941;
 XX 21-MAY-2002 (first entry)
 DE 5'-PCR primer used to produce single pattern characteristic by FokI.
 XX Identification of transcribed gene; mRNA profile; gene expression;
 KW cellular process; fingerprinting; susceptibility to external factor;
 KW development; disease; PCR; primer; ss.
 XX Synthetic.
 OS WO200208461-A2.
 PN 31-JAN-2002.
 PD 23-JUL-2001; 2001WO-IB001539.
 XX 21-JUL-2000; 2000GB-00018016.
 PR 21-JUL-2000; 2000US-0213925P.
 XX (GLOB-) GLOBAL GENOMICS AB.
 PA Linnarsson S, Ernfors P, Bauren G;
 PI WPI; 2002-217065/27.
 DR Providing mRNA profile, by generating two independent patterns
 PT characteristic of sample mRNA population, analyzing patterns, comparing
 FT gene expression by cell types under varied conditions, and identifying

PT genes.
 XX Disclosure; Fig 2; 67pp; English.
 PS The present invention relates to a method for providing a profile of mRNA
 CC molecules present in a sample. The method comprises generating two
 CC independent patterns characteristic of the population of mRNA molecules
 CC expressed in the sample and analysing the patterns using a combinatorial
 CC algorithm, comparing gene expression by different or same cell types
 CC under different conditions, and identifying genes having a role in
 CC various cellular processes. The method is useful for the analysis and
 CC identification of transcribed genes, and fingerprinting. The method can
 CC be used to identify genes which play a role in determining various
 CC cellular processes, including susceptibility to external factors,
 CC development, and disease. The present sequence for a PCR primer is used
 CC in the production of a single pattern characteristic of a sample.
 CC employing a Type IIS restriction enzyme (i.e. FokI) in the methods of the
 CC present invention
 XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 SQ

Query Match 0.9%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAA AAAAAAAAAA 1751
 |||||
 DB 16 AAAAAA AAAAAAAAAA 1

RESULT 870
 ABK49636/c
 ID ABK49636 standard; DNA; 17 BP.
 XX AC ABK49636;
 XX 15-JUL-2002 (first entry)
 DE Human Acetyltransferase-like protein 20-90-05 PCR primer GT15G.
 XX Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
 KW differential display; eosinophil; antiallergic; atopic dermatitis; GT15G.
 XX Homo sapiens.
 OS WO200224903-A1.
 PN 28-MAR-2002.
 PD 21-SEP-2001; 2001WO-JP008246.
 XX 25-SEP-2000; 2000JP-00291318.
 PR (GENO-) GENOX RES INC.
 PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
 XX (EISA) EISAI CO LTD.
 PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
 PI Takahashi E;
 PI WPI; 2002-315738/35.
 DR Examining allergic diseases by differential display of gene showing
 PT different expression particularly increased expression in remission stage
 PT in eosinophils of patients, also applicable in screening candidate
 PT compounds for remedies.
 XX Example 1; Page 57; 72pp; Japanese.
 PS The invention relates to a method for examining allergic diseases
 CC comprising determining the expression level of a gene containing, the
 CC human cDNA appearing as ABK49633 which has homology with
 CC acetyltransferases in the eosinophils of a patient and comparing the

expression level with that in the eosinophils of a healthy individual (i.e. differential display). Also included are methods of screening for candidate compounds which affect the expression level of the gene or the activity of the protein encoded by the gene (including related proteins and mutants), the use of probes based on the gene sequence in the examination of allergic diseases, the use of reporter constructs in the screening of candidate compounds, a vector containing a the transcription controlling region of the gene, cells transformed with the vector, an antibody against the protein and a model animal for allergic diseases which is a transgenic non-human vertebrate with lowering of expression intensity of the gene in eosinophils. The method is examining allergic diseases particularly atopic dermatitis which is also applicable in screening candidate compounds for remedies. Such method can be performed in high throughput, at low cost. The present sequence is a differential display PCR primer for the cDNA encoding the human acetyltransferase-like protein 20-90-05

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA... 1750
Db 17 CAAAAA... 2

RESULT 871
ABL59040/C
ID ABL59040 standard; DNA; 17 BP.

AC ABL59040;

DT 20-AUG-2002 (first entry)

DE Nucleotide sequence of PCR primer GT15G.

Human; allergy; eosinophil; PCR; primer; ss.

OS Homo sapiens.

PN JP2002095500-A.

PD 02-APR-2002.

PF 25-SEP-2000; 2000JP-00291316.

PR 25-SEP-2000; 2000JP-00291316.

PA (GENO-) GENOX SOYAKU KENKYUSHO KK.
PA (KOKU-) KOKURITSU SHONI BYOIN INCHO.

DR WPI; 2002-439993/47.

Examining allergosis, involves measuring the expression levels of a specific gene, and comparing it to the levels in the eosinophils of a healthy control.

Example 1; Page 17; 20pp; Japanese.

The specification describes a method for examining allergosis. The method comprises measuring the expression level of the gene given in ABL59037, and comparing it with the expression level of the gene in the eosinophils of a healthy person. The method is used for the examination of allergosis. The present sequence represents a PCR primer, which is used in the course of the invention

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA... 1750
Db 17 CAAAAA... 2

RESULT 872

ABN99831/C

ID ABN99831 standard; DNA; 17 BP.

AC ABN99831;

DT 15-AUG-2002 (first entry)

DE Human allergic disease related PCR primer SEQ ID NO: 20.

Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR; primer; ss.

OS Homo sapiens.

PN WO200233069-A1.

PD 25-APR-2002.

PF 28-SEP-2001; 2001WO-JP008574.

PR 13-OCT-2000; 2000JP-00314093.

PA (GENO-) GENOX RES INC.

PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;

DR WPI; 2002-372311/40.

Method for examining allergic diseases by differential display of seventeen genes showing different expression particularly significant increase in eosinophils in patients with mild atopic dermatitis, also applicable in screening compounds.

Example 1; Page 110; 165pp; Japanese.

The present invention relates to a method for examining allergic diseases which involves determining the expression level of a gene, having one of the 17 nucleotide sequences shown in ABN99812-ABN99828, in the eosinophils in a patient and comparing the expression level with that in the eosinophils of a healthy individual. The method can be used to examine allergic diseases, particularly atopic dermatitis, and its early diagnosis, which is also applicable in screening candidate compounds for remedies. The present sequence is a PCR primer described in the exemplification of the invention

Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA... 1750
Db 17 CAAAAA... 2

RESULT 873

AAL49950/C

ID AAL49950 standard; DNA; 17 BP.

AC AAL49950;

DT 10-DEC-2002 (first entry)

DE Human B153 expression in allergic disease related PCR primer GT15G.

```
XX Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
XX ss.
XX Unidentified.
XX WO200250269-A1.
XX 27-JUN-2002.
XX
XX 21-DEC-2001; 2001WO-JP011286.
XX
XX 21-DEC-2000; 2000JP-00389476.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX WPI; 2002-713252/77.
XX
XX Examination of allergic diseases comprises detecting gene B1153 over-
XX expressed in T cells of allergy patients for diagnosis treatment and
XX investigation of atopic skin inflammation and asthma.
XX
XX Example 6; Page 82; 102pp; Japanese.
XX
XX The present invention relates to a method of examining allergic diseases
XX which comprises comparing the expression level of gene B1153 in allergy
XX patients with the expression level in healthy subjects. The method is
XX useful for the treatment, prevention, diagnosis and study of allergic
XX diseases including atopic skin inflammation and asthma. The present
XX sequence is a PCR primer described in the exemplification of the
XX invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAA 1750
DB 17 CAAAAAAAAAAAAA 2
RESULT 874
AAL47236/c
ID AAL47236 standard; DNA; 17 BP.
XX
XX AAL47236;
XX
XX 22-AUG-2002 (first entry)
XX
XX Allergic disease examination method related anchor primer SEQ ID NO: 4.
DE
XX Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW atopic dermatitis; human; PCR; primer; ss.
XX
XX Unidentified.
XX
XX WO200233122-A1.
XX
XX 25-APR-2002.
XX
XX 11-OCT-2001; 2001WO-JP008937.
XX
XX 13-OCT-2000; 2000JP-00314093.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX (EISA ) EISAI CO LTD.
```

```
XX Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX WPI; 2002-372313/40.
XX
XX Method for examining allergic diseases by differential display of
XX intersectin 2 gene showing different expression particularly significant
XX increase in eosinophils in patients.
XX
XX Example 1; Page 53; 90pp; Japanese.
XX
XX The present invention relates to a method for examining allergic diseases
XX with intersectin 2 gene or a gene with equivalent function of intersectin
XX 2 as an indicator gene, which comprises determining the expression level
XX of the gene in the eosinophils in a patient, and comparing the expression
XX level with that in the eosinophils of a healthy individual. The method is
XX for examining allergic diseases, particularly atopic dermatitis, which is
XX also applicable in screening candidate compounds for remedies. The
XX present sequence is an anchor primer described in the exemplification of
XX the invention
XX
XX Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAA 1750
DB 17 CAAAAAAAAAAAAA 2
RESULT 875
ABK49758/c
ID ABK49758 standard; DNA; 17 BP.
XX
XX ABK49758;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human atopic dermatitis cDNA related PCR primer Grl5g.
DE
XX Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
KW allergic disease; antiallergic; dermatological; Grl5g.
XX
XX Synthetic.
XX
XX WO200226962-A1.
XX
XX 04-APR-2002.
XX
XX 21-SEP-2001; 2001WO-JP008247.
XX
XX 26-SEP-2000; 2000JP-00293021.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
PI WPI; 2002-330097/36.
XX
XX Examining allergic diseases by differential display of genes showing
XX different expression particularly increase in remission stage in
XX eosinophils in patients.
XX
XX Example 1; Page 55; 74pp; Japanese.
XX
XX This invention relates to gene sequences that are differentially
XX expressed in eosinophils from patients with atopic dermatitis in the
XX increment stage as compared with those in the remission stage. These
XX sequences are used in a novel method for examining allergic diseases
```

CC comprising determining the expression levels of these genes and comparing
CC the expression level with that in the eosinophils of a healthy
CC individual. The method of the invention may have antiallergic or
CC dermatological activities. The method can be used to diagnose allergic
CC diseases particularly atopic dermatitis, and may also be used to screen
CC candidate compounds for remedies. The method of the invention can be
CC performed in high throughput, at low cost. The present sequence
CC represents the Gr15g PCR primer used to amplify the differentially
CC amplified atopic dermatitis related cDNA sequences of the invention
XX

XX SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAA 2
|||||

RESULT 876
ADB04273/c
ID ADB04273 standard; DNA; 17 BP.
AC ADB04273;
XX
XX 20-NOV-2003 (first entry)
XX Human MD27 scanning oligonucleotide SEQ ID 5259.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5259; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.
XX
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1750
Db 16 CAAAAAAAAAAAAA 1
|||||

RESULT 877
ADB04271/c
ID ADB04271 standard; DNA; 17 BP.
XX
XX ADB04271;
AC
XX
XX 20-NOV-2003 (first entry)
XX Human MD27 scanning oligonucleotide SEQ ID 5257.
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX developmental disorder; ss.
XX Homo sapiens.
XX
XX EPI281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 5257; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
XX SQ Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAAAAAAAAAAAAA 2

RESULT 878
ABZ70578/c
ID ABZ70578 standard; DNA; 17 BP.
XX
XX
AC ABZ70578;
XX
DT 23-MAY-2003 (first entry)
XX
DE Primer.
XX
KW Aspergillus phenolics; oxalate decarboxylase; APOXD; transgenic plant;
KW crop protection; primer; ss.
XX
OS Synthetic.
XX
PN CA2350328-A1.
XX
PD 26-DEC-2002.
XX
PF 26-JUN-2001; 2001CA-02350328.
XX
PR 26-JUN-2001; 2001CA-02350328.
XX
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Scelonge C, Bidney D;
XX
DR WPI; 2003-248733/25.
XX
PT New isolated nucleic acid encoding oxalate decarboxylase from Aspergillus
PT phenolics, for degrading oxalic acid, identifying transformed plant
PT cells, and preventing pathogenic disease in plants.
XX
PS Disclosure; Page 50; 60pp; English.
XX
CC The present sequence is that of a primer used in the invention. The
CC invention relates to a novel nucleic acid (see ABZ70560) encoding
CC Aspergillus phenolics oxalate decarboxylase (APOXD) (see ABP72475). The
CC gene and its encoded protein are useful in degrading oxalate, in
CC diagnostic assays, for protecting plants against disease, and as a
CC selectable marker
XX
SQ Sequence 17 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 1 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAAAAAAAAAAAAA 2

RESULT 879
ACF36345/c
ID ACF36345 standard; DNA; 17 BP.
XX
XX
AC ACF36345;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA fragment.
XX
KW Gene variant identification; restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX
PN WO2003064689-A2.

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 17 AAAAAAAAAAAAAA 2

RESULT 880
ACF36370/c
ID ACF36370 standard; DNA; 17 BP.
XX
XX
AC ACF36370;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW electrophoresis; type II restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX
PN WO2003064691-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000843.
XX
PR 29-JAN-2002; 2002US-0352215P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
```

```
XX 07-AUG-2003.
XX 28-JAN-2003; 2003WO-IB000255.
XX 29-JAN-2002; 2002US-0352245P.
XX (GLOB-) GLOBAL GENOMICS AB.
XX Lommerberg P, Oldin M, Linnarsson S, Ernfors P;
XX WPI; 2003-627619/59.
XX
XX Determining polyadenylation sites within transcribed gene sequences
XX present in a sample comprises assigning to gene fragments gene candidates
XX within a database by comparing signals in the dataset with the database.
XX Example; Fig 3; 81pp; English.
XX
XX The invention relates to determining the presence of and/or identifying a
XX polyadenylation site within a sequence of a transcribed gene or variants
XX present in a sample. The method involves assigning to gene fragments gene
XX candidates within a database by comparing signals in the dataset with the
XX database, the database comprising data representing mRNAs with known
XX polyA sites and/or 'virtual genes' representing a possible
XX polyadenylation site within an actual gene. The method is useful for
XX determining the presence of and/or identifying a polyadenylation site or
XX alternative polyadenylation sites within a sequence of a transcribed gene
XX or sequences of transcribed gene variants present or potentially present
XX in a sample, in identifying gene features, particularly in identifying
XX differences between sequence variants that occur in a population of
XX nucleic acid molecules, especially in identifying or discovering polyA
XX site usage or determining polyA site usage in a nucleic acid sample, and
XX gene variants arising from alternative polyA sites. The present sequence
XX represents a double stranded product DNA fragment
XX
XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAA 1

RESULT 880
ACF36370/c
ID ACF36370 standard; DNA; 17 BP.
XX
XX
AC ACF36370;
XX
DT 04-DEC-2003 (first entry)
XX
DE Nucleotide sequence of a double stranded product DNA.
XX
KW Nucleic acid manipulation; mRNA profiling; polymerase chain reaction;
KW electrophoresis; type II restriction enzyme; FokI; ds.
XX
OS Synthetic.
XX
PN WO2003064691-A2.
XX
PD 07-AUG-2003.
XX
PF 28-JAN-2003; 2003WO-IB000843.
XX
PR 29-JAN-2002; 2002US-0352215P.
XX
PA (GLOB-) GLOBAL GENOMICS AB.
XX
PI Linnarsson S, Ernfors P, Bauren G, Metsis A, Pihlak A;
```

```
PI Montelius A;
XX WPI; 2003-618365/58.
XX Producing a population of double-stranded product DNA molecules, useful
PT for mRNA profiling, comprises amplification by nested polymerase chain
PT reaction.
XX Example; Fig 2; 105pp; English.
XX The invention relates to producing a population of double-stranded
CC product DNA molecules comprising amplification by a nested PCR method.
CC The method is useful in profiling mRNA transcribed in a system under
CC investigation. The oligonucleotides are used as size standards in
CC electrophoresis, and as internal controls allowing for calculation of
CC relative amounts of material present. The present sequence represents a
CC double stranded product DNA, which aids in outlining an approach to
CC production of a single pattern characteristic of a sample, employing a
CC type II restriction enzyme (FokI)
XX Sequence 17 BP; 0 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1751
Db 16 AAAAAAAAAAAAAAAAAA 1
RESULT 881
ADC84470/C
ID ADC84470 standard; DNA; 17 BP.
XX ADC84470;
XX 01-JAN-2004 (first entry)
XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 3.
XX Plant blastogenesis; transformation; gene expression; tissue specific;
XX PCR; primer; ss.
XX Synthetic.
XX JP2003159071-A.
XX 03-JUN-2003.
XX 22-NOV-2001; 2001JP-00358366.
XX 22-NOV-2001; 2001JP-00358366.
XX (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX WPI; 2003-818678/77.
XX New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX Example 3; SEQ ID NO 3; 43pp; Japanese.
XX The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
```

```
SQ Sequence 17 BP; 0 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2
RESULT 882
AAV54174/C
ID AAV54174 standard; cDNA; 18 BP.
XX AAV54174;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 11.
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
XX immunohistological staining.
XX Synthetic.
XX WO9839437-A1.
XX 11-SEP-1998.
XX 05-MAR-1998; 98WO-JP000905.
XX 05-MAR-1997; 97JP-00050302.
XX (KYOW ) KYOWA HAKKO KOGYO KK.
XX Sakaki Y;
XX WPI; 1998-495844/42.
XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX Example 1; Page 50; 70pp; Japanese.
XX This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAAAAAA 1750
Db 17 CAAAAAAAAAAAAAAAAA 2
RESULT 883
AAV54165/C
ID AAV54165 standard; cDNA; 18 BP.
XX AAV54165;
XX 21-DEC-1998 (first entry)
XX Nucleotide sequence PCR primer 2.
XX
```

KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX immunohistological staining.

OS Synthetic.

PN WO9839437-A1.

XX 11-SEP-1998.

PD 05-MAR-1998; 98WO-JP000905.

XX 05-MAR-1997; 97JP-00050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA Sakaki Y;

PI WPI; 1998-495844/42.

DR Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX treating diseases associated with apoptosis.

XX Example 1; Page 47; 70pp; Japanese.

CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

XX Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
 DB 17 CAAAAAAAAAAAAA 2

RESULT 884

AAV54171/c

ID AAV54171 standard; cDNA; 18 BP.

XX AAV54171;

XX 21-DEC-1998 (first entry)

XX Nucleotide sequence PCR primer 8.

KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX immunohistological staining.

OS Synthetic.

XX WO9839437-A1.

XX 11-SEP-1998.

XX 05-MAR-1998; 98WO-JP000905.

XX 05-MAR-1997; 97JP-00050302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PA Sakaki Y;

PI WPI; 1998-495844/42.

DR Novel apoptosis-related DNAs and proteins - for diagnosis, preventing, or
 PT treating diseases associated with apoptosis.

XX
 PS

Example 1; Page 49; 70pp; Japanese.

CC This is the nucleotide sequence of a PCR primer used in the method of the
 CC invention, involving the use of novel apoptosis-related DNAs and
 CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 CC immunohistological staining, as apoptosis inhibitors. It can also be used
 CC for treatment of apoptosis-related diseases

XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
 DB 17 CAAAAAAAAAAAAA 2

RESULT 885

AAZ90641/c

ID AAZ90641 standard; DNA; 18 BP.

XX AAZ90641;

XX 13-JUN-2000 (first entry)

DE Human adipose tissue gene amplifying primer #2.

KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

XX JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes

XX Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1750
 DB 17 CAAAAAAAAAAAAA 2

RESULT 886

AAZ90650/c

ID AA290650 standard; DNA; 18 BP.
 XX AA290650;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human adipose tissue gene amplifying primer #11.
 XX
 KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2000037190-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 23-JUL-1998; 98JP-00225228.
 XX
 PR 23-JUL-1998; 98JP-00225228.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-306578/27.
 XX
 PT A physiologically active protein specifically derived from mammal tissue.
 XX
 PS Example 2; Page 18; 50pp; Japanese.
 XX
 CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAA 1750
 Db 17 CAAAAA AAAAAAAAAA 2
 RESULT 887
 AA290647/C
 ID AA290647 standard; DNA; 18 BP.
 XX
 AC AA290647;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human adipose tissue gene amplifying primer #8.
 XX
 KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2000037190-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 23-JUL-1998; 98JP-00225228.
 XX
 PR 23-JUL-1998; 98JP-00225228.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-306578/27.
 XX
 PT A physiologically active protein specifically derived from mammal tissue.
 XX
 PS Example 2; Page 18; 50pp; Japanese.
 XX
 CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAA 1750
 Db 17 CAAAAA AAAAAAAAAA 2
 RESULT 887
 AA290647/C
 ID AA290647 standard; DNA; 18 BP.
 XX
 AC AA290647;
 XX
 DT 13-JUN-2000 (first entry)
 XX
 DE Human adipose tissue gene amplifying primer #8.
 XX
 KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2000037190-A.
 XX
 PD 08-FEB-2000.
 XX
 PF 23-JUL-1998; 98JP-00225228.
 XX
 PR 23-JUL-1998; 98JP-00225228.
 XX
 PA (NISR) JAPAN TOBACCO INC.
 XX

DR WPI; 2000-306578/27.
 XX
 PT A physiologically active protein specifically derived from mammal tissue.
 XX
 PS Example 2; Page 18; 50pp; Japanese.
 XX
 CC The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AA290631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AA290640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 4.8e+02; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAA AAAAAAAAAA 1750
 Db 17 CAAAAA AAAAAAAAAA 2
 RESULT 888
 AA290647/C
 ID AA290647 standard; DNA; 18 BP.
 XX
 AC AA290647;
 XX
 DT 10-MAY-2001 (first entry)
 XX
 DE Binary encoded sequence tag method anchored primer #3.
 XX
 KW Binary encoded sequence tag; BEST; nucleic acid analysis;
 KW gene expression; adaptor; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200112855-A2.
 XX
 PD 22-FEB-2001.
 XX
 PF 11-AUG-2000; 2000WO-US022164.
 XX
 PR 13-AUG-1999; 99US-0148870P.
 XX
 PR 06-APR-2000; 2000US-00544713.
 XX
 PA (UYVA) UNIV YALE.
 XX
 PI Kaufman JC, Roth ME, Lizardi PM, Feng L, Latimer DR;
 XX
 DR WPI; 2001-202878/20.
 XX
 PT Producing binary sequence tags, useful for analyzing nucleic acid
 PT sequence tags, gene expression or gene-expression patterns, involves
 PT generating nucleic acid fragments, which are mixed with offset adaptors
 PT and adaptor-indexers.
 XX
 PS Disclosure; Page 101; 101pp; English.
 XX
 CC The present invention describes a method of producing binary sequence
 CC tags from nucleic acid fragments in a sample, involving incubating the
 CC sample with cleaving reagents, mixing offset adaptors with the sample,
 CC incubating with more cleaving reagents and mixing the sample with adaptor
 CC indexers where the adaptors are coupled to binary sequence tags. The
 CC method is useful in sequence analysis, including analysis and comparison
 CC of gene expression, nucleic acid samples and genomes
 XX
 SQ Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 16; DB 1; Length 18;
 Query Match 0.9%; Score 16; DB 1; Length 18;

```
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAA 1751
DB 16 AAAAAAAAAAAAAAAA 1

RESULT 889
ABK51158/c
ID ABK51158 standard; DNA; 18 BP.
XX
AC ABK51158;
XX
DT 30-JUL-2002 (first entry)
XX
DE Human cytomegalovirus (HCMV) RT-PCR primer TXN.
XX
KW Human cytomegalovirus; HCMV; virucide; cytomegalovirus infection; CMV;
KW cellular kinase; RICK; RIP; Nck-Interacting kinase; MKK3; SRPK-2;
KW reverse transcriptase PCR; RT-PCR; primer; ss.
XX
OS Human cytomegalovirus.
XX
FH Key Location/Qualifiers
FT misc_difference 17
FT /*tag= a
FT /label= n
FT /note= "n= dATP, dCTP or dGTP"
XX
PN EP1201765-A2.
XX
PD 02-MAY-2002.
XX
PF 15-OCT-2001; 2001EP-00124604.
XX
PR 16-OCT-2000; 2000US-0240750P.
XX
PA (AXXI-) AXIMA PHARM AG.
XX
PI Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
XX WPI; 2002-373930/41.
XX
CC Identifying agents for treatment or prevention of cytomegalovirus
CC infection, comprises contacting test compound with cellular kinase and
CC detecting change in cellular kinase activity.
XX
PS Example 1; Page 13; 49pp; English.
XX
CC The present invention relates to a new method for identifying compounds
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC related diseases. The method of the invention comprises contacting a test
CC compound with at least one of the cellular kinases RICK, RIP, Nck-
CC interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
CC activity. The method of the invention can be used to treat and/or prevent
CC CMV infections and related diseases. Oligonucleotides that can detect the
CC specified kinases can also be used for diagnosis of infection. The
CC present nucleic acid sequence represents human CMV reverse transcriptase
CC (RT)-PCR primer TXN that was used in the methods of the invention for
CC preparation of radioactively labelled cDNA probes
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAA 1751
DB 16 AAAAAAAAAAAAAAAA 1
```

```
RESULT 890
AAD52799/c
ID AAD52799 standard; DNA; 18 BP.
XX
AC AAD52799;
XX
DT 14-MAY-2003 (first entry)
XX
DE Primer used to prepare radioactively labelled cDNA probes from RNA.
XX
KW Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;
KW cellular protein phosphatase; cellular signal transduction; prophylaxis;
KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;
KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;
KW TME; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;
KW fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic;
KW Alzheimer's disease; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200293164-A2.
XX
PD 21-NOV-2002.
XX
PF 16-MAY-2002; 2002WO-EP005420.
XX
PR 16-MAY-2001; 2001EP-00111858.
PR 29-MAY-2001; 2001US-0293528P.
PR 13-JUL-2001; 2001EP-00117113.
PR 18-JUL-2001; 2001US-0305898P.
XX
PA (AXXI-) AXIMA PHARM AG.
XX
PI Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;
XX WPI; 2003-120714/11.
XX
CC New pyridylpyrimidine derivatives useful in the treatment or prevention
CC of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease
CC (CJD).
XX
PS Example; Page 38; 96pp; English.
XX
CC The invention relates to novel pyridylpyrimidine derivatives and methods
CC of detecting prion infections and/or prion disease in an individual or in
CC cells, cell cultures and/or cell lysates. The method involves adding at
CC least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-
CC pyrimidine derivative to the sample or in cells, cell cultures and/or
CC cell lysates and detecting the activity of at least one human cellular
CC protein kinases (e.g., FGF-R1 (also known as flg, Fl-1, Flt-2, b-FGFR),
CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also
CC known as c-abl), ckl1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also
CC known as CDK1), PRK1, human cellular protein phosphatases such as PTP-SL
CC (also known as MCP8), and PTP-zeta, the cellular signal transduction
CC molecules HSP80 and GPR1-1. The invention is useful for regulating the
CC production of prions in cells and in the manufacture of pharmaceutical
CC composition for prophylaxis and/or treatment of infectious disease (e.g.
CC Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy
CC (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy
CC (BSE), variant CJD, Gerstmann-Strausler-Scheinker syndrome (GSS), fatal
CC familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD,
CC vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans
CC or ruminants. The present DNA sequence is a primer used to prepare
CC radioactively labelled cDNA probes from RNA. This sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 18 BP; 0 A; 0 C; 0 G; 16 T; 0 U; 2 Other;

Query Match 0.9%; Score 16; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAA 1751
```


Db 16 AAAAAAAAAAAAAA 1

RESULT 891
ABL51169
ID ABL51169 standard; DNA; 20 BP.
XX
AC ABL51169;
XX
DT 27-JUN-2002. (first entry)
XX
DE Human TNF inducible protein A20 antisense oligonucleotide SEQ ID:47.
XX
KW Human; tumour necrosis factor inducible protein A20; phosphorothioate;
KW antisense modulation; antisense oligonucleotide; antiinflammatory;
KW cytostatic; antiviral; gene therapy; TNF inducible protein A20;
KW inflammatory disorder; viral infection; hyperproliferative disorder;
KW cancer; inflammation; tumour formation; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /mod_base= OTHER
FT /note= "2'-methoxyethyl (MOE) nucleotide wings and a
FT deoxy gap with a phosphorothioate backbone"
FT modified_base 1..5
FT /*tag= b
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl nucleotides"
FT modified_base 15..20
FT /*tag= c
FT /mod_base= OTHER
FT /note= "2'-O-methoxyethyl nucleotides"
XX
WO200220545-A1.
XX
XX 14-MAR-2002.
XX
XX 07-SEP-2001; 2001WO-US028116.
XX
XX 08-SEP-2000; 2000US-00658687.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Wyatt JR;
XX
XX WPI; 2002-362238/39.
XX
XX New antisense compound useful for preventing or delaying infection,
XX inflammation or tumor formation, hybridizes and inhibits a nucleic acid
XX molecule encoding tumor necrosis factor inducible protein, A20.
XX
XX Claim 3; Page 92; 121pp; English.
XX
XX The present invention describes a compound (I) of 8 - 50 nucleotides
XX targeted to a nucleic acid molecule (II) encoding tumor necrosis factor
XX (TNF) inducible protein, A20, and which specifically hybridises with and
XX inhibits expression of A20, or a compound (Ia) of 8 - 50 nucleotides
XX which specifically hybridises with an 8-nucleotide portion of an active
XX site on (II). (I) have antiinflammatory, cytostatic and antiviral
XX activities. (I) can be used as inhibitors of TNF inducible protein, A20.
XX (I) is useful for inhibiting the expression of A20 in cells or tissues,
XX and for treating an animal having a disease condition associated with
XX A20, e.g. a inflammatory disorder, viral infection and hyperproliferative
XX disorder e.g. cancer. (I) is also useful prophylactically, e.g. to
XX prevent or delay infection, inflammation or tumour formation. (I) is also
XX useful as therapeutic, diagnostic and research reagent, for
XX distinguishing functions of various members of a biological pathway, and
XX in antisense gene therapy. The present sequence represents an antisense

CC oligonucleotide for human TNF inducible protein A20, from the present
CC invention
XX
SQ Sequence 20 BP; 6 A; 5 C; 3 G; 6 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 63 TTTCTGGAGTCCCAAA 78
|||||
Db 1 TTTCTGGAGTCCCAAA 16
|||||

RESULT 892
ABA05915/C
ID ABA05915 standard; DNA; 20 BP.
XX
AC ABA05915;
XX
DT 05-MAR-2002 (first entry)
XX
DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 5.
XX
KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
KW PCR primer; ss.
XX
OS Hepatitis B virus.
XX
PN EP1152063-A1.
XX
PD 07-NOV-2001.
XX
PF 03-MAY-2000; 2000EP-00109436.
XX
PR 03-MAY-2000; 2000EP-00109436.
XX
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX
PI Schroeder KH, Koike K;
XX
XX WPI; 2002-068256/10.
XX
XX Diagnosing hepatitis B virus (HBV) infection stages and determining the
XX risk for hepatocellular carcinoma, comprises identifying full length HBV
XX transcripts and truncated HBV transcripts in a serum sample.
XX
XX Example 1; Page 6; 25pp; English.
XX
XX The invention relates to diagnosis of hepatitis B virus (HBV) infection
XX stages comprising identification of full length HBV transcripts (I) and
XX truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
XX is indicative of a particular infection stage. The method is useful for
XX diagnosing HBV infection stages and determining the risk for developing
XX hepatocellular carcinoma. The present sequence is that of a HBV
XX diagnostic PCR primer, useful for the invention
XX
SQ Sequence 20 BP; 0 A; 1 C; 3 G; 16 T; 0 U; 0 Other;
Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1735 CAAAAAAAAAAAAA 1750
|||||
Db 16 CAAAAAAAAAAAAA 1
|||||

RESULT 893
AAD33499
ID AAD33499 standard; DNA; 20 BP.
XX
XX AAD33499;
XX

```
XX 01-JUL-2002 (first entry)
DT XX
DE DE T7T18Apad_P527-20-0003 probe for calibration of molecular array data.
DE XX
DE DE Molecular array; probe; ss.
KW XX
XX XX Unidentified.
XX XX
XX XX EP1186673-A2.
XX XX
XX PD 13-MAR-2002.
XX XX
XX PF 10-SEP-2001; 2001EP-00307665.
XX XX
XX PR 11-SEP-2000; 2000US-00659173.
XX XX
XX PA (AGIL-) AGILENT TECHNOLOGIES INC.
XX XX
XX PI Wobler PK, Delenstarr GC;
XX XX
XX DR WPI; 2002-282886/33.
XX XX
XX PT Calibration of molecular array data by employing calibration probes that
XX generate signals proportional to total concentrations of labeled target
XX molecules, and molecular arrays incorporating sets of calibration probes.
XX
XX PS Disclosure; Page 14; 32pp; English.
XX XX
XX CC The invention relates to a method for calibrating data scanned from a
XX molecular array. The method involves employing calibration probes that
XX generate signals proportional to the total concentrations of labelled
XX target molecules to which the molecular array probes are directed over an
XX entire range of sample solutions and molecular arrays incorporating sets
XX of calibration probes. Method is useful for calibrating different types
XX of signals scanned from a molecular array, or calibrating signals scanned
XX from different molecular arrays. The present sequence is poly (A)
XX normalisation probe used in calibration of molecular array data
XX
XX SQ Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1751
DB 1 AAAAAAAAAAAAAA 16

RESULT 894
ABZ86271/C
ID ABZ86271 standard; DNA; 20 BP.
XX
XX AC ABZ86271;
XX
XX DT 17-OCT-2003 (first entry)
XX
XX DE Human oligonucleotide sequence.
XX
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200285308-A2.
XX
XX XX 31-OCT-2002.
XX
```

```
PF 23-APR-2002; 2002WO-US013135.
XX
XX PR 24-APR-2001; 2001US-0286137P.
XX
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Fabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX DR
XX XX
XX PT Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX PS Claim 15; SEQ ID NO 1513; 872pp; English.
XX
XX CC The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1575 CACCACCTGACTGCTGA 1590
DB 19 CACCACCTGACTGCTGA 4

RESULT 895
AAZ09196/C
ID AAZ09196 standard; DNA; 21 BP.
XX
XX AC AAZ09196;
XX
XX DT 19-OCT-1999 (first entry)
XX
XX DE Oligonucleotide 8 for DNA analysis.
XX
XX KW Primer; DNA analysis; amplification; hybridisation; ss.
XX
XX OS Synthetic.
XX
XX XX JP11196874-A.
XX
XX PD 27-JUL-1999.
XX
XX PF 14-JAN-1998; 98JP-00005399.
XX
XX PR 14-JAN-1998; 98JP-00005399.
XX
XX PA (HITA ) HITACHI LTD.
```

XX DR WPI; 1999-496652/42.

XX XX Analysis of DNA fragment - comprises addition of known common

PT oligonucleotide, amplification of resultant DNA fragment and analysis and

PT labelling of amplified DNA.

XX XX

PS Example 1; Page 12; 17pp; Japanese.

XX XX

CC This invention describes a novel method for the analysis of a DNA fragment

CC which comprises: (i) addition of a known common oligonucleotide sequence

CC to at least one terminal of each DNA fragment, (ii) amplification of the

CC resultant DNA fragment as a primer using a first common primer containing

CC a complementary nucleotide sequence to the above mentioned known common

CC oligonucleotide sequence, a second common primer containing a

CC complementary nucleotide sequence to the prepared known common

CC oligonucleotide sequence optionally having been introduced with

CC complementary nucleotide sequence at a terminal, and a specific primer

CC capable of hybridisation with a DNA fragment containing whole or part of

CC the gene having known sequence, to give amplified DNA, (iii) analysis of

CC the amplified DNA to find the information of the DNA fragment, in which

CC the specific primer is designed to prepare fragments of the common first

CC and second primers and to give short fragment of amplified DNA and (iv)

CC labelling them to make their differentiation. Differentiation of

CC informations of known and unknown genes readily provides information of

CC unknown gene and simultaneous monitoring of signals derived from minor

CC genes. Furthermore, labelling of DNAs according to functions of known

CC genes can be performed. AA209189-209201 represent oligonucleotide primers

CC used to illustrate the method of the invention

XX XX

SQ Sequence 21 BP; 0 A; 0 C; 3 G; 18 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751

Db 21 AAAAAAAAAAAAAA 6

RESULT 896

AAH26601/c

ID AAH26601 standard; DNA; 21 BP.

AC AAH26601;

XX XX

DE 12-NOV-2001 (first entry)

XX XX

DE Mda-7 gene AP-1 and C/EBP binding site flanking sense PCR primer.

XX XX

XX Melanoma differentiation associated gene-7; Mda-7; human; promoter;

KW neuroblastoma; astrocytoma; glioblastoma multiforme; cervical cancer;

KW breast cancer; colon cancer; prostate cancer; osteosarcoma;

KW chondrosarcoma; tumour; therapy; PCR primer;

KW electrophoretic mobility shift assay; EMSA; ss.

XX XX

OS Homo sapiens.

XX XX

PN WO2000164921-A1.

XX XX

PD 07-SEP-2001.

XX XX

PP 28-FEB-2001; 2001WO-US006782.

XX XX

PR 29-FEB-2000; 2000US-00515369.

XX XX

PA (UYCO) UNIV COLUMBIA NEW YORK.

XX XX

PI Fisher PB, Madireddi MT;

XX XX

DR WPI; 2001-565508/63.

XX XX

PT Melanoma differentiation associated gene-7 promoter capable for treating

PT cancer comprises directing transcription of heterologous coding sequence

PT encoding tumor suppressor polypeptide positioned downstream, useful for

XX treating cancer.

PS Example 2; Page 70; 132pp; English.

XX XX

CC The present sequence is that of a sense primer flanking the region

CC corresponding to the putative AP-1 and C/EBP binding sites present

CC between NdeI and NheI restriction enzyme sites in the human melanoma

CC differentiation associated gene-7 (mda-7) promoter (see AAH26595). The

CC sense primer and an antisense primer (see AAH26602) were used in the PCR

CC amplification of this region of the promoter. The PCR product was used in

CC an electrophoretic mobility shift assay (EMSA) which demonstrated that

CC JUN/AP-1 and C/EBP-beta transcription factors bind to defined sites

CC within the mda-7 promoter during the process of terminal differentiation

CC in human melanoma cells. The invention provides recombinant expression

CC constructs in which the mda-7 promoter is operably linked to a coding

CC sequence encoding a tumour suppressor protein. A pharmaceutical

CC composition including the recombinant expression construct is used in a

CC claimed method of treating melanoma, neuroblastoma, astrocytoma,

CC glioblastoma multiforme, cervical cancer, breast cancer, colon cancer,

CC prostate cancer, osteosarcoma, chondrosarcoma or a cancer of the central

CC nervous system

XX XX

SQ Sequence 21 BP; 3 A; 3 C; 8 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 568 AAGCCAAATCCAGCCT 583

Db 16 AAGCCAAATCCAGCCT 1

RESULT 897

ABS97681

ID ABS97681 standard; DNA; 21 BP.

XX XX

AC ABS97681;

XX XX

DE 23-DEC-2002 (first entry)

XX XX

DE Histamine N-methyl transferase (HNMT) sequencing Primer #4.

XX XX

XX Human; ss; primer; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF;

KW adrenergic receptor beta1; ADRB1; aryl hydrocarbon; AHR; MRP3; NR1I2;

KW aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS;

KW cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

KW glutathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW NADPH quinone oxidoreductase 2; NQO2; sulfotransferase thermolabile; STM;

KW UDP-glucuronosyl transferase 2B4; UDP-glucuronosyl transferase 2B7;

KW UGT2B7; UDP-glucuronosyl transferase; UGT2B15; urokinase receptor; uPA;

KW multidrug resistance 1; lactotransferrin; orphan nuclear receptor;

KW multidrug resistance associated protein 3; cancer; prostate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR4; CHMR5;

KW altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; pulmonary; immunological; sequencing.

XX XX

OS Homo sapiens.

XX XX

PN WO200257410-A2.

XX XX

PD 25-JUL-2002.

XX XX

PF 28-NOV-2001; 2001WO-US044838.

XX XX

PR 28-NOV-2000; 2000US-00724389.

XX XX

CC haematological function, in CHMR3, CHMR4 or CHMR5 for altered central and
CC peripheral nervous system function. The present sequence represents a PCR
CC primer used to amplify the sequences of the invention

SQ Sequence 21 BP; 15 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1750

Db 2 CAAAAAAAAAAAAA 17

RESULT 899

AAD33500

ID AAD33500 standard; DNA; 21 BP.

AC AAD33500;

DT 01-JUL-2002 (first entry)

DE T7718pad_PS26-21-0003 probe for calibration of molecular array data.

KW Molecular array; probe; ss.

OS Unidentified.

PN EP1186673-A2.

PD 13-MAR-2002.

PF 10-SEP-2001; 2001EP-00307665.

PR 11-SEP-2000; 2000US-00659173.

PA (AGIL-) AGILENT TECHNOLOGIES INC.

PI Wobler PK, Delenstarr GC;

DR WPI; 2002-282886/33.

FT Calibration of molecular array data by employing calibration probes that
PT generate signals proportional to total concentrations of labeled target
PT molecules, and molecular arrays incorporating sets of calibration probes.

FS Disclosure; Page 14; 32pp; English.

CC The invention relates to a method for calibrating data scanned from a
CC molecular array. The method involves employing calibrations probes that
CC generate signals proportional to the total concentrations of labelled
CC target molecules to which the molecular array probes are directed over an
CC entire range of sample solutions and molecular arrays incorporating sets
CC of calibration probes. Method is useful for calibrating different types
CC of signals scanned from a molecular array, or calibrating signals scanned
CC from different molecular arrays. The present sequence is poly (A)
CC normalisation probe used in calibration of molecular array data

SQ Sequence 21 BP; 16 A; 3 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 16; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1751

Db 1 AAAAAAAAAAAAAA 16

RESULT 900

AAA84352

ID AAA84352 standard; DNA; 19 BP.

XX AAA84352;

DT 04-DEC-2000 (first entry)

DE Cyclin D2 ribozyme binding site #49.

KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.

OS Mammalia.

PN WO200032765-A2.

PD 08-JUN-2000.

PF 06-DEC-1999; 99WO-US028772.

PR 04-DEC-1998; 98US-0110954P.

PA (IMMU-) IMMUSOL INC.

PI Tritz R, Welch PJ, Barber JR, Robbins JM;

DR WPI; 2000-412314/35.

CC New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
CC RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
CC PCNA and Cyclin B1.

PS Disclosure; Page 75; 109pp; English.

CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AA82415 to AA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment

SQ Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 19;

Best Local Similarity 89.5%; Pred. No. 5.3e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1515 TGGGCACATCTTGTGCAAG 1533

Db 1 TGAGCACATCTTGTGCAAG 19

RESULT 901

AAH59514

ID AAH59514 standard; DNA; 19 BP.

AC AAH59514;

DT 10-SEP-2001 (first entry)

DE Cyclin D2 ribozyme binding site SEQ ID NO:1938.

CC Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
CC recognition site; target; ribozyme binding site; eye disease; vulnery;
CC proliferative disease; skin disease; psoriasis; diabetic retinopathy;
CC cytokine; inflammation; cell-cycle dependent kinase; cyclin; WWP;
CC matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
CC antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
CC antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
CC atopic dermatitis; actinic keratosis; squamous cell carcinoma;
CC basal cell carcinoma; seborrhic wart; vitreoretinopathy; scar;
CC sickle cell retinopathy; ss.

OS Homo sapiens.

```

OS Synthetic.
PN WO200130362-A2.
XX
XX
PD 03-MAY-2001.
XX
XX PF 26-OCT-2000; 2000WO-US029500.
XX
XX PR 26-OCT-1999; 99US-0161532P.
XX (IMMU-) IMMUSOL INC.
XX
XX PI Robbins JM, Tritz R;
XX
XX WPI; 2001-300427/31.
XX
XX PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
XX Example 1; Page 212; 408pp; English.
XX
XX CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antiproliferative,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulvular, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
XX SQ Sequence 19 BP; 5 A; 5 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 19;
Best Local Similarity 89.5%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1515 TGGGCACATCTTGTGCAAG 1533
DB 1 TGAGCACATCTTGGCAAG 19
||| ||||| ||||| |||||
1 TGAGCACATCTTGGCAAG 19

RESULT 902
AAQ44553/c
ID AAQ44553 standard; DNA; 20 BP.
XX
XX AAQ44553;
XX
XX 25-MAR-2003 (revised)
DT 26-SEP-1994 (first entry)
XX
XX Antisense oligonucleotide which targets human ELAM-1 3'-UTR.
XX
XX Human endothelial leukocyte adhesion molecule; ELAM-1; cell adhesion;
KW modulation; inflammation; psoriasis; malignant melanoma; inhibition;
KW inflammatory bowel disease; antisense oligonucleotide; therapy; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1..20
FT /tag= a
XX
XX Antisense oligonucleotide which targets human ELAM-1 3'-UTR.
XX
XX Human endothelial leukocyte adhesion molecule; ELAM-1; cell adhesion;
KW modulation; inflammation; psoriasis; malignant melanoma; inhibition;
KW inflammatory bowel disease; antisense oligonucleotide; therapy; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1..20
FT /tag= a

```

```

FT /note= "in phosphorothioate form"
XX
XX WO9405333-A1.
XX
XX 17-MAR-1994.
XX
XX 27-AUG-1993; 93WO-US008101.
XX
XX 02-SEP-1992; 92US-00939855.
PR 21-JAN-1993; 93US-00007997.
PR 17-MAY-1993; 93US-00063167.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Bennet CF, Mirabelli CK;
XX
XX WPI; 1994-100869/12.
XX
XX Oligo:nucleotide modulation of cell adhesion - used in the treatment of
PT e.g. psoriasis, inflammatory bowel disease or malignant melanoma.
XX
XX Claim 41; Page 62; 101pp; English.
XX
XX Antisense oligonucleotides which target human ELAM-1 were synthesised in
CC the phosphorothioate form. The oligonucleotides are useful to treat
CC diseases which are modulated by changes in intercellular adhesion
CC molecules. This sequence corresponds to nucleotides 2063-2082 of the 3'-
CC untranslated region of human ELAM-1 coding sequence. (Updated on 25-MAR-
CC 2003 to correct FN field.)
XX
XX SQ Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.8; DB 1; Length 20;
Best Local Similarity 89.5%; Pred. No. 5.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857
DB 19 CTCCTCGGGTCTCTGGCCC 1
||| ||||| ||||| |||||
19 CTCCTCGGGTCTCTGGCCC 1

RESULT 903
AAAT01782/c
ID AAAT01782 standard; DNA; 20 BP.
XX
XX AAAT01782;
XX
XX 22-DEC-1995 (first entry)
DT
XX
XX Peptide nucleic acid oligomer targetting ELAM-1 3'-UTR.
XX
XX peptide nucleic acid; PNA; intercellular adhesion molecule; ICAM-1;
KW endothelial leukocyte; ELAM-1; vascular; VCAM-1; antiinflammatory;
KW anticancer; antimetastatic; anti-AIDS; anti-rhinoviral; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT misc_feature 1..20
FT /tag= a
XX
XX /note= "at least one (and preferably all) of the backbone
FT subunits are composed of amide units, so that the
FT oligomer consists of the nucleobases attached covalently
FT to a polyamide backbone"
XX
XX WO9504749-A1.
XX
XX 16-FEB-1995.
PD
XX
XX 05-AUG-1994; 94WO-US009026.
PP
XX
XX 05-AUG-1993; 93US-00102650.
PR
XX
XX

```

```

PA (ISIS-) ISIS PHARM INC.
XX
XX Bennett CF, Mirabelli CK;
XX
XX WPI; 1995-090842/12.
XX
XX New peptide nucleic acid oligomers hybridising to adhesion molecule genes
PT - are stable anti-sense cpts. of high affinity, partic. for treating
PT inflammation, viral infection, cancer etc.
XX
XX Claim 10; Page 40; 57pp; English.
XX
XX New oligomers are claimed which (A) have at least one peptide nucleic
CC acid (PNA) subunit and (B) have a sequence hybridisable to AUG region,
CC coding region, 5'-untranslated region or 3'-untranslated region of ICAM-1
CC or ELAM-1, or hybridisable to AUG region, coding region, 5'- untranslated
CC region, exon/intron junction region or 3'-untranslated region of VCAM-1.
CC The PNAs can be used to target RNA and single stranded DNA (ssDNA) to
CC produce antisense-type gene regulation moieties. Hence they may be used
CC therapeutically for modulating cellular adhesion and thus as
CC AIDS agents and antiinflammatory agents. They may also be useful as
CC diagnostics, e.g. as probes for specific mRNAs. PNA oligomers have high
CC affinity for complementary single stranded DNA. They are also able to
CC form triple helices in which a first PNA strand binds with RNA or ssDNA
CC and a second PNA strand binds with the resulting double helix or with the
CC first PNA strand. The PNAs possess no significant charge and are water
CC soluble, which facilitates cellular uptake. Further, since they contain
CC amides of non-biological amino acids, they are biostable and resistant to
CC enzymatic degradation by proteases. The present sequence targets
CC endothelial leukocyte adhesion molecule-1 (ELAM-1) 3'-untranslated region
XX
XX Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15.8; DB 1; Length 20;
XX Best Local Similarity 89.5%; Pred. No. 5.5e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1
XX
RESULT 904
AAT33075/c
ID AAT33075 standard; DNA; 20 BP.
XX
XX AAT33075;
XX
XX 21-JAN-1997 (first entry)
XX
XX Antisense oligonucleotide ISIS 4729.
XX
XX Antisense oligonucleotide; human; intracellular adhesion molecule-1;
XX ICAM-1; endothelial leukocyte adhesion molecule-1; ELAM-1; E-selectin;
XX vascular cell adhesion molecule-1; VCAM-1; white blood cell; breguarin;
XX vascular endothelium; allograft rejection; immunosuppression; rapamycin;
XX anti-lymphocyte serum; monoclonal antibody; cardiac allograft; therapy;
XX renal allograft rejection; donor-specific transplant tolerance; LFA-1;
XX ss.
XX
XX Synthetic.
XX
XX WO9615780-A1.
XX
XX 30-MAY-1996.
XX
XX 22-NOV-1995; 95WO-US015536.
XX
XX 23-NOV-1994; 94US-00344155.
XX
XX (ISIS-) ISIS PHARM INC.
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX
XX Bennett CF, Stepkowski SM;
XX
XX WPI; 1996-268321/27.
XX
XX Oligo:nucleotide targetted to a nucleic acid sequence encoding ICAM-1,
PT ELAM-1 or VCAM-1 - useful for treating or preventing allo:graft
PT rejection.
XX
XX Example 9; Page 29; 92pp; English.
XX
XX AAT30211-T30233, AAT33058-T33112 and AAT36667-T36684 represent antisense
CC oligonucleotides of the invention. These sequences target regions of the
CC coding sequences for human intercellular adhesion molecule-1 (ICAM-1),
CC endothelial leukocyte adhesion molecule-1 (ELAM-1, also known as E-
CC selectin), or vascular cell adhesion molecule-1 (VCAM-1). This sequence
CC targets the 3' untranslated region (nucleotides 2063-2082) of ELAM-1.
CC ICAM-1, ELAM-1, and VCAM-1 represent three of the five cell adhesion
CC molecules involved in the adherence of white blood cells to vascular
CC endothelium. These sequences can be used in a composition for treating
CC allograft rejection. The composition contains one of these sequences in
CC combination with an immunosuppressive agent. The immunosuppressive agent
CC used in the compositions is breguarin, rapamycin, anti-lymphocyte serum,
CC a monoclonal antibody against LFA-1 or an antisense oligonucleotide. The
CC compositions can be used for treating or preventing allograft rejection,
CC such as cardiac or renal allograft rejection. By using these
CC compositions, allograft survival times are extended, and donor-specific
CC transplant tolerance is induced
XX
XX Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15.8; DB 1; Length 20;
XX Best Local Similarity 89.5%; Pred. No. 5.5e+02;
XX Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 839 CTGCTGGGGTCTCTGGCCC 857
Db 19 CTCCTCGGGTCTCTGGCCC 1
XX
RESULT 905
AAA29827/c
ID AAA29827 standard; DNA; 20 BP.
XX
XX AAA29827;
XX
XX 25-AUG-2000 (first entry)
XX
XX Human jun N-terminal kinase kinase-2 antisense oligonucleotide #12.
XX
XX Human; jun N-terminal kinase kinase-2; JNK-2; modulation; tumour;
XX antiinflammatory; cytostatic; antiinfectious; infection; inflammation;
XX detection; antisense therapy; phosphorothioate; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /note= "Phosphorothioate linkages"
XX
XX US6054440-A.
XX
XX 25-APR-2000.
XX
XX 24-JUN-1999; 99US-00344001.
XX
XX 24-JUN-1999; 99US-00344001.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Monia BP, Cowser LM;
XX
XX

```

DR WPI; 2000-338506/29.

XX Antisense compound specifically hybridizing and inhibiting the expression

PT of human Jun N-terminal kinase kinase-2 is useful for treating infection,

PT inflammation and tumor.

XX Claim 3; Col 40; 3lpp; English.

PS The present invention describes an antisense compound (I) of 8-30

CC nucleobases, specifically hybridizing to, and inhibiting expression of,

CC human Jun N-terminal kinase kinase-2 (JNK-2). Also described is a method

CC of inhibiting the expression of human JNK-2 in human cells or tissues,

CC comprising contacting the cells or tissues, with (I), in vitro. (I) has

CC antiinflammatory, cytostatic and antiinfectious activities. (I) is useful

CC for inhibiting the expression of JNK-2 in human cells or tissues and

CC prevents or delays infection, inflammation or tumour formation associated

CC with altered expression of JNK-2. (I) is also useful for detecting the

CC levels of JNK-2 in a sample. The present sequence represents a

CC phosphorothioate antisense oligonucleotide for human JNK-2, from the

CC present invention

XX Sequence 20 BP; 2 A; 12 C; 3 G; 3 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 5.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 997 GGTGGTGGCGGAGAGATG 1015

DB 19 GGTGGCGGCGGAGAGATG 1

RESULT 906

AAZ48939/c

ID AAZ48939 standard; DNA; 20 BP.

XX AAZ48939;

XX 29-MAR-2000 (first entry)

XX Human ELAM-1 antisense inhibitor, ISIS #4729.

XX Antisense inhibitor; human; ICAM-1; intercellular adhesion molecule-1;

KW vascular cell adhesion molecule-1; hyperproliferative disorder; VCAM-1;

KW endothelial leukocyte adhesion molecule-1; ELAM-1; skin condition;

KW cancer; viral infection; tumour; diapedesis; graft versus host disease;

KW arthritis; infection; autoimmune disorder; multiple sclerosis; stroke;

KW juvenile diabetes mellitus; arthritis; myasthenia gravis; therapy;

KW pemphigus vulgaris; systemic lupus erythematosus; acute myocarditis;

KW cardiovascular disorder; dilated cardiomyopathy; ischaemic heart disease;

KW ss.

XX Homo sapiens.

XX WO9961462-A1.

PN 02-DEC-1999.

XX 26-MAY-1999; 99WO-US011548.

XX 27-MAY-1999; 98US-00085759.

XX (ISIS-) ISIS PHARM INC.

PA Bennett CF, Mirabelli CK, Baker BF;

PI WPI; 2000-072600/06.

XX New antisense oligonucleotides, used for treating e.g. inflammatory

PT conditions, psoriasis, graft rejection, cancers, infections,

PT cardiovascular disorders or autoimmune disorders.

XX Example 16; Page 80; 199pp; English.

XX This sequence is an antisense oligonucleotide of the invention. The

CC antisense oligonucleotides are targeted to a nucleic acid encoding a

CC cellular adhesion molecule (CAM) and is capable of modulating the

CC expression of the CAM. They particularly inhibit intercellular adhesion

CC molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), or

CC endothelial leukocyte adhesion molecule-1 (ELAM-1). The antisense

CC oligonucleotides can be used to modulate CAM activity in mediating

CC cell-cell interactions and subsequent cellular and biological responses,

CC e.g. T cell activation, leukocyte transmigration and inflammation. The

CC antisense sequences can be used for modulating the synthesis of a CAM.

CC They can be used for treating an animal suspected of having or being

CC prone to a disease or condition associated with a CAM. Oligonucleotides

CC targeted to ICAM-1 can be used for treating an inflammatory disease or

CC condition e.g. inflammatory bowel disease such as Crohn's disease,

CC colitis or ulcerative colitis, a condition of the skin, e.g. psoriasis or

CC cytotoxic dermatitis, rheumatoid arthritis, allograft rejection, cancer,

CC pneumonia, multiple sclerosis or a viral infection. The ICAM-1 sequences

CC can also be used for reducing corticosteroid use in a patient or for

CC reducing cyclosporine use in a patient. The oligonucleotides can also be

CC used for detection and diagnosis. They can also be used for treating e.g.

CC hyperproliferative disorders, tumours, diapedesis, graft versus host

CC disease, arthritis, infections, autoimmune disorders, e.g. autoimmune

CC thyroid disorders, autoimmune forms of arthritis, multiple sclerosis,

CC some forms of juvenile diabetes mellitus, myasthenia gravis, pemphigus

CC vulgaris, systemic lupus erythematosus, cardiovascular disorders,

CC myocardial ischaemia/reperfusion injury, dilated cardiomyopathy, acute

CC myocarditis, ischaemic heart disease or stroke

XX Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;

SQ

Query Match 0.9%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 5.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 839 CTGCTGGGGTCTCTGGCCC 857

DB 19 CTCCTCGGGTCTCTGGCCC 1

RESULT 907

AAH56368

ID AAH56368 standard; DNA; 20 BP.

XX AAH56368;

XX 06-SEP-2001 (first entry)

DE Escherichia coli groE operon antisense oligonucleotide SEQ ID NO:16.

XX Antisense oligonucleotide; groE; groEL; groES; inhibitor; growth;

KW microorganism; Escherichia coli; Streptococcus pneumoniae; diagnosis;

KW Streptococcus pyogenes; Staphylococcus aureus; Pseudomonas aeruginosa;

KW antibacterial; antiviral; antiproliferative; antisense therapy;

XX microbial infection; ss.

OS Escherichia coli.

XX WO200136625-A2.

PN 25-MAY-2001.

XX 20-NOV-2000; 2000WO-CA001347.

XX 18-NOV-1999; 99US-0166249P.

XX (GENE-) GENESENSE TECHNOLOGIES INC.

PA Wright JA, Young AH, Dugourd D;

PI WPI; 2001-355633/37.

XX Novel antisense compounds targeting nucleic acid encoding groEL or groES

PT gene of microorganism, which hybridize with and inhibit expression of the
 PT genes, useful to inhibit growth of microorganism having the genes.

PS Claim 3; Page 40; 110pp; English.

XX The present invention specifically claims AAH56368 to AAH56832 which are
 CC antisense oligonucleotides to nucleotide sequences encoding groE. More
 CC generally, antisense compounds (I) comprising antisense oligonucleotides
 CC of 5-50 bases targeted to a nucleotide sequence encoding groEL (heat
 CC shock protein (HSP)60) (GL) and groES (HSP10) (GS) gene from a
 CC microorganism, where the antisense compound is complementary to GL or GS
 CC of a microorganism and specifically hybridizes with and inhibits the
 CC expression of GL or GS, is claimed. (I) have antibacterial, antiviral and
 CC antiproliferative activities, and can be used in antisense therapy and
 CC for inhibition of expression of groES or groEL. (I) are useful for
 CC inhibiting expression of GL or GS in cells or tissues in vitro. (I) are
 CC also useful for inhibiting the growth of a microorganism, or inhibiting
 CC the expression of GL or GS gene in a microorganism (a bacterial cell or a
 CC virus) having a GL or GS gene which involves administering to the
 CC microorganism or to a cell infected with the microorganism, (I). (I) are
 CC also useful for treating a mammalian pathological condition mediated by
 CC the microorganisms which involves identifying a eukaryotic organism
 CC having a pathological condition mediated by microorganisms having a GL or
 CC GS gene and administering (I) such that the growth of microorganism is
 CC inhibited. The antisense compounds are utilised for diagnostics,
 CC therapeutics, prophylaxis and as research reagents and kits, e.g., to
 CC prevent or delay microbial infections in humans. They are also useful as
 CC molecular weight markers. AAH56362 to AAH56367 and AAH56833 to AAH56854
 CC represent PCR primers for groE sequences which are used in the
 CC exemplification of the present invention. AAH56855 to AAH56870 represent
 CC groE nucleotide sequence given in the present invention

XX Sequence 20 BP; 13 A; 0 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 5.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 25 GGGGGAGAGGAAAAAAA 43
 ||||| | |||||
 Db 1 GGGGGAAAAAGAAAAAAA 19

RESULT 908

AAH91454

ID AAH91454 standard; DNA; 20 BP.

XX AAH91454;

AC AAH91454;

DT 09-OCT-2001 (first entry)

DE Human inflammatory bowel disease associated polymorphic site #529.

XX Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis;

KW single nucleotide polymorphism; SNP; chromosome 19p13; paternity test;

XX chromosome 5q31-33; forensic test; gene therapy; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FH misc_feature 12

FT /tag= a
 FT /note= "SNP, optionally insertion or deletion at this
 FT position"

XX WO200142511-A2.

PD 14-JUN-2001.

XX 11-DEC-2000; 2000WO-US033632.

XX 10-DEC-1999; 99US-0170257P.

PR 10-APR-2000; 2000US-0196046P.

XX

PA

(WHED) WHITEHEAD INST BIOMEDICAL RES.

PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.

XX

PI

Daly M, Hudson TJ, Lander ES, Rioux J, Siminovitch K;

XX

DR

WPI; 2001-367874/38.

XX

PT

Testing for the presence of polymorphisms associated with inflammatory
 PT bowel disease, using a hybridization assay.

XX

PS

Claim 1; Page 61; 463pp; English.

XX

CC

The present invention describes a method for detecting the presence of
 CC polymorphisms associated with inflammatory bowel diseases such as
 CC ulcerative colitis and Crohn's disease. The methods can be used to detect
 CC the presence of genetic polymorphisms associated with inflammatory bowel
 CC disease and correlating their occurrence with disease states. They may be
 CC used in this way for phenotypic correlations, forensics, paternity
 CC testing, medicine and genetic analysis. The present sequence is a
 CC polymorphic site described in the exemplification of the invention

XX

SQ

Sequence 20 BP; 17 A; 0 C; 2 G; 0 T; 0 U; 1 Other;

Query Match

Best Local Similarity 0.9%; Score 15.8; DB 1; Length 20;

Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 1736 AAAAAAAAAAAAAAAAAA 1755

||||| ||||| ||||| |||||

Db 1 AAAAAAGAAAAAAGAAAA 20

RESULT 909

ABQ96037

ID ABQ96037 standard; DNA; 20 BP.

XX

AC

ABQ96037;

XX

DT

28-OCT-2002 (first entry)

XX

DE

Tumour suppression-related oligonucleotide #1688.

XX

KW

Tumour; cytostatic; antiviral; neuroprotective; nootropic; neuroleptic;
 KW tumour suppression; tumour reversion; apoptosis; viral resistance; human;

KW

viral infection; cell degeneration disease; neurodegeneration; ds;

KW

Alzheimer's disease; schizophrenia; immune disease; inflammatory disease.

OS

Homo sapiens.

XX

XX

FR2819824-A1.

XX

XX

26-JUL-2002.

XX

PF

23-JAN-2001; 2001FR-00000899.

XX

XX

23-JAN-2001; 2001FR-00000899.

XX

PA

(MOLE-) MOLECULAR ENGINES LAB SA.

XX

XX

Telerman A, Amson R, Tuijnder M, Susini L;

XX

DR

WPI; 2002-610803/66.

XX

PT

New nucleic acid implicated e.g. in tumor suppression, useful for
 PT diagnosis of tumors, viral infection and cellular degeneration and for
 PT drug screening.

XX

PS

Claim 1; Page 468; 623pp; French.

XX

CC

The present invention relates to novel human nucleic acid sequences (I).
 CC The present sequence is one such nucleic acid sequence. Expression of (I)
 CC are implicated in tumour suppression or reversion and apoptosis and viral

CC resistance. (I) are useful as probes or primers for detecting,
 CC identifying, measuring and/or amplifying nucleic acid sequences, as
 CC antisense reagents and for recombinant production of polypeptides. (I).
 CC polypeptides (II) encoded by (I), vector containing (I), cells containing
 CC these vectors and antibodies (Ab) against (II) are all useful for
 CC treatment/prevention of viral, tumour and cell degeneration diseases
 CC (especially neurodegeneration, such as Alzheimer's disease and
 CC schizophrenia). Analysing the expression of (I) is also useful for
 CC diagnosis and/or prognosis of such diseases. Transgenic animals carrying
 CC (I) are used for studying the aetiology of these diseases (also immune
 CC and inflammatory diseases). Note: In the present specification, SEQ ID 1
 CC to 2280 are claimed in Claim 1, however only SEQ ID 1 to 2270 are shown
 CC in the specification

XX Sequence 20 BP; 17 A; 1 C; 1 G; 0 T; 0 U; 1 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 5.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755

DB 1 AAAAAAAAAAAAAAAAAAGGAAAA 20

RESULT 910
 AB282707/c
 ID AB282707 standard; DNA; 20 BP.

AC AB282707;

DT 14-MAY-2003 (first entry)

DE Human HSL chimeric phosphorothioate oligonucleotide SEQ ID NO:96.

XX Hormone-sensitive lipase; antisense oligonucleotide; inhibitor; obesity;
 KW phosphorothioate; antidiabetic; anorectic; cytostatic; antisense therapy;
 KW abnormal metabolic condition; hyperlipidaemia; type 2 diabetes; cancer;
 KW hyperproliferative disorder; human; ss.

OS Homo sapiens.
 OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= a
	/mod_base= OTHER
	/note= "phosphorothioate linkages"
modified_base	1..5
	/*tag= b
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) wing"
modified_base	16..20
	/*tag= c
	/mod_base= OTHER
	/note= "2'-O-methoxyethyl (2'-MOE) wing"

WO2003010139-A2.

PD 06-FEB-2003.

XX 15-JUL-2002; 2002WO-US022672.

XX 26-JUL-2001; 2001US-00915814.

PA (ISIS-) ISIS PHARM INC.

PI Butler MM, Watt AT, Freier SM, Wyatt JR;

DR WPI; 2003-239411/23.

XX New antisense oligonucleotides targeted against nucleic acids encoding
 PT hormone-sensitive lipase, useful for treating abnormal metabolic

PT condition, e.g. hyperlipidemia and obesity, or a hyperproliferative
 PT disorder, e.g. cancer.

PS Example 15; Page 89; 167pp; English.

XX The present invention describes a compound (I) 8-50 nucleobases in length
 CC targeted to a nucleic acid molecule encoding a hormone-sensitive lipase
 CC (HSL) or a splice variant of HSL. The compound specifically hybridises
 CC with and inhibits the expression of HSL or a splice variant of HSL, or
 CC specifically hybridises with at least an 8-nucleobase portion of an
 CC active site on a nucleic acid molecule encoding HSL. (I) have anorectic,
 CC antidiabetic and cytostatic activities, and can be used in antisense
 CC therapy. (I) is useful for treating an animal, particularly human,
 CC suspected of having an abnormal metabolic condition such as obesity,
 CC hyperlipidaemia, type 2 diabetes, a hyperproliferative disorder such as
 CC cancer (e.g. pituitary, colorectal, breast, testicular, pulmonary or
 CC epithelial cancer). (I) is also useful in modulating blood glucose
 CC levels, particularly plasma or serum glucose levels, in a diabetic
 CC animal. The present sequence represents a human hormone-sensitive lipase
 CC chimeric phosphorothioate antisense oligonucleotide, which is used in an
 CC example from the present invention

XX Sequence 20 BP; 4 A; 5 C; 9 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 5.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 167 GGGCCACCTGGCTGCCCCC 185

DB 19 GGCCTACCTGGCTGCCCTC 1

RESULT 911

AB222800

ID AB222800 standard; DNA; 20 BP.

AC AB222800;

DT 02-APR-2003 (first entry)

DE Human heparanase phosphorothioate oligonucleotide SEQ ID NO:1.

XX Human; heparanase; phosphorothioate; antisense oligonucleotide;
 KW cytostatic; gene therapy; tumour; ss.

XX Homo sapiens.

OS Synthetic.

Key	Location/Qualifiers
modified_base	1..20
	/*tag= a
	/mod_base= OTHER
	/note= "phosphorothioate linkages"

XX WO2003004705-A1.

XX 16-JAN-2003.

XX 01-JUL-2002; 2002WO-US020636.

XX 05-JUL-2001; 2001US-00899440.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Stein C;

XX WPI; 2003-201558/19.

XX New oligonucleotide having a sequence complementary to a sequence of
 PT ribonucleic acid encoding a heparanase, useful for preparing a
 PT composition for treating tumor.

XX

PS Example; Page 25; 48pp; English.

CC The present invention describes an oligonucleotide having a sequence complementary to a sequence of ribonucleic acid encoding a heparanase. The oligonucleotide hybridises with the ribonucleic acid under conditions of high stringency and has a sequence comprising 10-40 bp. The internucleoside linkages of the oligonucleotide comprise at least one phosphorothioate linkage. Hybridisation of the oligonucleotide to the ribonucleic acid inhibits expression of the heparanase, where inhibition of heparanase means at least a 50% reduction in the quality of heparanase in a cell; (2) a method of inhibiting expression of a heparanase in a cell; (3) a composition comprising the above oligonucleotide in an amount effective to inhibit the expression of heparanase in the cell and a carrier; and (3) a method of treating a tumour in a subject comprises administering to the subject an amount of the above oligonucleotide effective to inhibit expression of a heparanase in the subject. Heparanase antisense oligonucleotides have cytostatic activity, can be used in gene therapy, and can be used for preparing a composition for treating tumours. The present sequence represents a human heparanase phosphorothioate antisense oligonucleotide, which is used in the exemplification of the present invention

XX SQ Sequence 20 BP; 1 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 5.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 166 GGGCCACCTGGTGGCC 184
 |||||
 Db 2 GGGTCACCTGGTGTCC 20
 |||||

RESULT 912
 ADC39031/c
 ID ADC39031 standard; DNA; 20 BP.

XX AC ADC39031;

XX DT 18-DEC-2003 (first entry)

XX DE Human ELAM-1 targeted primer #18.

XX KW ss; primer; immunosuppressive; antisense therapy;
 KW corneal allograft rejection; intercellular adhesion molecule-1; ICAM-1;
 KW extracellular adhesion molecule-1; ELAM-1;
 KW vascular cell adhesion molecule-1; VCAM-1; corneal explant.

XX OS Synthetic.

XX OS Homo sapiens.

XX FN WO2003032920-A2.

XX PD 24-APR-2003.

XX PF 16-OCT-2002; 2002WO-US033236.

XX PR 18-OCT-2001; 2001US-00982262.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Mirabelli CK;

XX PI WPI; 2003-403142/38.

XX PT Inhibiting corneal allograft rejection, by contacting an allograft with a formulation having an oligonucleotide targeted to intercellular adhesion molecule-1, extracellular adhesion molecule-1 or vascular cell adhesion molecule-1.

XX PS Example 13; SEQ ID NO 57; 106pp; English.

XX CC The invention relates to a method of inhibiting corneal allograft

CC rejection, by contacting the allograft with a topical formulation comprising an antisense oligonucleotide targeted to intercellular adhesion molecule-1 (ICAM-1), extracellular adhesion molecule-1 (ELAM-1) or vascular cell adhesion molecule-1 (VCAM-1). The oligonucleotide is useful for inhibiting corneal allograft rejection or for preserving a corneal explant ex vivo, where the explant is human. This sequence corresponds to one of the oligonucleotide of the invention.

XX SQ Sequence 20 BP; 6 A; 5 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 20;
 Best Local Similarity 89.5%; Pred. No. 5.5e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 839 CTGCTGGGTCTCTGGCC 857
 |||||
 Db 19 CTCTCGGTCTCTGGCC 1
 |||||

RESULT 913
 ADC35554/c
 ID ADC35554 standard; DNA; 20 BP.

XX AC ADC35554;

XX DT 18-DEC-2003 (first entry)

XX DE Human CD81/TAPA-1 antisense oligonucleotide #14.

XX KW Antisense; ss; human; CD81; TAPA-1; tetraepanin; viral infection;
 KW cocaine addiction; autoimmune disorder; antiinflammatory; antibacterial;
 KW virucide; antiparasitic; inflammatory disorder; parasitic infection;
 KW bacterial infection.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT modified_base 1..20
 /*tag= b
 /mod_base= OTHER
 /note= "phosphorothioate backbone and all cytidines are 5-methyl cytidines"

FT modified_base 1..5
 /*tag= a
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"

FT modified_base 16..20
 /*tag= c
 /mod_base= OTHER
 /note= "2'-methoxyethyl nucleotide"

XX FN US2003113914-A1.

XX PD 19-JUN-2003.

XX PF 10-DEC-2001; 2001US-00006430.

XX PR 10-DEC-2001; 2001US-00006430.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Graham MJ, Dobie K;

XX PI WPI; 2003-810907/76.

XX PT Novel compound hybridizing with nucleic acid molecule encoding CD81 and inhibiting the expression of CD81, useful for treating infections and disease associated with expression of CD81 such as inflammation disorder.

XX PS Claim 3; SEQ ID NO 26; 55pp; English.

XX CC The invention relates to a compound (antisense oligonucleotide) hybridising with the eighth nucleobase portion of an active site on a

CC nucleic acid molecule encoding CD81 (also known as TAPA-1, a tetraspanin)
CC and inhibiting the expression of CD81. Also included is a composition
CC comprising the antisense oligonucleotide and a carrier or a diluent. The
CC antisense oligonucleotide is useful for inhibiting the expression of CD81
CC in cells or tissues. The antisense oligonucleotide is also useful for
CC treating infections preferably viral, bacterial and parasitic and
CC diseases such as inflammatory disorders and autoimmune disorders. The
CC disease or condition is characterised by chemical dependency (e.g.
CC cocaine addiction). The present sequence is a CD81 antisense
CC oligonucleotide of the invention.

XX Sequence 20 BP; 4 A; 8 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 20;

Best Local Similarity 89.5%; Pred. No. 5.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1146 GGGCTGCTACGTGGCCACC 1164

Db 19 GGGCTGCTACGGGGCCATC 1

RESULT 914

AAZ26004/c

ID AAZ26004 standard; DNA; 21 BP.

XX

AC AAZ26004;

XX

DT 30-NOV-1999 (first entry)

XX Human polymorphic region 193.

DE

XX Polymorphism; human; inhibitor; cancer; treatment; cell growth; LOH;

XX cell viability; loss of heterozygosity; precancerous condition; ASI;

XX allele specific inhibitor; somatic cell; diagnosis; prevention;

XX atherosclerotic plaque; premalignant metaplastic lesion; endometriosis;

XX dysplastic lesion; benign tumour; polycystic kidney disease; transplant;

XX graft versus host disease; malignant cell removal; bone marrow; ss.

XX

OS Homo sapiens.

XX

FN WO9841648-A2.

XX

PD 24-SEP-1998.

XX

PF 19-MAR-1998; 98WO-US005419.

XX

PR 20-MAR-1997; 97US-0041057P.

XX

PA (VARI-) VARIAGENICS INC.

XX

PI Housman D, Ledley FD, Stanton VP;

XX

DR WPI; 1998-521232/44.

XX

PT Identifying target genes for allele-specific drugs - used for diagnosis,

XX prevention and treatment of, e.g. cancers, atherosclerotic plaque,

XX dysplastic lesions, endometriosis or graft versus host disease.

XX

PS Disclosure; Fig 7; 605pp; English.

XX

CC This invention describes a novel method for identifying an inhibitor

CC potentially useful for treatment of cancer, where the inhibitor is active

CC on a gene vital for cell growth or viability, and where the gene is

CC subject to loss of heterozygosity (LOH) in a cancer. The inhibitor is

CC used for preventing the development of cancer in a patient having a

CC precancerous condition, by administering to the patient a first allele

CC specific inhibitor (ASI) targeted to an allele of a first essential gene

CC present in cells of the precancerous condition, where the normal somatic

CC cells of the patient are heterozygous for the first gene, the inhibitor

CC is active on at least one but less than all allelic forms of the gene

CC present in a population and targets only one allelic form present in the

CC normal somatic cells, and the first gene. The products and methods can be

CC used in the diagnosis, prevention and treatment of LOH disorders, e.g.
CC cancers, atherosclerotic plaques, premalignant metaplastic or dysplastic
CC lesions, benign tumours, endometriosis, polycystic kidney disease, and
CC graft versus host disease. The method can also be used to remove
CC malignant cells from bone marrow transplants. AAZ25812-226825 represent
XX human polymorphic sites described in the method of the invention

SQ Sequence 21 BP; 2 A; 6 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 21;

Best Local Similarity 89.5%; Pred. No. 5.7e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 459 GAGCACACGCTGGCCAAA 477

Db 19 GAGCACTACGCTGGCCAAA 1

RESULT 915

AAZ76115/c

ID AAZ76115 standard; DNA; 21 BP.

XX

AC AAZ76115;

XX

DT 10-SEP-2001 (first entry)

XX Human biallelic marker downstream amplification primer SEQ ID NO:10471.

DE

XX Human genome; biallelic marker; high density disequilibrium map;

XX genomic map; haplotype; phenotype; polymorphic base; genotyping;

XX haplotyping; hybridisation; identification; characterisation;

XX amplification; single nucleotide polymorphism; SNP; PCR primer;

XX diagnosis; ss.

XX

OS Homo sapiens.

XX

FN WO9954500-A2.

XX

PD 28-OCT-1999.

XX

PF 21-APR-1999; 99WO-IB000822.

XX

PR 21-APR-1998; 98US-0082614P.

XX

PR 23-NOV-1998; 98US-0109732P.

XX

PA (GEST) GENSET.

XX

PI Cohen D, Blumenfeld M, Chumakov I;

XX

DR WPI; 2000-013267/01.

XX

PT Novel biallelic markers used to construct a high density disequilibrium

XX map of the human genome.

XX

PS Claim 9; Page 2463; 2745pp; English.

XX

CC AAZ65654 to AAZ69578 represent human biallelic markers from the present

CC invention, which contain a polymorphic base at position 24 of their

CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification

CC primers for the biallelic markers. The biallelic markers of the invention

CC have a variety of uses: they can be used for high density mapping of the

CC human genome, and in complex association studies and haplotyping studies.

CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the

CC identification of the targets for the development of pharmaceutical

CC agents and diagnostic methods, as well as the characterisation of the

CC differential efficacious responses to and side effects from

CC pharmaceutical agents acting on a disease as well as other treatment.

CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and

CC 3367, are not actually given a sequence in the Sequence Listing from the

XX present invention

SQ Sequence 21 BP; 11 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 89.5%; Pred. No. 5.7e+02;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 289 GTCAATTTTGGCCCTTC 307
 Db 19 GTCAATTTTGGCTCTTC 1

RESULT 916

AAV19118/c
 ID AAC80155 standard; DNA; 21 BP.

XX AC AAC80155;
 XX AC AAC80155;

DT 03-MAY-2001 (first entry)

DE Forward primer #26 used for amplification of HLA-A exon 3.

XX HLA-A; HLA-B; HLA-C; typing; primer; human; ss.

XX Homo sapiens.

OS Synthetic.

XX WO200061795-A2.

PD 19-OCT-2000.

PF 05-APR-2000; 2000WO-EP002998.

XX 09-APR-1999; 99EP-00870068.

PR 11-JUN-1999; 99US-0138614P.

PA (INNO-) INNOGENETICS NV.

PI De Canck I, Rombout A, Rossau R;

XX WPI; 2000-647426/62.

XX Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
 primer sets, useful for subtyping or typing of HLA Class I alleles.

PS Claim 4; Page 37; 128pp; English.

XX The present invention relates to a method for the locus-specific,
 separate amplification of exon 2, exon 3, and/or exon 4 of human
 leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 for subtyping or typing of HLA class I alleles. The present sequence is
 an amplification primer used in the method

XX Sequence 21 BP; 3 A; 10 C; 7 G; 0 T; 0 U; 1 Other;

Query Match 0.9%; Score 15.8; DB 1; Length 21;
 Best Local Similarity 81.0%; Pred. No. 5.7e+02;
 Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 182 CCCCAGACCGCCGAGCCCG 202
 Db 1 CCCCAGACCGCCGAGCCCG 21

RESULT 917

AAV19118/c
 ID AAV19118 standard; DNA; 17 BP.

XX AC AAV19118;

DT 28-AUG-1998 (first entry)

DE Anchored oligo(T) primer.

XX

KW Secreted apoptosis-related protein; SARP; mSARP1; mouse; prostate cancer;
 XX breast cancer; diagnosis; gene therapy; PCR; primer; ss.
 OS Synthetic.

PN WO9813493-A2.

XX 02-APR-1998.

XX 24-SEP-1997; 97WO-US017154.

XX 24-SEP-1996; 96US-0026603P.

PR 11-OCT-1996; 96US-0028363P.

XX (LXRB-) LXR BIOTECHNOLOGY INC.

XX Umansky S, Melkonyan H;

XX WPI; 1998-230704/20.

XX New secreted apoptosis-related proteins - useful for modulating
 PT apoptosis, particularly for treatment of prostatic or breast cancer, also
 PT for diagnosis and monitoring of disease.

PS Example 1; Page 30; 101pp; English.

XX This oligo(T) synthetic oligonucleotide was used for first strand cDNA
 CC synthesis from total RNA isolated from either logarithmically growing or
 CC quiescent 10T1/2 mouse fibroblast cells. It was also used with an
 CC arbitrary d(N10) primer in PCR. The PCR products were used in a
 CC differential display to identify the mSARP1 gene (see AAV19112) that
 CC codes for novel murine secreted apoptosis-related protein mSARP1 (see
 CC AAV37814). The invention relates to SARP polynucleotides (see also
 CC AAV19113-15) and polypeptides (see also AAV37815-17), antibodies specific
 CC for SARP, and use of such polynucleotides and antibodies in diagnostic
 CC and therapeutic methods, and methods for treating diseases related to the
 CC regulation of SARP expression in tissue and body fluid samples, including
 CC cancers

XX Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.9%; Score 15.6; DB 1; Length 17;

Best Local Similarity 88.2%; Pred. No. 5.2e+02;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAATAAAAAA 1751

Db 17 SNAATAAAAAAATAAAAA 1

RESULT 918

AAV18371/c

ID AAV18371 standard; DNA; 17 BP.

XX AC AAV18371;

XX 11-MAY-1999 (first entry)

DE RT-PCR primer of the invention SEQ ID 12.

XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

XX Synthetic.

XX JPI1032765-A.

XX 09-FEB-1999.

XX 18-JUL-1997; 97JP-00208312.

XX 18-JUL-1997; 97JP-00208312.

XX (TAKI) TAKARA SHUZO CO LTD.

CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0

Qy 1732 TTACAAAAA 1748
||| |||||
Db 17 TTA 1

RESULT 920
AA25456/C
ID AA25456 standard; DNA; 17 BP.
XX
AC AA25456;
XX
DT 19-JUL-2000 (first entry)
XX
DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1954.
XX
KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX
PN W09954459-A2.
XX
PD 28-OCT-1999.
XX
PF 19-APR-1999; 99WO-US008547.
XX
PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
DR WPI; 2000-013248/01.
XX
PT New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
XX
PS Claim 77; Page 79; 148pp; English.

CC The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphorothioate
CC link, having endonuclease activity, (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention

XX SQ Sequence 17 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 5.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1730 GTTTACAAAAA 1746
 |||||
 Db 17 GTATACAAAAA 1

RESULT 921
 AAA25455/c
 ID AAA25455 standard; DNA; 17 BP.
 XX AC
 XX AAA25455;
 XX DT 19-JUL-2000 (first entry)
 XX DE
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1953.
 DE KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX OS Homo sapiens.
 XX PN WO9954459-A2.
 XX PD 28-OCT-1999.
 XX PF 19-APR-1999; 99WO-US008547.
 XX PR 20-APR-1998; 98US-0082404P.
 XX PR 23-JUN-1998; 98US-00103636.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX DR WPI; 2000-013248/01.
 XX PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX PS Claim 77; Page 79; 148pp; English.
 XX CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype.
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX SQ Sequence 17 BP; 2 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 5.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1731 TTTTACAAAAA 1747
 |||||
 Db 17 TATACAAAAA 1

RESULT 922
 AAA25457/c
 ID AAA25457 standard; DNA; 17 BP.
 XX AC
 XX AAA25457;
 XX DT 19-JUL-2000 (first entry)
 XX DE
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1955.
 DE KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX OS Homo sapiens.
 XX PN WO9954459-A2.
 XX PD 28-OCT-1999.
 XX PF 19-APR-1999; 99WO-US008547.
 XX PR 20-APR-1998; 98US-0082404P.
 XX PR 23-JUN-1998; 98US-00103636.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX DR WPI; 2000-013248/01.
 XX PT New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX PS Claim 77; Page 80; 148pp; English.
 XX CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype.
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention

XX SQ Sequence 17 BP; 2 A; 1 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 17;

Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1729 AGTTTACAAAAA 1745
DB 17 AGTATACAAAAA 1

RESULT 923
ABK02364
ID ABK02364 standard; RNA; 17 BP.
XX
AC ABK02364;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Amberzyme #36.
XX

Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic; cerebroprotective; neurotropic; neuroprotective; antiparkinsonian; muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme; DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia; B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia; human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma; MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia; inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.
OS Synthetic.
XX
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
DR
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury.
XX
PS Claim 88; Page 131; 200pp; English.
XX

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to

CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NOGO-targeting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg²⁺. Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an amberzyme molecule of the invention

XX
SQ Sequence 17 BP; 7 A; 0 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 861 AGGAAGAGGAGGAG 877
DB 1 AGGAGGAGGAGGAG 17

RESULT 924
ABA91530/c
ID ABA91530 standard; DNA; 17 BP.
XX
AC ABA91530;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA-RNA-DNA oligonucleotide AGT02014 used to test RNase H cleavage.
XX
KW DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 8
FT /*tag= a
FT /label= RNA
XX
PN WO200206531-A2.
XX
PD 24-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US022166.
XX
PR 14-JUL-2000; 2000US-00616761.
PR 30-MAR-2001; 2001US-00823647.
XX
PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI Dattagupta N;
XX
DR WPI; 2002-171819/22.
XX
PT Probes for detecting target nucleotide sequence in sample, has sequence that forms hairpin structure having a double-stranded segment and single-stranded loop collectively forming region complementary to target sequence.
XX
PS Example 4; Page 49; 72pp; English.
XX
CC The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide AGT02014. This is one of a set of oligonucleotides (see ABA91527-30) used

CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric
 CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of
 CC the set had a different number of ribonucleotides, 1 in the present case.
 CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
 CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
 CC minutes. The results showed that 4 ribonucleotides were the minimum
 CC number for RNA cleavage. The invention provides probes for nucleic acid
 CC hybridisation. The probes form a hairpin structure comprising a double-
 CC stranded stem and a single-stranded loop, and are capable of both
 CC intramolecular and intermolecular hybridisation. The double-stranded stem
 CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
 CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
 CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
 CC can be removed. Arrays and methods for nucleic acid hybridisation using
 CC the probes are provided

XX
 SQ Sequence 17 BP; 1 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 94.1%; Pred. No. 5.5e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1752
 Db ||||| ||||| |||||
 17 AAAAAAAAAATAAAAAA 1

RESULT 925
 ABK1820
 ID ABK1820 standard; RNA; 17 BP.
 AC
 AC ABK1820;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human ERG DNazyme target sequence Seq ID No 1467.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulvular; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 FN WO20018124-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 XX
 DR WPI; 2002-082995/11.
 XX
 PT Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 PS Claim 4; Page 92; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention

XX
 SQ Sequence 17 BP; 2 A; 12 C; 2 G; 0 T; 1 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 5.5e+02;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 268 GCACCTCCAGCCACCC 284
 Db ||:|||||||
 1 GCCCUCACGCCACCC 17

RESULT 926
 AAD44151/C
 ID AAD44151 standard; DNA; 17 BP.
 XX
 AC AAD44151;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Oligo-AT PCR primer #2 used to illustrate the method of the invention.
 XX
 KW Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
 KW primer; ss.
 XX
 OS Unidentified.
 XX
 FN US6277571-B1.
 XX
 PD 21-AUG-2001.
 XX
 PF 30-SEP-1998; 98US-00163485.
 XX
 PR 03-OCT-1997; 97US-00943162.
 PR 03-OCT-1997; 97US-0108152P.
 XX
 XX (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
 XX
 XX Fillmore H, Broadus W, Gillies G;
 PI WPI; 2002-412824/44.
 XX
 DR WPI; 2002-412824/44.
 XX
 PT Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.
 XX
 PS Example; Fig 1D; 19pp; English.
 XX
 CC The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or


```

RESULT 929
ACC63788/c
ID ACC63788 standard; DNA; 17 BP.
XX
AC ACC63788;
XX
DT 01-JUL-2003 (first entry)
XX
DE Murine oligonucleotide associated with tumour suppression, SEQ ID 1035.
XX
KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
OS Mus musculus.
XX
PN WO2003025176-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004210.
XX
PR 17-SEP-2001; 2001FR-00011979.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijinder M;
XX
XX WPI; 2003-333167/31.
XX
DR New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; Page 152; 738pp; French.
XX
CC The present invention relates to murine oligonucleotides (ACC62754-
CC ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
SQ Sequence 17 BP; 2 A; 7 C; 3 G; 5 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 17;
Best Local Similarity 94.1%; Pred. No. 5.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 102 GTGAAGGCCACAGGCTC 118
| | | | | | | | | | | | | | | | | |
Db 17 GTGAAGGCCACAGGATC 1

RESULT 930
AAQ20109/c
ID AAQ20109 standard; DNA; 18 BP.
XX
AC AAQ20109;
XX
DT 01-APR-1992 (first entry)
XX
DE Cross-linking oligomer 943 to target human TNF Receptor mRNA.
XX
KW deoxyribonucleic acid; major groove; ethanoino group;
KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW cross-linking group; ss.

```

```

XX Synthetic.
OS Key Location/Qualifiers
XX modified_base 5
FT /*tag= a
FT /mod_base= OTHER
FT /note= "N-methyl-8-oxo-2'-deoxyadenine"
FT 18
FT /*tag= b
FT /mod_base= OTHER
FT /note= "N4N4-ethanocytosine"
XX WO9118997-A.
XX 12-DEC-1991.
XX 25-MAY-1990; 90US-00529346.
XX 25-MAY-1990; 90US-00529346.
XX 14-JAN-1991; 91US-00640654.
XX (GILE-) GILEAD SCIE INC.
XX Matteucci MD, Krawczyk S;
XX WPI; 1992-007480/01.
XX New sequence-specific non-photo-activated crosslinking agents - bind to
PT the major groove of duplex DNA and are esp. useful for treating latent
PT infections e.g. HIV.
XX Example 4; Page 27; 42pp; English.
XX The oligomer was designed to target human TNF receptor mRNA beginning at
CC nucleotide 2354 and to covalently cross-link to the target via the N4N4-
CC ethanocytosine group. See also AAQ20108
XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1752
| | | | | | | | | | | | | | | | | |
Db 17 AAAAAAAAAAAAAAAAAA 1

RESULT 931
AAQ20108/c
ID AAQ20108 standard; DNA; 18 BP.
XX
AC AAQ20108;
XX
DT 01-APR-1992 (first entry)
XX
DE Cross-linking oligomer 942 to target human TNF Receptor mRNA.
XX
KW deoxyribonucleic acid; major groove; ethanoino group;
KW tumour necrosis factor; receptor; messenger RNA; aziridinylcytosine;
KW cross-linking group; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 5
FT /*tag= a
FT /mod_base= m5c
FT 18
FT /*tag= b
FT /mod_base= OTHER
FT /note= "N4N4-ethanocytosine"

```


DR WPI; 1992-217083/26.
 XX New oligomers contg. modified bases - which form a triplex with G-C
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
 PT herpes malignancy and inflammation.
 XX Claim 11; Page 64; 77pp; English.
 XX The sequence depicts a HUMNFR (tumour necrosis factor receptor) mRNA
 CC sequence beginning at nucleotide 2354. The sequence is a viral duplex
 CC sequence contg. a purine-rich region concentrated on one chain of the
 CC duplex. The sequence may be prep'd. by standard DNA synthesis. The HUMNFR
 CC duplex sequence is used as a target for novel oligomers which are capable
 CC of forming a triplex at physiological pH by coupling into the major
 CC groove of the DNA duplex. Three such oligomers TNFR 941-32 are capable of
 CC forming a triplex with this sequence. The oligomers are used in the
 CC treatment of inflammation. Similar oligomers may be used to target viral
 CC DNA duplexes specific for HIV, herpes and other viruses. The triple
 CC helices form under mild conditions thus assays may be carried out without
 CC subjecting the test specimen to harsh conditions. The oligomer is able to
 CC inhibit gene expression, as verified by in vitro systems. See also
 CC AAQ25452-25500 and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN
 CC field.)
 XX Sequence 18 BP; 16 A; 0 C; 2 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.9%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 5.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 1 AAAAAAAAAAAAAAAAAA 17
 RESULT 934
 AAQ30448/c
 ID AAQ30448 standard; DNA; 18 BP.
 XX AAQ30448;
 XX 25-MAR-2003 (revised)
 DT 07-DEC-1992 (first entry)
 XX Oligomer TNFR943 for forming triplex with HUMNFR target duplex.
 XX Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
 KW HPV; malignancy; hepatitis; inflammation; ss.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX modified_base 5 /*tag= a
 FT /mod_base= OTHER
 FT /note= "N6 methyl-8-oxo-2' deoxyadenine"
 FT modified_base 18
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 XX WO9209705-A1.
 XX 11-JUN-1992.
 XX 25-NOV-1991; 91WO-US008811.
 XX 23-NOV-1990; 90US-00617907.
 PR 18-JAN-1991; 91US-00643382.
 PR 08-APR-1991; 91US-00683420.
 PR 17-APR-1991; 91US-00866544.
 PR 17-APR-1991; 91US-00866546.
 PR 17-APR-1991; 91US-00866547.

PR 27-SEP-1991; 91US-00766733.
 XX (GILE-) GILEAD SCI INC.
 XX Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 XX WPI; 1992-217083/26.
 XX New oligomers contg. modified bases - which form a triplex with G-C
 PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
 PT herpes malignancy and inflammation.
 XX Claim 12; Page 72; 77pp; English.
 XX The synthetic oligomer is capable of forming a triplex at physiological
 CC pH with a purine rich target sequence by coupling into the major groove
 CC of the duplex. The specific target sequence of this oligomer is the human
 CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
 CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
 CC and others like it are useful in diagnosis and therapy of diseases
 CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
 CC hepatitis B, herpes, malignant tumours and inflammation. The triple
 CC helices form under mild conditions thus assays may be carried out without
 CC subjecting the test specimen to harsh conditions. See also AAQ25452-25501
 CC and AAQ30226-447. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PD field.)
 XX Sequence 18 BP; 1 A; 1 C; 0 G; 16 T; 0 U; 0 Other;
 SQ Query Match 0.9%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 5.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 935
 AAQ30447/c
 ID AAQ30447 standard; DNA; 18 BP.
 XX AAQ30447;
 XX 25-MAR-2003 (revised)
 DT 07-DEC-1992 (first entry)
 XX Oligomer TNFR942 for forming triplex with HUMNFR target duplex.
 XX Human tumour necrosis factor receptor mRNA; AIDS; modified; HIV; RSV;
 KW HPV; malignancy; hepatitis; inflammation; ss.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX modified_base 5 /*tag= a
 FT /mod_base= m5c
 FT modified_base 18
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "OTHER= N4 N4 ethanocytosine"
 XX WO9209705-A1.
 XX 11-JUN-1992.
 XX 25-NOV-1991; 91WO-US008811.
 PR 23-NOV-1990; 90US-00617907.
 PR 18-JAN-1991; 91US-00643382.
 PR 08-APR-1991; 91US-00683420.
 PR 17-APR-1991; 91US-00866544.
 PR 17-APR-1991; 91US-00866546.
 PR 17-APR-1991; 91US-00866547.

```

PR 17-APR-1991; 91US-00686546.
PR 17-APR-1991; 91US-00686547.
PR 27-SEP-1991; 91US-00766733.
XX
PA (GILE-) GILEAD SCI INC.
XX
PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;
XX
DR WPI; 1992-217083/26.
XX
PT New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
XX
PS Claim 12; Page 72; 77pp; English.
XX
CC The synthetic oligomer is capable of forming a triplex at physiological
CC pH with a purine rich target sequence by coupling into the major groove
CC of the duplex. The specific target sequence of this oligomer is the human
CC tumour necrosis factor receptor mRNA beginning at nucleotide 2354 contg.
CC a purine rich sequence concd. on one strand of the duplex. The oligomer,
CC and others like it are useful in diagnosis and therapy of diseases
CC characterised by specific DNA duplex targets, e.g. HPV, HER, HIV,
CC hepatitis B, herpes, malignant tumours and inflammation. The triple
CC helices form under mild conditions thus assays may be carried out without
CC subjecting the test specimen to harsh conditions. See also AAO25452-25501
CC and AAO30226-448. (Updated on 25-MAR-2003 to correct PN field.) (Updated
CC on 25-MAR-2003 to correct PD field.)
XX
SQ Sequence 18 BP; 0 A; 2 C; 0 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AAAAAAAAAAAAAAAAAA 1751

RESULT 936
AAV54170/c
ID AAV54170 standard; cDNA; 18 BP.
XX
AC AAV54170;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 7.
XX
PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
immunohistological staining.
XX
Synthetic.
XX
WO9839437-A1.
XX
11-SEP-1998.
XX
05-MAR-1998; 98WO-JP000905.
XX
05-MAR-1997; 97JP-00050302.
XX
(KYOW ) KYOWA HAKKO KOGYO KK.
XX
Sakaki Y;
XX
WPI; 1998-495844/42.
XX
Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
treating diseases associated with apoptosis.
XX
Example 1; Page 49; 70pp; Japanese.
XX
This is the nucleotide sequence of a PCR primer used in the method of the
invention, involving the use of novel apoptosis-related DNAs and
proteins. The inventions can be used as diagnostic reagents for apoptosis
e.g. (monoclonal) antibodies for the protein, as a reagent in
immunohistological staining, as apoptosis inhibitors. It can also be used
for treatment of apoptosis-related diseases
XX
Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTAACAAAAAAAAAAAAAAAAA 1748
DB 18 TTAACAAAAAAAAAAAAAAAAA 2

RESULT 938
AAV54169/c

```

```

XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
DB 18 CAAAAAAAAAAAAAAAAA 2

RESULT 937
AAV54164/c
ID AAV54164 standard; cDNA; 18 BP.
XX
AC AAV54164;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 1.
XX
PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
immunohistological staining.
XX
Synthetic.
XX
WO9839437-A1.
XX
11-SEP-1998.
XX
05-MAR-1998; 98WO-JP000905.
XX
05-MAR-1997; 97JP-00050302.
XX
(KYOW ) KYOWA HAKKO KOGYO KK.
XX
Sakaki Y;
XX
WPI; 1998-495844/42.
XX
Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
treating diseases associated with apoptosis.
XX
Example 1; Page 47; 70pp; Japanese.
XX
This is the nucleotide sequence of a PCR primer used in the method of the
invention, involving the use of novel apoptosis-related DNAs and
proteins. The inventions can be used as diagnostic reagents for apoptosis
e.g. (monoclonal) antibodies for the protein, as a reagent in
immunohistological staining, as apoptosis inhibitors. It can also be used
for treatment of apoptosis-related diseases
XX
Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAAAAAAAAAAAAA 1748
DB 18 TTACAAAAAAAAAAAAAAAA 2

RESULT 938
AAV54169/c

```

ID AAV54169 standard; cDNA; 18 BP.
 XX AC AAV54169;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 6.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.
 XX OS Synthetic.
 XX XX WO9839437-A1.
 XX PD 11-SEP-1998.
 XX PF 05-MAR-1998; 98WO-JP000905.
 XX PR 05-MAR-1997; 97JP-00050302.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX XX WPI; 1998-495844/42.
 XX XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX PT treating diseases associated with apoptosis.
 XX PS Example 1; Page 49; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 XX CC invention, involving the use of novel apoptosis-related DNAs and
 XX CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 XX CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 XX CC immunohistological staining, as apoptosis inhibitors. It can also be used
 XX CC for treatment of apoptosis-related diseases
 XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 5.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 AAAAAAAAAAAAAAAAAA 1750
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 939
 AAV54172/c
 ID AAV54172 standard; cDNA; 18 BP.
 XX AC AAV54172;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 9.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.
 XX OS Synthetic.
 XX XX WO9839437-A1.
 XX PD 11-SEP-1998.
 XX PF 05-MAR-1998; 98WO-JP000905.
 XX PR 05-MAR-1997; 97JP-00050302.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX XX WPI; 1998-495844/42.
 XX XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX PT treating diseases associated with apoptosis.
 XX PS Example 1; Page 49; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 XX CC invention, involving the use of novel apoptosis-related DNAs and
 XX CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 XX CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 XX CC immunohistological staining, as apoptosis inhibitors. It can also be used
 XX CC for treatment of apoptosis-related diseases
 XX SQ Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 5.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1734 AAAAAAAAAAAAAAAAAA 1750
 DB 18 AAAAAAAAAAAAAAAAAA 2
 RESULT 939
 AAV54172/c
 ID AAV54172 standard; cDNA; 18 BP.
 XX AC AAV54172;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 9.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.
 XX OS Synthetic.
 XX XX WO9839437-A1.
 XX PD 11-SEP-1998.
 XX PF 05-MAR-1998; 98WO-JP000905.
 XX PR 05-MAR-1997; 97JP-00050302.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX XX WPI; 1998-495844/42.
 XX XX Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX PT treating diseases associated with apoptosis.
 XX PS Example 1; Page 48; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 XX CC invention, involving the use of novel apoptosis-related DNAs and
 XX CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 XX CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 XX CC immunohistological staining, as apoptosis inhibitors. It can also be used
 XX CC for treatment of apoptosis-related diseases
 XX SQ Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 18;

PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX XX WPI; 1998-495844/42.
 XX DR Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX PT treating diseases associated with apoptosis.
 XX XX Example 1; Page 50; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 XX CC invention, involving the use of novel apoptosis-related DNAs and
 XX CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 XX CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 XX CC immunohistological staining, as apoptosis inhibitors. It can also be used
 XX CC for treatment of apoptosis-related diseases
 XX XX SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 18;
 Best Local Similarity 94.1%; Pred. No. 5.7e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1735 CAAAAAAAAAAAAAAAAA 1751
 DB 18 CGAAAAAAAAAAAAAAAAA 2
 RESULT 940
 AAV54167/c
 ID AAV54167 standard; cDNA; 18 BP.
 XX AC AAV54167;
 XX DT 21-DEC-1998 (first entry)
 XX DE Nucleotide sequence PCR primer 4.
 XX KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
 XX KW immunohistological staining.
 XX OS Synthetic.
 XX XX WO9839437-A1.
 XX PD 11-SEP-1998.
 XX PF 05-MAR-1998; 98WO-JP000905.
 XX PR 05-MAR-1997; 97JP-00050302.
 XX PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX PI Sakaki Y;
 XX XX WPI; 1998-495844/42.
 XX DR Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
 XX PT treating diseases associated with apoptosis.
 XX PS Example 1; Page 48; 70pp; Japanese.
 XX CC This is the nucleotide sequence of a PCR primer used in the method of the
 XX CC invention, involving the use of novel apoptosis-related DNAs and
 XX CC proteins. The inventions can be used as diagnostic reagents for apoptosis
 XX CC e.g. (monoclonal) antibodies for the protein, as a reagent in
 XX CC immunohistological staining, as apoptosis inhibitors. It can also be used
 XX CC for treatment of apoptosis-related diseases
 XX XX SQ Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 18;

```
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1750
DB 18 ATAAAAAAAAAAAAAA 2

RESULT 941
AAV22960
ID AAV22960 standard; DNA; 18 BP.
XX
AC AAV22960;
XX
DT 04-AUG-1998 (first entry)
XX
DE Probe used to isolate cDNA encoding human BMP-16.
XX
KW Human; bone morphogenetic protein-16; BMP-16; murine protein; nodal;
KW formation; bone; cartilage; treatment; wound healing; reduction;
KW fibrosis; scar tissue formation; probe; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9812322-A1.
PD 26-MAR-1998.
XX
PF 09-JUL-1997; 97WO-US011954.
XX
PR 18-SEP-1996; 96US-00715202.
XX
PA (GENY ) GENETICS INST INC.
XX
PI Celeste AJ, Murray BL;
XX
DR WPI; 1998-217262/19.
XX
PT New isolated bone morphogenetic protein-16 - used to develop products for
PT inducing formation of bone, cartilage and other connective tissue,
PT particularly for wound healing and tissue repair.
XX
PS Example 1; Page 19; 43pp; English.
XX
CC The present sequence represents a probe used to isolate human bone
CC morphogenetic protein-16 (BMP-16) cDNA. Human BMP-16 is a homologue of a
CC murine protein called nodal, which is expressed in the mouse node during
CC gastrulation. BMP-16 cDNA is isolated from a human genomic library
CC screened with a probe derived from the nodal DNA sequence. The BMP-16
CC proteins can induce the formation of bone, cartilage or other connective
CC tissue. They can be used for treating bone, cartilage or other connective
CC tissue defects, periodontal disease or healing of various types of
CC tissues and wounds. They can also increase neuronal, astrocytic and glial
CC cell survival and therefore be useful in transplantation and treatment of
CC conditions exhibiting a decrease in neuronal survival and repair. They
CC can also exhibit properties such as angiogenic, chemotactic and/or
CC chemoattractant properties, and effects on cells including induction of
CC collagen synthesis, fibrosis, differentiation responses, cell
CC proliferative responses and responses involving cell adhesion, migration
CC and extracellular matrices. These properties make the proteins potential
CC agents for wound healing, reduction of fibrosis and reduction of scar
CC tissue formation
XX
SQ Sequence 18 BP; 2 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1479 CTCTGAGGCGGAGTCTC 1495
DB 1 CTGTGAGGCGGAGTGTCT 17

Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
DB 18 CGAAAAAAAAAAAAAAAAA 2

RESULT 943
AAZ90646/c
ID AAZ90646 standard; DNA; 18 BP.
XX
AC AAZ90646;
XX
DT 13-JUN-2000 (first entry)
XX
DE Human adipose tissue gene amplifying primer #7.
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN JP2000037190-A.
PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 0 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAAAAAA 1751
DB 18 CGAAAAAAAAAAAAAAAAA 2
```


PR 23-JUL-1998; 98JP-00225228.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis, hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention and treatment of adipose tissue related diseases. Sequences AAZ90640-51 represent PCR primers amplifying the human adipose tissue genes

SQ Sequence 18 BP; 2 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 5.7e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1748

DB 18 TTA 2

RESULT 944

AAZ90640/C

ID AAZ90640 standard; DNA; 18 BP.

XX AC AAZ90640;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #1.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

XX JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral

XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,

XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the

XX proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention

XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51

XX represent PCR primers amplifying the human adipose tissue genes

XX Sequence 18 BP; 1 A; 0 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 5.7e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAA 1751

DB 18 CTA 2

RESULT 945

AAZ90645/C

ID AAZ90645 standard; DNA; 18 BP.

XX AC AAZ90645;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #6.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

XX JP2000037190-A.

XX 08-FEB-2000.

XX 23-JUL-1998; 98JP-00225228.

XX 23-JUL-1998; 98JP-00225228.

XX (NISB) JAPAN TOBACCO INC.

XX WPI; 2000-306578/27.

XX A physiologically active protein specifically derived from mammal tissue.

XX Example 2; Page 18; 50pp; Japanese.

XX The invention relates to identification of genes and proteins of adipose tissue relating to obesity, particularly complications of visceral

XX obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,

XX hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the

XX proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention

XX and treatment of adipose tissue related diseases. Sequences AAZ90640-51

XX represent PCR primers amplifying the human adipose tissue genes

XX Sequence 18 BP; 0 A; 1 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;

Best Local Similarity 94.1%; Pred. No. 5.7e+02;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 AAAAAA 1750

DB 18 AGA 2

RESULT 946

AAZ90643/C

ID AAZ90643 standard; DNA; 18 BP.

XX AC AAZ90643;

XX 13-JUN-2000 (first entry)

XX Human adipose tissue gene amplifying primer #4.

XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;

XX arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.

XX Homo sapiens.

XX JP2000037190-A.

XX

PD 08-FEB-2000.
XX
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
XX
PS Example 2; Page 18; 50pp; Japanese.
XX
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAY67598-Y67600) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 1 A; 0 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 18;
Best Local Similarity 94.1%; Pred. No. 5.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1750
DB 18 ATAAAAAAAAAAAAA 2

RESULT 947
AAC60415
ID AAC60415 standard; DNA; 19 BP.
XX
AC AAC60415;
XX
DT 19-FEB-2001 (first entry)
XX
DE Primer eGFP2 used to modify eGFP coding region.
XX
KW Disease; intron; plant; animal; ds.
XX
OS Synthetic.
XX
PN WO200063359-A2.
XX
PD 26-OCT-2000.
XX
PF 17-APR-2000; 2000WO-CB001454.
XX
PR 16-APR-1999; 99GB-00008788.
XX
PA (UNLO) UNIV COLLEGE LONDON.
XX
PI Roes JT;
XX
DR WPI; 2000-679594/66.
XX
PT Polynucleotides having a heterologous intron, useful for manufacturing
PT medicaments for treating human and animal diseases, by stable
PT introduction into cells.
XX
PS Example 1; Page 25; 40pp; English.
XX
CC The present invention relates to a coding sequence with a heterologous
CC intron for treating diseases. The invention is also useful for obtaining
CC a transgenic plant having increased resistance to an external stress such
CC as herbicide, a pathogen or pest or an unfavourable environmental factor
XX
SQ Sequence 19 BP; 4 A; 5 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 19;
Best Local Similarity 94.1%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 765 CCCAGGCCGAGGTGAAG 781
DB 3 CCCGCGCCGAGGTGAAG 19

RESULT 948
AAT73293/C
ID AAT73293 standard; DNA; 20 BP.
XX
AC AAT73293;
XX
DT 12-DEC-1997 (first entry)
XX
DE Primer for pUC19 DNA amplification.
XX
KW primer; PCR; polymerase chain reaction; sequencing; walking;
KW Complementary extension reaction; low redundancy; universal primer; ss.
XX
OS Synthetic.
XX
PN EP767240-A2.
XX
PD 09-APR-1997.
XX
PF 17-SEP-1996; 96EP-00114907.
XX
PR 18-SEP-1995; 95JP-00238141.
PR 30-JAN-1996; 96JP-00013634.
XX
PA (HITA) HITACHI LTD.
XX
PI Kambara H, Okano K;
XX
DR WPI; 1997-205424/19.
XX
PT Efficient sequencing of long DNA by fragment walking - with simultaneous
PT sequencing of restriction enzyme fragment and adjacent region of intact
PT DNA, avoids the need for cloning and requires fewer primers.
XX
PS Example 1; Page 23; 50pp; English.
XX
CC A method for DNA analysis based on a complementary extension reaction
CC using a DNA polymerase, comprises a combination of fragment walking and
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC restriction enzyme and the targeted DNA sequence can be determined
CC directly from the digested DNA fragments. By exploring the overlapping
CC sequence of the determined base sequence, the overall base sequence of a
CC lengthy DNA can be determined with low redundancy without cloning or
CC subcloning. In addition, the method can be done with commercially
CC available universal primers or with fewer primers than required in
CC existing methods. AAT73291-92 are primers used in determination of the
CC pUC19 sequence. Primer extension was carried out using 16 primers
CC AAT73293
XX
SQ Sequence 20 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 2 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1751
DB 17 CGAAAAAAAAAAAAA 1

RESULT 949
AAT73291/C
ID AAT73291 standard; DNA; 20 BP.

```
XX AC AAT73291;
XX DT 12-DEC-1997 (first entry)
XX DE Primer 1 for pUC19 DNA amplification.
XX KW primer; PCR; polymerase chain reaction; sequencing; walking;
XX KW complementary extension reaction; low redundancy; universal primer; ss.
XX OS Synthetic.
XX PN EP767240-A2.
XX PD 09-APR-1997.
XX PF 17-SEP-1996; 96EP-00114907.
XX PR 18-SEP-1995; 95JP-00238141.
XX PR 30-JAN-1996; 96JP-00013634.
XX PA (HITA ) HITACHI LTD.
XX PI Kambara H, Okano K;
XX WPI; 1997-205424/19.
XX Efficient sequencing of long DNA by fragment walking - with simultaneous
PT sequencing of restriction enzyme fragment and adjacent region of intact
PT DNA, avoids the need for cloning and requires fewer primers.
XX Example 1; Page 11; 50pp; English.
XX A method for DNA analysis based on a complementary extension reaction
CC using a DNA polymerase, comprises a combination of fragment walking and
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC restriction enzyme and the targeted DNA sequence can be determined
CC directly from the digested DNA fragments. By exploring the overlapping
CC sequence of the determined base sequence, the overall base sequence of a
CC lengthy DNA can be determined with low redundancy without cloning or
CC subcloning. In addition, the method can be done with commercially
CC available universal primers or with fewer primers than required in
CC existing methods. AAT73291-92 are primers used in determination of the
CC pUC19 sequence. Primer extension was carried out using 16 primers
XX AAT73293
XX SQ Sequence 20 BP; 1 A; 2 C; 3 G; 14 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15.4; DB 1; Length 20;
XX Best Local Similarity 94.1%; Pred. No. 6.1e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1749
DB 17 TGCAAAAA 1
RESULT 950
AAT73292/C
ID AAT73292 standard; DNA; 20 BP.
XX AC AAT73292;
XX DT 12-DEC-1997 (first entry)
XX DE Primer 2 for pUC19 DNA amplification.
XX KW primer; PCR; polymerase chain reaction; sequencing; walking;
XX KW complementary extension reaction; low redundancy; universal primer; ss.
XX OS Synthetic.
XX PN EP767240-A2.
```

```
XX PD 09-APR-1997.
XX PF 17-SEP-1996; 96EP-00114907.
XX PR 18-SEP-1995; 95JP-00238141.
XX PR 30-JAN-1996; 96JP-00013634.
XX PA (HITA ) HITACHI LTD.
XX PI Kambara H, Okano K;
XX WPI; 1997-205424/19.
XX Efficient sequencing of long DNA by fragment walking - with simultaneous
PT sequencing of restriction enzyme fragment and adjacent region of intact
PT DNA, avoids the need for cloning and requires fewer primers.
XX Example 1; Page 11; 50pp; English.
XX A method for DNA analysis based on a complementary extension reaction
CC using a DNA polymerase, comprises a combination of fragment walking and
CC DNA sequencing. DNA fragments are formed by digestion of DNA with a
CC restriction enzyme and the targeted DNA sequence can be determined
CC directly from the digested DNA fragments. By exploring the overlapping
CC sequence of the determined base sequence, the overall base sequence of a
CC lengthy DNA can be determined with low redundancy without cloning or
CC subcloning. In addition, the method can be done with commercially
CC available universal primers or with fewer primers than required in
CC existing methods. AAT73291-92 are primers used in determination of the
CC pUC19 sequence. Primer extension was carried out using 16 primers
XX AAT73293
XX SQ Sequence 20 BP; 1 A; 1 C; 3 G; 15 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15.4; DB 1; Length 20;
XX Best Local Similarity 94.1%; Pred. No. 6.1e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1733 TACAAAAA 1749
DB 17 TGCAAAAA 1
RESULT 951
AAA72164
ID AAA72164 standard; DNA; 20 BP.
XX AC AAA72164;
XX DT 15-SEP-2003 (revised)
XX DT 24-NOV-2000 (first entry)
XX DE Humanised anti-Fas antibody heavy chain primer, SEQ ID NO:94.
XX KW Anti-Fas antibody; monoclonal antibody HFETA; FERM-BP-5828; murine;
XX KW humanised antibody; complementarity determining region; CDR; human Fas;
XX KW Fas ligand; apoptosis modulator; programmed cell death;
XX KW autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX KW cardiomyopathy; glomerulonephritis; aplastic anaemia; pancytopenia;
XX KW hepatitis; AIDS; graft rejection; heavy chain; sequencing primer; ss.
XX OS Mus musculus.
XX OS Homo sapiens.
XX OS Chimeric.
XX PN JP2000169393-A.
XX DT 20-JUN-2000.
XX PF 30-SEP-1999; 99JP-00278301.
XX PR 30-SEP-1998; 98JP-00276883.
```

```

XX PA (SANY ) SANKYO CO LTD.
XX PS WPI; 2000-485645/43.
XX DR
XX PT Preventive or treating agent for the diseases caused by an abnormality in
XX PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
XX PT antibody.
XX PS
XX PS Example 15; Page 49; 139pp; Japanese.
XX CC
XX CC The invention relates to compositions for the prevention or treatment or
XX CC diseases caused by an abnormality in the Fas/Fas ligand system containing
XX CC an anti-Fas antibody as the active component. The anti-Fas antibody is
XX CC either the murine anti-human Fas monoclonal antibody HFE7A, or a
XX CC humanised version of HFE7A containing identical CDRs (complementarity
XX CC determining regions) to antibody HFE7A. Via its interaction with Fas, the
XX CC antibody of the invention acts as a modulator of apoptosis. The
XX CC compositions of the invention may therefore be used in the treatment or
XX CC prevention of conditions such as autoimmune diseases, allergy, atopy,
XX CC arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
XX CC aplastic anaemia (panmyelophthisis), hepatitis, AIDS and organ graft
XX CC rejection. The present sequence represents a humanised HFE7A-derived anti
XX CC -Fas antibody heavy chain sequencing primer used in an exemplification of
XX CC the invention. (Updated on 15-SEP-2003 to standardise OS field)
XX SQ Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15.4; DB 1; Length 20;
XX Best Local Similarity 94.1%; Pred. No. 6.1e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 TTAGGGGGGAAGAGGAA 37
DB 3 TTGGGGGGAAGAGGAA 19
XX
XX RESULT 952
XX AAA72168/c
XX ID AAA72168 standard; DNA; 20 BP.
XX
XX AC AAA72168;
XX
XX 15-SEP-2003 (revised)
XX 24-NOV-2000 (first entry)
XX
XX Humanised anti-Fas antibody heavy chain primer, SEQ ID NO:98.
XX
XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
XX humanised antibody; complementarity determining region; CDR; human Fas;
XX Fas ligand; apoptosis modulator; programmed cell death;
XX autoimmune disease; allergy; atopy; arteriosclerosis; myocarditis;
XX cardiomyopathy; glomerulonephritis; aplastic anaemia; panmyelophthisis;
XX hepatitis; AIDS; graft rejection; heavy chain; sequencing primer; ss.
XX
XX Mus musculus.
XX OS Homo sapiens.
XX OS Chimeric.
XX
XX JP2000169393-A.
XX
XX 20-JUN-2000.
XX
XX 30-SEP-1999; 99JP-00278301.
XX
XX 30-SEP-1998; 98JP-00276883.
XX
XX (SANY ) SANKYO CO LTD.
XX
XX WPI; 2000-485645/43.
XX
XX Preventive or treating agent for the diseases caused by an abnormality in
XX the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
XX antibody.
XX
XX Query Match 0.9%; Score 15.4; DB 1; Length 20;
XX Best Local Similarity 94.1%; Pred. No. 6.1e+02;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 21 TTAGGGGGGAAGAGGAA 37
DB 18 TTGGGGGGAAGAGGAA 2
XX
XX RESULT 953
XX AAZ57075
XX ID AAZ57075 standard; DNA; 20 BP.
XX
XX AC AAZ57075;
XX
XX 19-MAY-2000 (first entry)
XX
XX Murine melanocortin receptor MC3-R amplifying primer.
XX
XX Medicament; agonist; melanocortin receptor type 3; ACTH; PMN; MC3-R;
XX adrenocorticotrophic hormone; neutrophil chemoattractant; antigen;
XX polymorphonuclear cell; septic shock; skin disorder; antiarthritic;
XX melanocortin receptor; anti-inflammatory; antiasmatic; PCR primer; ss.
XX
XX Mus sp.
XX
XX WO200005263-A2.
XX
XX 03-FEB-2000.
XX
XX 22-JUL-1999; 99WO-GB002392.
XX
XX 24-JUL-1998; 98GB-00016234.
XX
XX (HARV-) HARVEY RES LTD WILLIAM.
XX
XX Perretti M, Getting S, Flower R;
XX
XX WPI; 2000-182651/16.
XX
XX Inhibition of neutrophil chemoattractant production, inhibition of
XX polymorphonuclear cell accumulation or reduction/treatment of
XX inflammation using compounds comprising the peptide sequence HFRW.
XX
XX Disclosure; Page 8; 20pp; English.
XX
XX The invention relates to the use of a compound comprising an amino acid
XX sequence His-Phe-Arg-Trp (HFRW) in the manufacture of a medicament and/or
XX an agonist of melanocortin receptor type 3 (MC3-R) where the compound is
XX not adrenocorticotrophic hormone (ACTH)1-39. The compounds are used to
XX inhibit neutrophil chemoattractant production, polymorphonuclear cell
XX (PMN) accumulation or reduction/treatment of inflammation. Especially,

```

CC these compounds are agonists of the MC3-R. The inflammatory response/
 CC disease is selected from gout, gouty arthritis, rheumatoid arthritis,
 CC asthma, reperfusion injury or damage, stroke, myocardial infarction,
 CC septic shock, or a skin disorder. Sequences AA257073-80 represent PCR
 CC primers used for amplifying murine melanocortin receptors

XX
 SQ Sequence 20 BP; 0 A; 7 C; 4 G; 9 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 6.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1689 CTGTCCTCTCTCTCC 1705
 Db 3 CTGTCCTCTCTCTCC 19

RESULT 954
 AAA11602
 ID AAA11602 standard; DNA; 20 BP.
 XX AC AAA11602;
 XX 08-AUG-2000 (first entry)
 DT Humanised HFE7A designed heavy chain DNA primer #5.
 DE
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiartherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection;
 KW primer; ss.
 XX Synthetic.
 OS
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-00307711.
 PF
 XX 30-SEP-1998; 98JP-00276881.
 PR
 XX 30-SEP-1998; 98JP-00276882.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI
 XX WPI; 2000-258930/23.
 DR
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.
 XX
 XX Example reference 15; Page 137; 263pp; English.
 PS
 XX This invention describes a novel humanized anti-Fas antibody-like
 CC molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas
 CC ligand system, by binding to Fas on the cell surface, and prevents
 CC apoptosis in cells with a normal system, by inhibiting binding between
 CC Fas and its ligand. The products of the invention have anti-inflammatory,
 CC anti-anemic, antidiabetic, anti-allergic, anti-arthritis, antiviral,
 CC immunomodulatory, dermatological, immunosuppressive, thymimetic,
 CC antirheumatic, nephrotropic, antiinfertility, neuroprotective,
 CC antiarteriosclerotic, cardiant and hepatropic activity. (I) induce
 CC apoptosis by binding to cell surface Fas or inhibit it by competitive

CC inhibition of ligand binding. (I) are used to treat and/or prevent
 CC diseases associated with the Fas/Fas ligand system, especially systemic
 CC lupus erythematosus, Hashimoto disease, rheumatoid arthritis, graft
 CC versus host disease, Sjorgen's syndrome, pernicious or hypoplastic
 CC anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's
 CC disease, autoimmune hemolytic anemia, sterility, myasthenia gravis,
 CC multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
 CC dependent diabetes mellitus, allergy, arteriosclerosis, myocarditis,
 CC cardiomyopathy, glomerulonephritis, hepatitis (fulminant, chronic, viral
 CC (B, C or D) or alcoholic), and transplant rejection. (I) selectively
 CC inhibit apoptosis in normal cells but selectively induce it in abnormal
 CC cells. They bind to both human and murine Fas, so can be evaluated in
 CC murine disease models. (I) act on the active site of Fas, i.e. they mimic
 CC the native ligand, do not induce liver disease, and have reduced risk of
 CC inducing a human anti-murine antibody response. This sequence represents
 CC primer used in the construction of a humanised anti-Fas antibody HFE7A
 CC designed heavy chain which is used in the method described in the
 CC invention

XX
 SQ Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 6.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 TTAGGGGGGAAGAGAA 37
 Db 3 TTTGGGGGAAGAGAA 19

RESULT 955
 AAA11606/c
 ID AAA11606 standard; DNA; 20 BP.
 XX AC AAA11606;
 XX 08-AUG-2000 (first entry)
 DT Humanised HFE7A designed heavy chain DNA primer #9.
 DE
 XX Fas; antibody; human; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritis; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thymimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiartherosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection;
 KW primer; ss.
 XX Synthetic.
 OS
 XX EP990663-A2.
 PN
 XX 05-APR-2000.
 PD
 XX 29-SEP-1999; 99EP-00307711.
 PF
 XX 30-SEP-1998; 98JP-00276881.
 PR
 XX 30-SEP-1998; 98JP-00276882.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 XX Serizawa N, Haruyama H, Nakahara K, Tamaki I, Takahashi T;
 PI
 XX WPI; 2000-258930/23.
 DR
 XX New humanized anti-Fas antibody, useful for treating or preventing e.g.
 PT inflammatory or autoimmune disease, induces apoptosis selectively in
 PT cells with abnormal Fas-Fas ligand systems.
 XX


```

Qy 21 TTAGGGGGGAAGAGGAA 37
Db 18 TTTGGGGGAAGAGGAA 2

RESULT 958
ABA05917/c
ID ABA05917 standard; DNA; 20 BP.
XX AC ABA05917;
XX DT 05-MAR-2002 (first entry)
XX DE Hepatitis B virus diagnostic PCR primer SEQ ID NO 7.
XX KW Hepatitis B virus; HBV; infection; hepatocellular carcinoma; diagnosis;
XX KW PCR primer; ss.
XX OS Hepatitis B virus.
XX PN EP1152063-A1.
XX PD 07-NOV-2001.
XX PF 03-MAY-2000; 2000EP-00109436.
XX PR 03-MAY-2000; 2000EP-00109436.
XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX PI Schroeder KH, Koike K;
XX DR WPI; 2002-068256/10.
XX PT Diagnosing hepatitis B virus (HBV) infection stages and determining the
PT risk for hepatocellular carcinoma, comprises identifying full length HBV
PT transcripts and truncated HBV transcripts in a serum sample.
XX PS Example 1; Page 6; 25pp; English.
XX CC The invention relates to diagnosis of hepatitis B virus (HBV) infection
CC stages comprising identification of full length HBV transcripts (I) and
CC truncated HBV transcripts (II) in a serum sample, where the ratio of I:II
CC is indicative of a particular infection stage. The method is useful for
CC diagnosing HBV infection stages and determining the risk for developing
CC hepatocellular carcinoma. The present sequence is that of a HBV
CC diagnostic PCR primer, useful for the invention
XX SQ Sequence 20 BP; 1 A; 2 C; 1 G; 16 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA...AAAAA 1751
Db 17 CTA...AAAAA 1

RESULT 959
ABL45981
ID ABL45981 standard; DNA; 20 BP.
XX AC ABL45981;
XX DT 26-APR-2002 (first entry)
XX DE Humanised anti-Fas antibody related PCR primer SEQ ID NO 19.
XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
XX KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
XX KW autoimmune disease; allergy; atopic; PCR primer; ss.

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAA...AAAAA 1751
Db 17 CTA...AAAAA 1

RESULT 959
ABL45981
ID ABL45981 standard; DNA; 20 BP.
XX AC ABL45981;
XX DT 26-APR-2002 (first entry)
XX DE Humanised anti-Fas antibody related PCR primer SEQ ID NO 19.
XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
XX KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
XX KW autoimmune disease; allergy; atopic; PCR primer; ss.

```

```

OS Synthetic.
XX JP2001342148-A.
XX PD 11-DEC-2001.
XX PF 28-MAR-2001; 2001JP-00093106.
XX PR 29-MAR-2000; 2000JP-00090918.
XX PA (SANY ) SANKYO CO LTD.
XX WPI; 2002-145113/19.
XX PT Drug containing humanized anti-Fas antibody, used for preventing and
XX PT treating autoimmune diseases, allergy, and atopy.
XX PS Example 4 (Preparatory); Page 23; 194pp; Japanese.
XX CC The invention relates to a preventive or treating agent for diseases
XX CC caused by abnormality in Fas/Fas ligand system containing as the active
XX CC component an antibody having as the light chain subunit a polypeptide
XX CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
XX CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
XX CC fully defined in the specification and having an activity of combining
XX CC specifically with mammalian Fas and an activity of inducing apoptosis in
XX CC a cell expressing Fas. The agent has immunosuppressive and antiallergic
XX CC activity and is used for preventing and treating autoimmune diseases,
XX CC allergy, atopy and others. The present sequence is that of a PCR primer,
XX CC useful to the invention
XX SQ Sequence 20 BP; 5 A; 0 C; 11 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
Best Local Similarity 94.1%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 21 TTAGGGGGGAAGAGGAA 37
Db 3 TTTGGGGGAAGAGGAA 19

RESULT 960
ABL45985/c
ID ABL45985 standard; DNA; 20 BP.
XX AC ABL45985;
XX DT 26-APR-2002 (first entry)
XX DE Humanised anti-Fas antibody related PCR primer SEQ ID NO 23.
XX KW Human; mouse; humanised anti-Fas antibody; Fas/Fas ligand;
XX KW light chain subunit; apoptosis; immunosuppressive; antiallergic;
XX KW autoimmune disease; allergy; atopic; PCR primer; ss.
XX OS Synthetic.
XX PN JP2001342148-A.
XX PD 11-DEC-2001.
XX PF 28-MAR-2001; 2001JP-00093106.
XX PR 29-MAR-2000; 2000JP-00090918.
XX PA (SANY ) SANKYO CO LTD.
XX WPI; 2002-145113/19.
XX PT Drug containing humanized anti-Fas antibody, used for preventing and
XX PT treating autoimmune diseases, allergy, and atopy.
XX

```

PS Example 5 (Preparatory); Page 25; 194pp; Japanese.

CC The invention relates to a preventive or treating agent for diseases
 CC caused by abnormality in Fas/Fas ligand system containing as the active
 CC component an antibody having as the light chain subunit a polypeptide
 CC containing residues 1-218 of one of 3, 239 residue amino acid sequences,
 CC or residues 1-451 of one of 3, 470 residue amino acid sequences, all
 CC fully defined in the specification and having an activity of combining
 CC specifically with mammalian Fas and an activity of inducing apoptosis in
 CC a cell expressing Fas. The agent has immunosuppressive and anti-allergic
 CC activity and is used for preventing and treating autoimmune diseases,
 CC allergy, atopy and others. The present sequence is that of a PCR primer,
 CC useful to the invention

XX Sequence 20 BP; 4 A; 11 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 6.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 21 TTAGGGGGGAGAGGAA 37
 |||||
 DB 18 TTGGGGGAGAGGAA 2

RESULT 961

ABZ89489
 ID ABZ89489 standard; DNA; 20 BP.

XX AC ABZ89489;

XX DT 17-OCT-2003 (first entry)

XX DE Human oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 4731; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, anti-allergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction.
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 20 BP; 16 A; 2 C; 0 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 6.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAAAAAA 1750
 |||||
 DB 1 ACATAAAAAAAAAAAAA 17

RESULT 962

ABZ99051/c

XX ID ABZ99051 standard; DNA; 20 BP.

XX AC ABZ99051;

XX DT 17-OCT-2003 (first entry)

XX DE Human PDE4C oligonucleotide sequence.

XX Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti-allergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX OS Homo sapiens.

XX PN WO200285308-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013135.

XX PR 24-APR-2001; 2001US-0286137P.

XX PA (EPIG-) EPIGENESIS PHARM INC.

XX NYce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-229219/22.

XX Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiquinone.

PS Disclosure; SEQ ID NO 14293; 872pp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiquinone. A composition of the invention

CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 20 BP; 2 A; 1 C; 2 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 6.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1735 CAAAAAAGAAAAA 1751
 Db 17 CAAAAAAGAAAAA 1

RESULT 963
 ACF04183
 ID ACF04183 standard; DNA; 20 BP.
 XX
 AC ACF04183;
 DT 06-NOV-2003 (first entry)
 XX
 DE Human IL-22BP coding sequence PCR primer #1.
 XX
 KW Human; IL-22BP; chromosome 1; LICR-2; STAT activation; Class II;
 KW cytokine receptor; neutropic; antiinflammatory; antineumatic;
 KW antiarthritic; antidiabetic; antiallergic; antiasthmatic; diabetes;
 KW autoimmune disease; multiple sclerosis; inflammatory bowel disease;
 KW rheumatoid arthritis; allergy; asthma; PCR; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2003057711-A2.
 PN
 XX 17-JUL-2003.
 PD
 XX 09-DEC-2002; 2002WO-US039231.
 PF
 XX 21-DEC-2001; 2001US-00026106.
 PR
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA
 XX Renauld J, Fickensicher H, Dumoutier L, Hor S;
 PI WPI; 2003-587107/55.
 DR
 XX New LICR-2 nucleic acid molecule encoding a cytokine receptor useful for
 XX treating autoimmune diseases such as multiple sclerosis, inflammatory
 PT bowel disease, rheumatoid arthritis, type I and type II diabetes,
 PT allergies and asthma.
 XX
 XX Example 3; Page 4; 41pp; English.
 PS
 XX The present invention provides the protein and coding sequences of a
 CC Class II cytokine receptor, designated LICR-2. Two splice variants of
 CC this sequence are given. The nucleic acid molecules, proteins and methods
 CC are useful for treating autoimmune diseases such as multiple sclerosis,
 CC inflammatory bowel disease, rheumatoid arthritis, type I and type II
 CC diabetes, allergies and asthma. The present sequence is a PCR primer used
 CC to isolate the human IL-22BP gene, also known as LICR-2
 XX
 XX Sequence 20 BP; 4 A; 6 C; 9 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.4; DB 1; Length 20;
 Best Local Similarity 94.1%; Pred. No. 6.1e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 155 AGCCCATGTCGGGGCCC 171
 Db 2 AGCCCATGTCGGGGCCC 18

RESULT 964
 AAX18388/c
 ID AAX18388 standard; DNA; 17 BP.
 XX
 AC AAX18388;
 DT 11-MAY-1999 (first entry)
 XX
 DE RT-PCR primer of the invention SEQ ID 29.
 XX
 KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 FN JPI1032765-A.
 XX
 PD 09-FEB-1999.
 XX
 PF 18-JUL-1997; 97JP-00208312.
 XX
 PR 18-JUL-1997; 97JP-00208312.
 XX
 PA (TAKI) TAKARA SHUZO CO LTD.
 XX
 DR WPI; 1999-183822/16.
 XX
 KW Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX
 XX Example 1; Page 12; 19pp; Japanese.
 PS
 XX This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX
 XX Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAGAAAAA 1750
 Db 16 BAAAAAAGAAAAA 1

RESULT 965
 AAS14174/c
 ID AAS14174 standard; DNA; 17 BP.
 XX
 AC AAS14174;
 XX
 DT 18-DEC-2001 (first entry)
 XX

DE Modified Poly-T Primer #1 used in construction of probe sets.
 XX
 KW WRAP-Probe; gene expression array; global amplification; RNA array; ss;
 KW tissue microarray; drug discovery assay; reporter binding site; forensic;
 KW diagnostic; genomic analysis; universal linker; poly-T primer.
 XX
 OS Synthetic.
 XX
 PN WO200166802-A1.
 XX
 PD 13-SEP-2001.
 XX
 PF 09-MAR-2001; 2001WO-US007508.
 XX
 PR 09-MAR-2000; 2000US-0187982P.
 XX
 PA (GENE-) GENETAG TECHNOLOGY INC.
 XX
 PI Shafer DA;
 XX
 DR WPI; 2001-596845/67.
 XX
 XX Novel probe sets with common universal linkers at one or both ends (WRAP
 PT probes) for gene expression arrays to provide global amplification of
 PT probe set and to provide common equivalent signaling regardless of
 PT length.
 XX
 PS Disclosure; Page 88; 97pp; English.
 XX
 CC The invention relates to a probe set for gene expression arrays to
 CC provide common equivalent signalling per probe and global amplification
 CC of the set. The probe set has a pool of modified cDNA probes, each probe
 CC having a central target specific segment copied from a portion of a
 CC single mRNA transcript and a universal linker (a WRAP-probe) located on
 CC one or both terminal ends. The universal linker has reporter binding
 CC sites to join common reporters to the probes and primer binding sites to
 CC copy and amplify the probe. The probes and reporters are useful in
 CC diagnostic or drug discovery assays for a wide range of biomedical
 CC samples, including detection of nucleic acids and gene expression
 CC profiles in human diagnostics, forensics and genomic analysis. The
 CC methods are useful for amplifying and identifying any unknown DNA
 CC fragment and also for improving sensitivity with tissue microarrays or
 CC RNA arrays. The methods improve the quantification of gene expression and
 CC allow highly improved detection of rare transcripts or very small
 CC samples. This sequence represents a poly-T primer used in the
 CC construction of probe sets
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;
 Query Match 0.9%; Score 15.2; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 5.8e+02;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1735 CAAAAAATAAAAAA 1750
 Db :|||||
 16 BAAAAAATAAAAAA 1
 RESULT 966
 ID AAQ55833 standard; DNA; 20 BP.
 AC AAQ55833;
 XX
 DT 21-JUL-1994 (first entry)
 XX
 DE HCV detection primer (DNA type 4 SS3).
 XX
 KW HCV; hepatitis C virus; detection; primer; PCR; mixer primer set;
 KW polymerase chain reaction; DNA polymerase; ss.
 XX
 OS Synthetic.
 XX

PN JP05337000-A.
 XX
 PD 21-DEC-1993.
 XX
 PF 04-JUN-1992; 92JP-00168226.
 XX
 PR 04-JUN-1992; 92JP-00168226.
 XX
 PA (SAYA/) SAYAMA K.
 XX
 DR WPI; 1994-037380/05.
 XX
 PT Detection of type C hepatitis virus - using one step DNA polymerase chain
 PT reaction with mixed primer set.
 XX
 PS Claim 2; Page 2; 7pp; Japanese.
 XX
 CC The primers (AAQ5811-841) are used to detect various types of hepatitis
 CC C virus. The primers are made from oligo DNA fragments selected from
 CC specific hepatitis C virus subtypes. The primers can be used in a one
 CC step PCR reaction which can determine the subtypes of a large number of
 CC samples
 XX
 SQ Sequence 20 BP; 3 A; 2 C; 8 G; 7 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1000.GGCTCGCGAGAGATGGT 1019
 Db 1 GTCTGCGGAGATGTTGGT 20
 RESULT 967
 ID AAQ82253/c
 ID AAQ82253 standard; DNA; 20 BP.
 XX
 AC AAQ82253;
 XX
 DT 25-MAR-2003 (revised)
 DT 07-SEP-1995 (first entry)
 XX
 DE Chromosome 11 (locus D11S1113) STS primer cSRL-4b4-tA.
 XX
 KW sequence sampled mapping; genomic analysis; complex genome mapping;
 KW cosmid library; chromosome 11; sequence tagged site; STS analysis; ss.
 XX
 OS Synthetic.
 XX
 PN WO9429486-A1.
 XX
 PD 22-DEC-1994.
 XX
 PF 15-JUN-1994; 94WO-US006810.
 XX
 PR 15-JUN-1993; 93US-00078471.
 PR 07-SEP-1993; 93US-00117952.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Evans GA, Smith MW;
 XX
 DR WPI; 1995-036508/05.
 XX
 PT Sequencing complex genomes, present as fragments in a cosmid library - by
 PT sequencing end-specific nucleotides of each clone then correlating with
 PT spatial relationship of cosmid, esp. for mammalian chromosomes.
 XX
 PS Example 4; Page 73; 128pp; English.
 XX
 CC Sequences were determined from the ends of chromosome 11-specific cosmids
 CC by automated sequencing without intermediate subcloning. A sample of 371


```

Db      1  CCTGAGGGCAAGAGGAAGC 20

RESULT 970
AAT97431/c
ID  AAT97431 standard; DNA; 20 BP.
XX  AC
XX  AAT97431;
XX  14-APR-1998 (first entry)
XX  DE
XX  Oligomer si4102 Common probe from WO9722719 Example 7.
XX  KW
XX  Detection; target site; nucleic acid; fluorophore; labelled; fluorescent;
XX  inherited disease; tissue typing; PCR; ss.
XX  OS
XX  Synthetic.
XX  FH
XX  Key Location/Qualifiers
XX  modified_base 20
XX  /*tag= a
XX  /*note= "Labelled with fluorescein"
XX  PN
XX  WO9722719-A1.
XX  PD
XX  26-JUN-1997.
XX  PF
XX  17-DEC-1996; 96WO-US020379.
XX  PR
XX  18-DEC-1995; 95US-0008743P.
XX  PA
XX  (UNIW ) UNIV WASHINGTON.
XX  PI
XX  Kwok P, Chen X;
XX  WPI; 1997-341707/31.
XX  DR
XX  Detecting target site in nucleic acid by forming a fluorophore-labelled
XX  oligonucleotide at the site - and detecting fluorescent energy following
XX  denaturation, used e.g. to detect inherited diseases, in tissue typing
XX  etc.
XX  PS
XX  Example 7; Page 49; 68pp; English.
XX  CC
XX  A method has been developed for detecting the presence of a target site
XX  (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method
XX  comprises: (a) forming an oligonucleotide (ON), consisting of two
XX  fluorophores (F1, F2) each covalently linked to separate nt, bound to TS;
XX  and (b) detecting fluorescence energy transfer (FET) between F1 and F2
XX  when ON is released from TS. The present sequence represents a synthetic
XX  polynucleotide used in an example of the present invention. The method is
XX  used to diagnose hereditary and other diseases; to determine infectious
XX  agents; in tissue typing for histocompatibility; in forensic
XX  identification and paternity testing, and in monitoring the genetic make
XX  up of plants and animals. Specifically it is used to detect single nt
XX  polymorphisms. The method provides inexpensive, simple, accurate and
XX  automatable nucleic acid analyses
XX  SQ
XX  Sequence 20 BP; 5 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
XX  Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX  Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX  QY 1729 AGTTTACAAAAA 1748
XX  Db 20 ATTTTACAAAAATAAACAA 1
XX  RESULT 971
XX  AAT97419/c
XX  ID  AAT97419 standard; DNA; 20 BP.
XX  XX

```

```

AC  AAT97419;
XX  14-APR-1998 (first entry)
XX  DE
XX  Donor Sequence oligomer from WO9722719 Example 6.
XX  KW
XX  Detection; target site; nucleic acid; fluorophore; labelled; fluorescent;
XX  inherited disease; tissue typing; PCR; ss.
XX  OS
XX  Synthetic.
XX  PN
XX  WO9722719-A1.
XX  PD
XX  26-JUN-1997.
XX  PF
XX  17-DEC-1996; 96WO-US020379.
XX  PR
XX  18-DEC-1995; 95US-0008743P.
XX  PA
XX  (UNIW ) UNIV WASHINGTON.
XX  PI
XX  Kwok P, Chen X;
XX  WPI; 1997-341707/31.
XX  DR
XX  Detecting target site in nucleic acid by forming a fluorophore-labelled
XX  oligonucleotide at the site - and detecting fluorescent energy following
XX  denaturation, used e.g. to detect inherited diseases, in tissue typing
XX  etc.
XX  PS
XX  Example 6; Page 46; 68pp; English.
XX  CC
XX  A method has been developed for detecting the presence of a target site
XX  (TS), of at least one nucleotide (nt) in a nucleic acid (NA). The method
XX  comprises: (a) forming an oligonucleotide (ON), consisting of two
XX  fluorophores (F1, F2) each covalently linked to separate nt, bound to TS;
XX  and (b) detecting fluorescence energy transfer (FET) between F1 and F2
XX  when ON is released from TS. The present sequence represents a synthetic
XX  polynucleotide used in an example of the present invention. The method is
XX  used to diagnose hereditary and other diseases; to determine infectious
XX  agents; in tissue typing for histocompatibility; in forensic
XX  identification and paternity testing, and in monitoring the genetic make
XX  up of plants and animals. Specifically it is used to detect single nt
XX  polymorphisms. The method provides inexpensive, simple, accurate and
XX  automatable nucleic acid analyses
XX  SQ
XX  Sequence 20 BP; 5 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
XX  Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX  Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX  Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX  QY 1729 AGTTTACAAAAA 1748
XX  Db 20 ATTTTACAAAAATAAACAA 1
XX  RESULT 972
XX  AAX38359
XX  ID  AAX38359 standard; DNA; 20 BP.
XX  AC
XX  AAX38359;
XX  DT
XX  16-JUN-1999 (first entry)
XX  DE
XX  E. coli K12 R1 antisense oligonucleotide 59.
XX  KW
XX  Microorganism inhibitor; antisense; nuclease resistant; treatment;
XX  ribonucleotide reductase; secA gene; pathological condition; R1 subunit;
XX  antimicrobial agent; crop protection; primer; R2 subunit; ss.
XX  OS
XX  Synthetic.
XX  OS
XX  Escherichia coli.

```

XX PN WO9902673-A2.
 XX PD 21-JAN-1999.
 XX PF 10-JUL-1998; 98WO-CA000666.
 XX PR 10-JUL-1997; 97US-0052160P.
 XX PA (GENE-) GENESENSE TECHNOLOGIES INC.
 XX PI Wright JA, Young AH, Dugourd D;
 XX WPI; 1999-120874/10.
 XX New oligonucleotides complementary to RR or SecA genes - useful to
 PT inhibit growth of microorganisms.
 XX Disclosure; Page 18; 103pp; English.
 XX This invention describes novel antisense oligonucleotides (AA38301-
 CC X38552) which are nuclease resistant, and comprises about 3-50
 CC nucleotides complementary to the ribonucleotide reductase gene or the
 CC secA gene of a microorganism. The antisense oligonucleotides are used to
 CC treat mammalian pathological conditions mediated by microorganisms. The
 CC oligonucleotides are particularly useful as antimicrobial agents in crop
 CC protection
 XX Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1204 CGGATCCTCGCGGCTATGGG 1223
 DB 1 CGGATCAACGGGCTATGGG 20
 RESULT 973
 AA237137/C
 ID AA237137 standard; cDNA; 20 BP.
 AC AA237137;
 XX 01-FEB-2000 (first entry)
 XX Primer used for amplifying human TANGO 125 (T125) gene.
 XX TANGO 125; T125; alternative splice variant; EGF domain; antibody;
 KW secreted protein; agonist; antagonist; predictive medicine; treatment;
 KW forensic biology; PCR primer; ss.
 XX Homo sapiens.
 XX WO9954437-A2.
 XX 28-OCT-1999.
 XX 23-APR-1999; 99WO-US008900.
 XX 23-APR-1998; 98US-00065363.
 XX 23-APR-1999; 99US-00298531.
 XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 XX Holtzman DA;
 XX WPI; 2000-013240/01.
 XX Novel polynucleotides and polypeptides used to modulate a variety of
 PT cellular processes.
 XX

PS Disclosure; Page 22; 120pp; English.
 XX PCR primers AA237136-237137 are used to amplify the TANGO 125 (T125) gene
 CC (AA237131). The T125 protein has two epidermal growth factor (EGF)-like
 CC domains at amino acids 107-134 and 141-176 and is predicted to have a
 CC molecular weight of approximately 30kD. T125 is predicted to have no
 CC transmembrane domains and appears to be a secreted protein. There are
 CC three alternatively spliced forms of T125: T125a, T125b and T125c
 CC (AA237132-237135). The sequences of all variants of T125 are used in the
 CC invention to create antibodies which selectively bind to T125. The T125
 CC polypeptide is used to modulate a variety of cellular processes. It can
 CC be used to produce fusion proteins. The protein may also be used to
 CC produce antibodies, and to identify T125 antagonists and agonists. The
 CC T125 polynucleotides, polypeptides, homologues and antibodies can be used
 CC in screening assays; predictive medicine; and methods of treatment of
 CC T125 associated disorders. The T125 polynucleotides can be used to
 CC express the protein; to detect T125 mRNA; to detect genetic alterations
 CC in the T125 gene; in forensic biology; and as a source of primers and
 CC probes
 XX
 SQ Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 681 GGCACAGCCAGTGAGGGGCT 700
 DB 20 GGCACAGCCAGTGAGGGGCT 1
 RESULT 974
 AA243822
 ID AA243822 standard; DNA; 20 BP.
 AC AA243822;
 XX 10-MAR-2000 (first entry)
 XX Human fetal brain cDNA clone vc10_1 DNA probe.
 XX Human; secreted protein; treatment; nutritional activity; cytokine;
 KW cell proliferation; cell differentiation; hematopoiesis regulation;
 KW tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic;
 KW thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
 KW gene therapy; ss.
 XX Synthetic.
 XX Homo sapiens.
 XX WO9955721-A1.
 XX 04-NOV-1999.
 XX 23-APR-1999; 99WO-US008504.
 XX 24-APR-1998; 98US-0082904P.
 XX 11-JUN-1998; 98US-0088994P.
 XX 12-JUN-1998; 98US-0089278P.
 XX 02-JUL-1998; 98US-0091647P.
 XX 24-AUG-1998; 98US-0097639P.
 XX 22-APR-1999; 99US-00097639.
 XX (ALPH-) ALPHAGENE INC.
 XX Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;
 XX WPI; 2000-052801/04.
 XX New polynucleotides encoding secreted human proteins, derived from human
 PT fetal brain, adult skin, adult brain, adult heart, adult thymus and adult
 PT aorta cDNA libraries.
 XX

PS Disclosure; Page 267; 282pp; English.

XX This invention describes novel human secreted proteins which are encoded
CC by polynucleotides obtained from fetal brain, adult skin, adult brain,
CC adult heart, adult thymus and adult aorta cDNA libraries. The
CC polynucleotides and proteins are predicted to have biological activities
CC which would make them suitable for treating, preventing or ameliorating
CC medical conditions in humans and animals, although no supporting data is
CC given. Suggested activities include nutritional activity, cytokine and
CC cell proliferation/differentiation activity, immune stimulating (e.g. as
CC vaccines) or suppressing activity, hematopoiesis regulating activity,
CC tissue growth activity, activin/inhibin activity,
CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumor
CC invasion suppressor activity, and tumor inhibition activity. The
CC polynucleotides are also stated to be useful for gene therapy. AAZ43809-
CC Z43840 represent DNA probes used to isolate the polynucleotides
CC represented in AAZ43777-243808 which encode the secreted proteins
CC represented in AAZ50905-Y50947

XX Sequence 20 BP; 3 A; 1 C; 10 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1009 GAAGATGTGTTGGGATGG 1028
|||||
DB 1 GAAGTCTGTTGGTATGG 20
|||||

RESULT 975
AAZ14012
ID AAA14012 standard; DNA; 20 BP.
XX
AC AAA14012;
DT 18-JUL-2000 (first entry)
DE Human liver glycogen phosphorylase antisense oligo, SEQ ID NO:12.
XX
KW Liver glycogen phosphorylase; PYGL gene; human; chromosome 14;
KW 1,4-alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase; HGLPa;
KW glycogenolysis; carbohydrate metabolism; blood glucose homeostasis;
KW expression inhibition; hypoglycaemic; type II diabetes;
KW non insulin-dependent; antisense; phosphorothioate; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "Phosphorothioate linkages"

XX US6043091-A.
PN 28-MAR-2000.
XX
PD 19-JUL-1999; 99US-00357071.
XX
PF 19-JUL-1999; 99US-00357071.
XX
PR 19-JUL-1999; 99US-00357071.
XX
XX (ISIS-) ISIS PHARM INC.
PA
XX Monia BP, Cowser LM;
PI WPI; 2000-270346/23.
XX
DR Antisense compounds particularly oligonucleotides useful for prophylaxis,
PT diagnosis and treatment of diseases associated with expression of liver
PT glycogen phosphorylase.
XX
PS Claim 3; Col 39; 33pp; English.

XX Sequences AAA14008-A14047 represent phosphorothioate antisense
CC oligonucleotides targeted to the human liver glycogen phosphorylase gene
CC (PYGL gene), which inhibit its expression. The antisense oligonucleotides
CC were designed to target different regions of human liver glycogen
CC phosphorylase RNA, and were analysed for their effect on liver glycogen
CC phosphorylase levels by quantitative real-time PCR. Liver glycogen
CC phosphorylase is one of three glycogen phosphorylase isozymes, which
CC differ in their tissue-specific distribution, immunological properties
CC and electrophoretic mobilities and are encoded by three different genes.
CC Liver glycogen phosphorylase is encoded by the PYGL gene, which is
CC located on chromosome 14. Liver glycogen phosphorylase (also known as 1,4
CC alpha-D-glucan:orthophosphate alpha-D-glucosyltransferase, and HGLPa in
CC its phosphorylated, active form) catalyses the degradation of stored
CC glycogen in the liver to glucose-1-phosphate via the cleavage of the
CC alpha-1,4-glycosidic bonds. It therefore plays a critical role in
CC carbohydrate metabolism and blood glucose homeostasis. Inhibition of
CC liver glycogen phosphorylase and therefore glycogenolysis may provide a
CC means of reducing blood glucose levels in diabetic patients, particularly
CC those with type II (non insulin-dependent) diabetes. The antisense
CC oligonucleotides of the invention are useful for diagnosis, prevention
CC and treatment of conditions associated with liver glycogen phosphorylase
CC expression, or those which may benefit from inhibition of liver glycogen
CC phosphorylase expression, such as type II diabetes

XX Sequence 20 BP; 3 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1176 TGCCACGTGTCGCCAGCCCA 1195
|||||
DB 1 TGCCACGTCTCCAGCCCA 20
|||||

RESULT 976
AAZ72207
ID AAZ72207 standard; DNA; 20 BP.
XX
AC AAZ72207;
DT 10-SEP-2001 (first entry)
DE Human biallelic marker upstream amplification primer SEQ ID NO:6563.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /note= "Phosphorothioate linkages"

XX US6043091-A.
PN 28-MAR-2000.
XX
PD 21-APR-1999; 99WO-IB000822.
XX
PF 21-APR-1999; 98US-0082614P.
XX
PR 21-APR-1999; 98US-0082614P.
XX
PR 23-NOV-1998; 98US-0109732P.
XX
XX (GEST) GENSET.
PA
XX Cohen D, Blumenfeld M, Chumakov I;
PI WPI; 2000-013267/01.
XX
DR Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
PT
XX Claim 9; Page 1630; 2745pp; English.

XX AA265654 to AA269578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.
 CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 20 BP; 2 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1014 TGTGTTGGGATGGGCTG 1033
 Db 1 TCTGATTTGGGATGGGCTG 20
 RESULT 977
 AA275831/C
 ID AA275831 standard; DNA; 20 BP.
 XX
 AC AA275831;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human biallelic marker downstream amplification primer SEQ ID NO:10187.
 XX
 KW Human genome; biallelic marker; high density disequilibrium map;
 KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
 KW haplotyping; hybridisation; identification; characterisation;
 KW amplification; single nucleotide polymorphism; SNP; PCR primer;
 KW diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954500-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 21-APR-1999; 99WO-IB000822.
 XX
 PR 21-APR-1998; 98US-0082614P.
 PR 23-NOV-1998; 98US-0109732P.
 XX
 PA (GIST) GENSET.
 XX
 PI Cohen D, Blumenfeld M, Chumakov I;
 XX
 DR WPI; 2000-013267/01.
 XX
 PT Novel biallelic markers used to construct a high density disequilibrium
 PT map of the human genome.
 XX
 PS Claim 9; Page 2402; 2745pp; English.
 XX
 CC AA265654 to AA269578 represent human biallelic markers from the present
 CC invention, which contain a polymorphic base at position 24 of their
 CC nucleotide sequences. AA269579 to AA277440 represent amplification
 CC primers for the biallelic markers. The biallelic markers of the invention
 CC have a variety of uses: they can be used for high density mapping of the
 CC human genome, and in complex association studies and haplotyping studies
 CC which are useful in determining the genetic basis for disease states.

CC Compositions and methods of the invention can also be useful for the
 CC identification of the targets for the development of pharmaceutical
 CC agents and diagnostic methods, as well as the characterisation of the
 CC differential efficacious responses to and side effects from
 CC pharmaceutical agents acting on a disease as well as other treatment.
 CC N.B. The SEQ ID NOS 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
 CC 3367, are not actually given a sequence in the Sequence Listing from the
 CC present invention
 XX
 SQ Sequence 20 BP; 2 A; 2 C; 9 G; 7 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 564 CCTGAAGCCCAATCCAGCCT 583
 Db 20 CCTGAAGCCCAACACACCCT 1
 RESULT 978
 AAC80118
 ID AAC80118 standard; DNA; 20 BP.
 XX
 AC AAC80118;
 XX
 DT 03-MAY-2001 (first entry)
 XX
 DE Reverse primer #30 used for amplification of HLA-A exon 2.
 XX
 KW HLA-A; HLA-B; HLA-C; typing; primer; human; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200061795-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 05-APR-2000; 2000WO-EP002998.
 XX
 PR 09-APR-1999; 99EP-00870068.
 PR 11-JUN-1999; 99US-0138614P.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI De Canck I, Rombout A, Rossau R;
 XX
 DR WPI; 2000-647426/62.
 XX
 PT Locus-specific, separate amplification of exon 2, exon 3, and/or exon 4
 PT of human leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles using defined
 PT primer sets, useful for subtyping or typing of HLA Class I alleles.
 XX
 PS Claim 4; Page 36; 128pp; English.
 XX
 CC The present invention relates to a method for the locus-specific,
 CC separate amplification of exon 2, exon 3, and/or exon 4 of human
 CC leukocyte antigen (HLA)-A, HLA-B, or HLA-C alleles. The method is useful
 CC for subtyping or typing of HLA class I alleles. The present sequence is
 CC an amplification primer used in the method
 XX
 SQ Sequence 20 BP; 1 A; 9 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15.2; DB 1; Length 20;
 Best Local Similarity 85.0%; Pred. No. 6.5e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 728 AGGCTTCTGGGCCCTCCCG 747
 Db 1 AGGGCCCTGGGCCCTCTCCCG 20

```
RESULT 979
ID AAI71234/c
XX AAI71234 standard; DNA; 20 BP.
XX AC AAI71234;
XX DT 23-JAN-2002 (first entry)
XX DE Human Toll like receptor 4 PCR sense primer 1 SEQ ID NO:7.
XX KW Human: Toll like receptor; TLR; CD14; antibody; anti-CD14 antibody;
XX KW TLR/CD14 binding inhibitor; antibacterial; immunosuppressive;
XX KW antipyretic; hypertensive; immunostimulant; haemostatic; vasotropic;
XX KW bacterial infection; sepsis; fever; hypotension; leukopaenia;
XX KW thrombopaenia; shock; multi-organ failure; ss.
XX OS Homo sapiens.
XX PN WO200172993-A1.
XX PD 04-OCT-2001.
XX PF 02-APR-2001; 2001WO-JP002869.
XX PR 31-MAR-2000; 2000JP-00099617.
XX PR 22-NOV-2000; 2000JP-00356719.
XX PR 28-MAR-2001; 2001US-00806158.
XX PA (MOCH ) MOCHIDA PHARM CO LTD.
XX PI Furusako S, Mori S, Shirakawa K, Takahashi T;
XX WPI; 2001-616487/71.
XX PT Anti-CD14 antibody or its fragment inhibiting the binding of CD14 to Toll
XX PT -like receptor, applicable in drugs for treating bacterial infection as
XX PT well as sepsis, fever, hypotension, leukopenia, thrombopenia and shock.
XX PS Example 2; Page 169; 202pp; Japanese.
XX CC The present invention describes an anti-CD14 antibody, which has a
XX CC function of inhibiting the binding of CD14 to the Toll-like receptor
XX CC (TLR). The anti-CD14 antibody can specifically recognise the epitope
XX CC containing the domain from numbers 269-315 in human CD14 of the sequence
XX CC in AAG68127 or a part of it. Anti-CD14 antibody has antibacterial,
XX CC immunosuppressive, antipyretic, hypertensive, immunostimulant,
XX CC haemostatic and vasotropic activities. The antibody together with other
XX CC polypeptides are applicable in drugs for treating bacterial infection as
XX CC well as sepsis, fever, hypotension, leukopaenia, thrombopaenia, shock and
XX CC multi-organ failure. AAG68127 to AAG68137 and AAI71230 to AAI71295
XX CC represent sequences used in the exemplification of the present invention
XX SQ Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1687 TCGTCTCTCTCTTCTTCTCA 1706
DB 20 TGGTGTCTTCTCTTCTCTCA 1
RESULT 980
ID AAF28352
XX AAF28352 standard; DNA; 20 BP.
XX AC AAF28352;
XX DT 02-APR-2001 (first entry)
XX DE DNA oligomer #2.
XX OS Homo sapiens.
KW Deoxynucleic S-Methylthiouraea; DNmt; antisense therapy;
KW cardiovascular disease; inflammatory disease; neurocellular disease;
KW antiviral therapy; human immunodeficiency virus; human-cytomegalovirus;
KW influenza; herpes; infection; ss.
XX OS Unidentified.
XX PN US6169176-B1.
XX PD 02-JAN-2001.
XX PF 28-SEP-1999; 99US-00407675.
XX PR 02-JUL-1998; 98US-0091481P.
XX PR 11-DEC-1998; 98US-0111800P.
XX PR 02-JUL-1999; 99US-00347443.
XX PA (REGC ) UNIV CALIFORNIA.
XX PI Dev AP, Bruice TC;
XX WPI; 2001-122276/13.
XX PT Preparing novel deoxynucleic alkyl thiourea oligonucleotide for use in
XX PT antisense therapy, by synthesizing oligonucleotides comprising backbone
XX PT of alkyl or alkoxy thiourea linkages in solution or on solid phase.
XX PS Example 7; Fig 16; 48pp; English.
XX CC The present sequence was used to demonstrate the ability of deoxynucleic
XX CC S-Methylthiouraea (DNmt) compounds to form triplexes with DNA oligomers. An
XX CC increase in the C content of the oligos resulted in a large decrease in
XX CC binding. This experiment was performed as an example of a method for
XX CC preparing oligonucleotides comprising a backbone of alkyl or alkoxy
XX CC thiourea linkages. The method is useful for preparing oligonucleotides
XX CC for use in antisense or antigene therapy, to inhibit production of
XX CC proteins associated with genetic diseases, cardiovascular, inflammatory
XX CC and neurocellular diseases, and for antiviral therapy, e.g. to treat
XX CC human immunodeficiency virus, human-cytomegalovirus, influenza and herpes
XX CC infections. The compounds are also useful as diagnostic reagents to
XX CC detect the presence or absence of the target DNA or RNA sequences to
XX CC which they specifically bind and by antagonising the normal biological
XX CC activity of a target protein, they can be used in the manipulation of
XX CC tissue e.g. tissue differentiation, both in vivo and in ex vivo tissue
XX CC cultures. The method provides an efficient and rapid solid-phase method
XX CC for the synthesis of thiourea and S-methylthiouraea
XX SQ Sequence 20 BP; 16 A; 4 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1735 CAAAAAATAAAAAAAAAA 1754
DB 1 CAAAAAATAAAAAAAAAA 20
RESULT 981
ID AAC82913/c
XX AAC82913 standard; DNA; 20 BP.
XX AC AAC82913;
XX DT 21-MAR-2001 (first entry)
XX DE Human beta-actin derived oligonucleotide #6.
XX KW Recognition system; screening; identification; pharmaceutical; toxin;
XX KW plant protection agent; toxin; venom; carcinogen; venom; teratogen;
XX KW herbicide; fungicide; pesticide; beta-actin; human; ss.
XX OS Homo sapiens.
```


CC the cabh gene encoding A. chrysogenum CPC-AH, under conditions where it
CC is either expressed or inactivated. The genes and proteins are used for
CC removal of acetyl groups, especially from the 3'-carbon of CPC or from 7-
CC aminoccephalosporanic acid, to give deacetylated products useful as
CC intermediates for cephalosporin antibiotics. Inactivation of the gene
CC that expresses CPC increases production of cephalosporins by A.
CC chrysogenum. This sequence represents a PCR primer used to clone the cabh
CC gene encoding A. chrysogenum:CPC-AH
XX
XX Sequence 20 BP; 1 A; 8 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. NO. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1462 TGTGGCTGCTGCTCTCTC 1481
DB 1 TCGGTGCTGCTACTCTCTC 20

RESULT 984
ABA91537
ID ABA91537 standard; DNA; 20 BP.
XX
AC ABA91537;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA oligonucleotide AGT02025 used to test RNase H cleavage.
XX
KW Nucleic acid detection; probe; mismatch; ss.
XX
OS Synthetic.

FH Key Location/Qualifiers
FT misc_feature 12
FT /*tag= a
FT /note= "mismatch to target DNA"

PN WO200206531-A2.
XX
PD 24-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US022166.
XX
PR 14-JUL-2000; 2000US-00616761.
PR 30-MAR-2001; 2001US-00823647.

XX (GENE-) APPLIED GENE TECHNOLOGIES INC.

XX Dattagupta N;
XX
DR WPI; 2002-171819/22.

XX Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.

XX Example 5; Page 50; 72pp; English.

XX The present sequence is that of oligonucleotide AGT02025, which contains
CC a single mismatch with a target DNA oligonucleotide (see ABA91531). It is
CC one of a set of oligonucleotides (see ABA91532-37) containing
CC mismatch(es) to the target DNA that were tested in a hybridisation/RNase
CC H cleavage assay. The results showed that 2 mismatches between the target
CC and the probe ablated RNase H cleavage. The effect of one mismatch site
CC was less than that of two mismatch sites, and showed a polarity effect.
CC with weaker inhibition shown in assays with AGT02021 than in assays using
CC an oligonucleotide in which the mismatch was at an adjacent position.
CC Oligonucleotides in which the mismatch was G or C rather than A showed
CC similar inhibition of RNase H cleavage. The invention provides probes for
CC nucleic acid hybridisation. The probes form a hairpin structure

CC comprising a double-stranded stem and a single-stranded loop, and are
CC capable of both intramolecular and intermolecular hybridisation. The
CC double-stranded stem may comprise a methylphosphonate DNA:RNA hybrid that
CC is resistant to RNase H cleavage. When the probe hybridises with a target
CC DNA, the RNA strand in the DNA:RNA duplex becomes sensitive to RNase H
CC treatment and can be removed. Arrays and methods for nucleic acid
CC hybridisation using the probes are provided

XX Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. NO. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1755
DB 1 AAAAAAAAAATTATAAAAA 20

RESULT 985
AAL41013/C
ID AAL41013 standard; DNA; 20 BP.
XX
AC AAL41013;
XX
DT 11-OCT-2002 (first entry)
XX
DE Anti-CD14 monoclonal antibody related oligonucleotide #1.
XX
KW Immunosuppressive; antibacterial; anti-CD14 antibody; epitope; sepsis;
KW human CD14; ds.
XX
OS Unidentified.

XX WO200242333-A1.
XX
PD 30-MAY-2002.
XX
PF 28-SEP-2001; 2001WO-JP008563.
XX
PR 22-NOV-2000; 2000JP-00356719.

XX (MOCH) MOCHIDA PHARM CO LTD.
XX
PI Furusako S, Shirakawa K, Mori S;
XX
DR WPI; 2002-454920/48.

XX Anti-CD14 monoclonal antibody which inhibits CD14/T lymphocyte receptor
PT binding by specifically recognizing epitope in human CD14 domain to
PT prevent interaction and suppress cell activation, useful for treating
PT sepsis.
XX
PS Example 2; Page 45; 156pp; Japanese.
XX
CC The invention relates to an anti-CD14 antibody which can specifically
CC recognise an epitope containing a part of a domain with not less than 8
CC amino acids in human CD14 in the region from positions 269-315 in a fully
CC defined sequence of 356 amino acids as given in the specification. The
CC antibody is useful in drug compositions for treating sepsis and for
CC screening remedies for sepsis. This polynucleotide sequence represents
CC anti-CD14 related oligonucleotide of the invention

XX Sequence 20 BP; 9 A; 4 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. NO. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1687 TCGTGTCTTCTCTTCTTCTCA 1706
DB 20 TGGTGTCTTCTTCTTCTCTCA 1

DE	Oligonucleotide synthesis method related DNA #9.
XX	
KW	Oligonucleotide synthesis; polynucleotide array; protecting group;
KW	oxidation; ss.
XX	
OS	Synthetic.
PN	BPI176151-A1.
XX	
PD	30-JAN-2002.
XX	
PF	27-JUL-2001; 2001EP-00118360.
XX	
PR	28-JUL-2000; 2000US-00627249.
XX	
PA	(AGIL-) AGILENT TECHNOLOGIES INC.
XX	
PI	Dellinger DJ, Perbost MGM, Betley JR, Caruthers M;
XX	
DR	WI; 2002-156732/21.
XX	
PT	Synthesis of polynucleotide useful during fabrication of an array
PT	involves coupling nucleoside phosphoramidite and a solid-supported
PT	nucleoside and treating the product with an oxidation/deprotection
PT	composition.
XX	
PS	Example 2; Page 17; 36pp; English.
XX	
CC	The present invention relates to a method for the synthesis of a
CC	polynucleotide which involves coupling a second nucleoside to a first
CC	nucleoside through a phosphite linkage, where the second nucleoside has a
CC	non-carbonate protecting group protecting a hydroxyl, and exposing the
CC	product to a composition which concurrently oxidizes the phosphite formed
CC	to a phosphate and deprotects the protected hydroxyl of the second
CC	nucleoside. The method is useful for synthesizing the polynucleotides,
CC	for carrying out either 3' to 5' or 5' to 3' synthesis and for
CC	fabricating an addressable array of polynucleotides on a substrate. The
CC	present sequence is an oligonucleotide produced to demonstrate the method
CC	of the invention
XX	
SQ	Sequence 20 BP; 0 A; 10 C; 0 G; 10 T; 0 U; 0 Other;
	Query Match 0.9%; Score 15.2; DB 1; Length 20;
	Best Local Similarity 85.0%; Pred. No. 6.5e+02;
	Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0
QY	26 GGCGAAGACGAAAAAAAAAA 45 DB 20 GGCGGGGGGGAAAAAAAAAA 1
RESULT 988	
AAD33542/C	
ID	AAD33542 standard; DNA; 20 BP.
XX	
AC	AAD33542;
XX	
DT	01-JUL-2002 (first entry)
XX	
DE	PCR primer #4 used in the invention.
XX	
KW	Haematopoiesis; clotting; kidney failure; wound healing; cancer;
KW	neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;
KW	heart disorder; ischaemic heart disease; neuroprotective; vulnaray;
KW	cerebrovascular disorder; ischaemic heart disease; immunosuppressive;
KW	glomerular disease; glomerulonephritis; uterine disorder; hyperplasia;
KW	fetal spleen; prostate disorder; inflammatory disease; Crohn's disease;
KW	proliferative disorder; gynaecological; haemostatic; antibacterial;
KW	systemic lupus erythematosus; immunodeficiency disorder; antiasthmatic;
KW	cytostatic; nephrotropic; antidiabetic; cerebroprotective; tranquilizer;
KW	hypertensive; tumour; injury; trauma; antiangular; vasotropic; antitumor;
KW	apoptotic disorder; rheumatoid arthritis; cardiac; renal disorder;
KW	hepatotropic; antipsoptic; antiallergic; dermatological; virucide; PCR;

Db 20 GCCGAGCTCCGCCCCAGCA 1

RESULT 990
ABZ89486
ID ABZ89486 standard; DNA; 20 BP.
XX
AC ABZ89486;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandreasgra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 4728; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 15 A; 4 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1733 TACAAAAA 1752
||||| ||| |||||

Db 1 TACAACCAACCAAAAAA 20

RESULT 991
ABZ90374
ID ABZ90374 standard; DNA; 20 BP.
XX
AC ABZ90374;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandreasgra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 5616; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytosstatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 17 A; 3 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 AAAAAA 1755
||||| ||| |||||

Db 1 AAACAAACAAACAAA 20

RESULT 992
ABZ89084
ID ABZ89084 standard; DNA: 20 BP.

DT 17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antisense; lung dysfunction

KW antiinflammatory steroid; leukotriene; antiinflammatory; antiallergic;
KW antihistamic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antitense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; db.

OS Homo sapiens.

PN WO200285308-A2.

PD 31-OCT-2002.

23-APR-2002:

XX
PR 24-APR-2007: 2001US-0286137P

XX PA (EPIC-) EPICGENESIS PHARM INC

XX	Nr 00	TW	1:1	V	Bandw
BT					

PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.

Pharmaceutical compo

PT ubiquinone.

PS Disclosure; SEQ ID NO 4326; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' and genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published/pct](http://wipo.int/pub/published/pct) sequences

Sequence 20 BP; 16 A; 1 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.9%: Score 15.2: DB 1: Length 20:

Best Local Similarity 85.0%; Pred. NO. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1734 ACACAAAAA AAAAAAAAAA 1753

Db 1 ACGAGAGCAAAAAAAAAAAAAA 20

RESULT 993
ABZ85668/C

ID ABZ85668 standard; DNA; 20 BP.

AC ABZ85668;

17-OCT-2003 (first entry)

Human oligonucleotide sequence.

Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; anti allergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.

XX Homo sapiens.

XX PN WO200285308-A2.

31-OCT-2002.

XX
PF
23-APR-2002:XX
PP 24-APR-2001. 2001US-0286137P

XX
BA
/EDIC-1 EDICENETS: BUAPM INC

XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tanq L, Shahabuddin S;

WPI: 2003-229219/22.

PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

PS Claim 15; SEQ ID NO 910; 872pp: English.

The invention relates to a novel pharmaceutical composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine or receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at <http://www.wipo.int/pub/published> pct sequences

Sequence 20 BP; 0 A; 3 C; 0 G; 17 T; 0 U; 0 Other;

Query Match 0.9%: Score 15.2: DB 1: Length 20:

Best Local Similarity 85.0%; Pred. NO. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755

Db 20 AAGAGAAAAAAGAAAAA 1

RESULT 994
ABZ85670/C
ID ABZ85670 standard; DNA; 20 BP.
XX AC ABZ85670;
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI: 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX PS Claim 15; SEQ ID NO 912; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 1 A; 2 C; 0 G; 17 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAAAAAA 1755
||||| ||||||| |||||

Db 20 AAAAAATAGAAAAAGAAAAA 1

RESULT 995
ABZ89131/C
ID ABZ89131 standard; DNA; 20 BP.
XX AC ABZ89131;
XX DT 17-OCT-2003 (first entry)
XX DE Human oligonucleotide sequence.
XX KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX OS Homo sapiens.
XX PN WO200285308-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013135.
XX PR 24-APR-2001; 2001US-0286137P.
XX PA (EPIG-) EPIGENESIS PHARM INC.
XX PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI: 2003-229219/22.
XX PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX PS Disclosure; SEQ ID NO 4373; 872pp; English.
XX CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 20 BP; 0 A; 8 C; 1 G; 11 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 23 AGGGGGGAGAGAAAAA 42
||||| ||||||| |||||

Db 20 CAGAGGGAGCCTGGGCCAAG 1

RESULT 998
ACC83605
ID ACC83605 standard; DNA; 20 BP.
XX
AC ACC83605;
XX
DT 08-SEP-2003 (first entry)
XX
DE Human Toll-like receptor 4 antisense oligonucleotide ISIS #114628.
XX
KW Human; Toll-like receptor 4; receptor; antiinflammatory; immunomodulator;
KW phosphorothioate; antisense; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..20
FT /*tag= a
FT /*mod_base= OTHER
FT /note= "OTHER = phosphorothioate nucleotides, the
FT oligonucleotide comprises a central gap region of 10 2'-
FT deoxynucleotides, flanked on both sites by 5-nucleotides
FT wings composed of 2'-methoxyethyl nucleotides"
FT modified_base 11
FT /*tag= b
FT /*mod_base= m5c
FT modified_base 16
FT /*tag= c
FT /*mod_base= m5c
FT modified_base 18
FT /*tag= d
FT /*mod_base= m5c
FT modified_base 19
FT /*tag= e
FT /*mod_base= m5c
XX
XX WO2003044163-A2.
XX
XX 30-MAY-2003.
XX
XX 14-NOV-2002; 2002WO-US036390.
XX
XX 19-NOV-2001; 2001US-00001863.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Karras JG, Koller E;
XX
XX WPI; 2003-468766/44.
XX
XX New antisense oligonucleotides for modulating Toll-like receptor 4 gene
XX expression, particularly useful for preventing, delaying or treating e.g.
XX inflammatory disorders, or conditions involving Th1 or Th2 immune
XX responses.
XX
XX Example 14; Page 95; 110pp; English.
XX
XX The present sequence is that of antisense oligonucleotide ISIS #114628.
XX This chimeric phosphorothioate oligonucleotide, having 2'-MOE wings and a
XX deoxy gap, is targeted to the 5' untranslated region of human Toll-like
XX receptor 4 mRNA. It exhibits 32% inhibition of human Toll-like receptor 4
XX expression in THP-1 cells. It is useful for inhibiting the expression of
XX Toll-like receptor 4 in cells or tissues. The oligonucleotide is
XX particularly useful for treating or preventing a disease or condition
XX associated with Toll-like receptor 4, e.g. an inflammatory disorder or a
XX condition involving an immune response, particularly Th1 or Th2 responses
XX
XX Sequence 20 BP; 3 A; 4 C; 10 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15.2; DB 1; Length 20;

Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 101 GGTGAGGCCAGAGGCTCGG 120
|||||
Db 1 GGTGAGGGGCTGAGGCTCCG 20
|||||

RESULT 999
ABX95028
ID ABX95028 standard; DNA; 20 BP.
XX
AC ABX95028;
XX
DT 13-JUN-2003 (first entry).
XX
DE Human bcr-abl gene rearrangement assay primer BCR-P2,P3F.
XX
KW Human; primer; PCR; ss; Philadelphia chromosome; bcr-abl; CML; ALL;
KW chronic myeloid leukaemia; acute lymphoblastic leukaemia;
KW translocation rearrangement.
XX
OS Homo sapiens.
XX
FN US2002192645-A1.
XX
PD 19-DEC-2002.
XX
PF 22-DEC-2000; 2000US-00747165.
XX
PR 24-DEC-1999; 99US-0173050P.
XX
PA (TSEN/) TSENG R W.
PA (SAMO/) SAMOSZUK M K.
XX
PI Teeng RW, Samoszuk MK;
XX
XX WPI; 2003-361830/34.
XX
XX Determining bcr-abl translocation rearrangements in a biological sample,
XX useful for diagnosing chronic myeloid leukemia or acute lymphoblastic
XX leukemia, comprises performing real time polymerase chain reaction on the
XX cDNA.
XX
XX Disclosure; Page 6; 18pp; English.
XX
XX The invention relates to a method of determining bcr-abl translocation
XX rearrangements (the Philadelphia chromosome) in a biological sample,
XX which comprises reverse transcribing extracted RNA from the sample to
XX cDNA and performing polymerase chain reaction (PCR) on the cDNA. Also
XX included is a method of diagnosing chronic myeloid leukaemia (CML) or
XX acute lymphoblastic leukaemia (ALL) by performing the assay cited above.
XX The method is useful in assaying biological samples for bcr-abl
XX translocation rearrangements and reporting the results of such assays
XX useful in the diagnosis of CML and/or ALL. The present sequence
XX represents the human bcr-abl gene rearrangement assay primer BCR-P2,P3F
XX
XX Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 922 GAGCTGGATAGGCTGACGAA 941
|||||
Db 1 GAGCTGCAGATGCTGACGAA 20
|||||

RESULT 1000
AAD49622
ID AAD49622 standard; DNA; 20 BP.
XX
XX AAD49622;
XX

```
XX DT 24-MAR-2003 (first entry)
XX DE Human EPO gene fragment amplifying antisense PCR primer #1.
XX KW Human; erythropoietin; single nucleotide polymorphism; psoriasis; SNP;
XX KW acquired immune deficiency syndrome; venereal disease; carcinoma; EPO;
XX KW autoimmune disease; gastrointestinal disorder; cardiovascular disease;
XX KW Kaposi's sarcoma; ulcerative colitis; central nervous system disease;
XX KW renal insufficiency; inflammatory process; radiotherapy; chemotherapy;
XX KW metabolic disease; Alzheimer's disease; Parkinson's disease; melanoma;
XX KW schizophrenia; Crohn's disease; rheumatoid arthritis; cancer; obesity;
XX KW tumour; depression; lymphoma; leukaemia; infection; pneumonia; asthma;
XX KW genital wart; allergy; multiple myeloma; anaemia; therapy; AIDS; PCR;
XX KW primer; ss.
XX OS Homo sapiens.
XX XX WO200285940-A2.
XX PN 31-OCT-2002.
XX PD 29-MAR-2002; 2002WO-EP004331.
XX PF 04-APR-2001; 2001PR-00004603.
XX PR 21-DEC-2001; 2001US-0343163P.
XX PR 04-JAN-2002; 2002US-0345440P.
XX PR 21-FEB-2002; 2002US-0358598P.
XX XX (GENO-) GENODYSSE.
XX PA Escary J;
XX PI WPI; 2003-093099/08.
XX DR Novel polypeptide encoded by nucleotide sequence derived from human
XX PT erythropoietin gene with single nucleotide polymorphisms, for diagnosing,
XX PT preventing and treating cancers, infections and autoimmune diseases.
XX XX Example 2; Page 74; 76pp; English.
XX PS The invention relates to polypeptides encoded by nucleotide sequences
XX CC derived from human erythropoietin gene (EPO) with single nucleotide
XX CC polymorphisms. Sequences of the invention are useful for preventing or
XX CC treating diseases such as cancers and tumours which include melanomas,
XX CC metastasising renal carcinomas, lymphomas such as follicular lymphomas,
XX CC and cutaneous T cell lymphoma, leukaemias including chronic lymphocytic
XX CC leukaemia and chronic myeloid leukaemia, cancers of the liver, neck, head
XX CC and kidneys, multiple myeloid leukaemia, carcinoid tumours and tumours that appear
XX CC following an immune deficiency comprising Kaposi's sarcoma in the case of
XX CC AIDS; infectious diseases such as viral infections including chronic
XX CC hepatitis B and C and human immunodeficiency virus (HIV)/acquired immune
XX CC deficiency syndrome (AIDS) and infectious pneumonias; venereal diseases
XX CC such as genital warts; immunologically related diseases and/or autoimmune
XX CC diseases and disorders which include rejection of tissue or organ grafts,
XX CC allergies, asthma, psoriasis, rheumatoid arthritis, multiple sclerosis,
XX CC Crohn's disease and ulcerative colitis; cardiovascular diseases such as
XX CC brain injury and anaemias including anaemia in patients under dialysis in
XX CC renal insufficiency, as well as anaemia resulting from chronic
XX CC infections, inflammatory processes, radiotherapies and chemotherapies;
XX CC metabolic diseases such as non-immune associated diseases such as
XX CC obesity, central nervous system diseases including Alzheimer's disease,
XX CC Parkinson's disease, schizophrenia and depression. Gastrointestinal
XX CC disorders and disorders connected with chemotherapy treatments. The
XX CC present sequence is human EPO gene fragment amplifying PCR primer
XX XX Sequence 20 BP; 3 A; 8 C; 1 G; 8 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1644 GATCACTCTCCTGCATCC 1663
```

```
DB 1 GATCATTCTCCTTCATCC 20
||||| ||||| ||||| |||||
RESULT 1001
AAL53968
ID AAL53968 standard; DNA; 20 BP.
XX AC AAL53968;
XX DT 18-FEB-2003 (first entry)
XX DE DNA mutation detection related ribonucleotide, SEQ ID No 18.
XX KW Detecting; point mutation; hybridising; target DNA; duplex; RNase H;
XX KW single nucleotide polymorphism; ss.
XX OS Unidentified.
XX PN US2002142308-A1.
XX PD 03-OCT-2002.
XX PF 30-MAR-2001; 2001US-00823634.
XX PR 30-MAR-2001; 2001US-00823634.
XX PA (DAT/) DATTAGUPTA N.
XX PA (TSEN/) TSENG T.
XX PI Dattagupta N, Tseng T;
XX DR WPI; 2003-102506/09.
XX DR Detecting point mutation in DNA strand, by hybridizing target DNA strand
XX PT having mutation with test DNA strand to form duplex, contacting the
XX PT duplex with RNase H and determining the cleavage of test strand by RNase
XX PT H.
XX XX Example 5; Fig 4; 26pp; English.
XX PS The invention relates to a novel method for detecting a point mutation in
XX CC a DNA strand. The novel method comprises hybridising a target DNA strand
XX CC containing or suspected of containing a point mutation with a test
XX CC nucleic acid strand complementary to the DNA strand to form a target DNA
XX CC strand/test nucleic acid strand duplex, contacting the duplex with an
XX CC RNase H, and determining whether the ribonucleotide residues within the
XX CC nucleotide sequence are cleaved by RNase H. The method is useful for
XX CC detecting a point mutation in a DNA strand, where the point mutation to
XX CC be detected is a single nucleotide polymorphism, preferably a
XX CC polymorphism in a genome, e.g., a viral, bacterial, eukaryotic, mammalian
XX CC or human genome. The method is useful to detect any nucleic acids from
XX CC any species of organisms such as Acinetobacter, Bacillus, Candida,
XX CC Enterococcus, Haemophilus, Mycobacterium and Streptococcus, and viruses.
XX CC This polynucleotide sequence represents a ribonucleotide relating to the
XX CC mutation detecting method of the invention
XX XX Sequence 20 BP; 17 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15.2; DB 1; Length 20;
XX Best Local Similarity 85.0%; Pred. No. 6.5e+02;
XX Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1755
||||| ||||| ||||| |||||
DB 1 AAAAAAAAAATATTAAAAAAAAA 20
RESULT 1002
AAD61440/c
ID AAD61440 standard; DNA; 20 BP.
XX AC AAD61440;
```

XX 15-JAN-2004 (first entry)
XX Human TANGO cDNA related PCR primer #4.
XX
XX Human; TANGO; kidney failure; hyperplasia; inflammatory disorder; cancer;
KW angiogenesis; haematopoietic disorder; pancreatic disorder; hypertension;
KW heart disorder; hepatic disorder; diabetes mellitus; placental disorder;
KW cerebrovascular disease; Goodpasture's syndrome; cardiovascular disorder;
KW fetal spleen associated disease; reproductive disorder; atherosclerosis;
KW glomerular disease; intestinal disorder; proliferative disorder; tumour;
KW ovulation disorder; testicular disorder; lung disorder; Crohn's disease;
KW prostate disorder; Whipple's disease; haemophilia; anaemia; thalassaemia;
KW gene therapy; tranquilizer; vulnary; vasotropic; psoriasis; leukaemia;
KW jaundice; immunosuppressive; abortion; ischaemia; arthritis; allergy;
KW asthma; PCR; primer; ss.
XX
XX Homo sapiens.
XX
XX US2003104447-A1.
XX
XX 05-JUN-2003.
XX
XX 11-OCT-2002; 2002US-00269353.
XX
XX 23-APR-1998; 98US-00065661.
PR 23-APR-1999; 99US-00298531.
PR 21-FEB-2001; 2001US-00790264.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Holtzman DA, Goodearl ADJ, McCarthy SA;
XX WPI; 2003-787050/74.
XX
XX New TANGO polypeptides useful as modulating agents in regulating cellular
PT processes and for diagnosing, treating heart, liver, lung, kidney,
PT inflammatory and cellular proliferative disorders.
XX
XX Disclosure; Page 65; Opp; English.
XX
XX The invention relates to an isolated polypeptide termed human T139 (TANGO
CC -139), T125, T110, murine T175, human T175 or murine WDNM-2. T139 is
CC useful for treating kidney defects such as kidney failure or hyperplasia,
CC T125 is useful for treating wound healing and cancer, T110 is useful for
CC treating neoplasia, inappropriate angiogenesis or tissue regeneration and
CC T177 or WDNM-2 is useful for treating cancer, inflammatory disorders and
CC haematopoietic disorders. T125 and T110 are useful to treat pancreatic
CC disorders such as pancreatitis, diabetes mellitus, and Zollinger-Ellison
CC syndrome, placental disorders such as placental edema, cerebrovascular disease
CC disorders of the brain such as cerebral edema, cerebrovascular disease
CC and tumours and injury or trauma to the brain. T125, T110, T175 molecules
CC treat heart disorders e.g., ischaemic heart disease, atherosclerosis,
CC hypertension, angina pectoris, pulmonary (lung) disorders such as
CC rheumatoid lung disease, bronchial asthma and Goodpasture's syndrome,
CC disorders of skeletal muscle such as muscular dystrophy, motor neuron
CC disease e.g., amyotrophic lateral sclerosis, cardiovascular disorders
CC such as rheumatic heart disease or myocardial disease, hepatic disorder
CC including jaundice, hepatic failure, Crigler-Najjar syndromes or
CC malignant tumours. T139, T125, T110 and T175 molecules are useful to treat
CC renal (kidney) disorders such as glomerular disease (e.g., acute and
CC chronic glomerulonephritis) and reproductive disorders including
CC ovulation disorder, disorders due to infections and ovarian disorders.
CC T139, T125 and T175 are useful to treat testicular disorders and sperm cell
CC disorders. T175 is useful to treat uterine disorders, hyperplasia of the
CC endometrium, uterine cancer, bone marrow, blood and haematopoietic
CC associated diseases and disorders, e.g., acute myeloid leukaemia,
CC haemophilia, anaemia and thalassaemia. T-110 is useful to treat spleen
CC e.g., the fetal spleen associated diseases and disorder e.g., splenic
CC lymphoma and/or splenomegaly. T125 treats prostate disorders such as
CC inflammatory diseases, ovarian disorders such as ovarian endometriosis,
CC non-neoplastic cysts and tumours, intestinal disorders such as infective
CC enterocolitis, Crohn's disease and Whipple's disease, colonic disorders

CC such as congenital anomalies and tumours. T139, T125, T110, T175 or WDNM-2
CC are useful for treating proliferative disorders, inflammatory disorders
CC e.g., bacterial infection, psoriasis, e.g., ulcerative colitis, arthritis
CC and allergic inflammatory disorders (e.g., asthma, psoriasis). The
CC invention is useful in gene therapy. The present sequence is human TANGO
CC cDNA related PCR primer
XX
SQ Sequence 20 BP; 2 A; 9 C; 5 G; 4 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Oy 681 GGCACAGCCAGTGAGGGCT 700
Db 20 GGCACAGCCATGAGGGCT 1
RESULT 1003
ADD71322
ID ADD71322 standard; DNA; 20 BP.
XX
XX AC ADD71322;
XX
XX 15-JAN-2004 (first entry)
XX
XX Nucleic acid detection method-related universal DNA sequence #2.
DE Nucleic acid detection; nucleic acid quantitation; universal sequence;
KW nucleic acid detection; nucleic acid quantitation; universal sequence;
KW ss.
XX
XX Synthetic.
XX
XX WO2003078587-A2.
XX
XX 25-SEP-2003.
XX
XX 13-MAR-2003; 2003WO-US007818.
XX
XX 13-MAR-2002; 2002US-0364230P.
XX
XX (SYCN) SYNGENTA PARTICIPATIONS AG.
XX (SHIL//) SHI L.
XX
XX Shi L;
XX
XX WPI; 2003-803888/75.
XX
XX Detecting the presence of a target nucleic acid molecule in templates by
PT combining a detection probe, a first oligonucleotide, second
PT oligonucleotide, a primer and templates suspected of containing the
PT target nucleic acid molecule.
XX
XX Example 2; SEQ ID NO 9; 42pp; English.
XX
XX The invention comprises a method for detecting a target nucleic acid
CC molecule in a plurality of templates, the method involves combining a
CC detection probe, a first oligonucleotide, second oligonucleotide, a
CC primer and a plurality of templates suspected of containing the target
CC nucleic acid molecule. The method of the invention is useful for
CC detecting the presence of a target nucleic acid molecule in a plurality
CC of templates. The method is also useful for quantitating a particular
CC nucleic acid molecule in a sample. The invention provides a rapid,
CC reliable and cost-effective method for detecting a particular nucleic
CC acid molecule in a sample. The present DNA sequence represents a
CC universal sequence that was used in an example of the invention.
XX
SQ Sequence 20 BP; 7 A; 0 C; 13 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15.2; DB 1; Length 20;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
QY      862  GGAAGAGGAGGAGGAGCGA 881
Db      1  GGAGGAGGAGGAGGAGGAGA 20

RESULT 1004
AAQ79185
ID  AAQ79185 standard; DNA; 15 BP.
XX
AC  AAQ79185;
XX
XX  25-MAR-2003 (revised)
DT  21-JUN-1995 (first entry)
XX
DE  Nuclease resistant oligonucleotide.
XX
KW  Nuclease resistant oligonucleotide; inhibition of gene expression;
KW  9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS  Synthetic.
FH  Key Location/Qualifiers
FT  modified_base 13
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "9-methyl-acyclo-adenosine"
XX
PN  WO9422864-A1.
XX
PD  13-OCT-1994.
XX
PF  21-MAR-1994; 94WO-US002995.
PR  30-MAR-1993; 93US-00040326.
XX
PA  (STER ) STERLING WINTHROP INC.
XX
PI  Cook PD, Delecki DJ, Guinasso C;
XX
DR  WPI; 1994-333078/41.
XX
PT  New acyclic nucleoside analogues - used to prepare nuclease resistant
PT  oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS  Example 11; Page 20; 37pp; English.
XX
CC  AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
CC  nucleoside analogues which inhibit nuclease degradation. The nuclease
CC  resistant oligonucleotides can themselves be used to inhibit gene
CC  expression as antisense agents, in nucleic acid sequencing and diagnostic
CC  assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX  Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736  AAAAAAAAAAAAAA 1750
Db      1  AAAAAAAAAAAAAA 15

RESULT 1005
AAQ79184
ID  AAQ79184 standard; DNA; 15 BP.
XX
AC  AAQ79184;
XX
XX  25-MAR-2003 (revised)
DT  21-JUN-1995 (first entry)
XX
DE  Nuclease resistant oligonucleotide.
XX
```

```
XX
KW  Nuclease resistant oligonucleotide; inhibition of gene expression;
KW  9-methyl-8-acyclo-adenosine; antisense agents; ss.
XX
OS  Synthetic.
FH  Key Location/Qualifiers
FT  modified_base 14
FT  /*tag= a
FT  /mod_base= OTHER
FT  /note= "9-methyl-acyclo-adenosine"
XX
PN  WO9422864-A1.
XX
PD  13-OCT-1994.
XX
PF  21-MAR-1994; 94WO-US002995.
PR  30-MAR-1993; 93US-00040326.
XX
PA  (STER ) STERLING WINTHROP INC.
XX
PI  Cook PD, Delecki DJ, Guinasso C;
XX
DR  WPI; 1994-333078/41.
XX
PT  New acyclic nucleoside analogues - used to prepare nuclease resistant
PT  oligo-nucleotide(s) used partic. for inhibiting gene expression.
XX
PS  Example 10; Page 20; 37pp; English.
XX
CC  AAQ79182-Q79186 contain one or more 9-methyl-acyclo-adenosines, acyclic
CC  nucleoside analogues which inhibit nuclease degradation. The nuclease
CC  resistant oligonucleotides can themselves be used to inhibit gene
CC  expression as antisense agents, in nucleic acid sequencing and diagnostic
CC  assays. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX  Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1736  AAAAAAAAAAAAAA 1750
Db      1  AAAAAAAAAAAAAA 15

RESULT 1006
AAT52136/c
ID  AAT52136 standard; RNA; 15 BP.
XX
AC  AAT52136;
XX
XX  25-MAR-2003 (revised)
DT  25-MAR-1997 (first entry)
XX
DE  Human ICAM hammerhead ribozyme target sequence (nt. position 2910).
XX
KW  Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW  gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW  intercellular adhesion molecule; rel A; tumour necrosis factor;
KW  TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW  translocation; chronic myelogenous leukaemia; CML; cancer;
KW  Philadelphia chromosome; inflammation; autoimmune disease;
KW  atherosclerosis; myocardial infarction; stroke; restenosis;
KW  transplant rejection; rheumatoid arthritis; psoriasis;
KW  myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW  human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX
XX  ss.
XX  Homo sapiens.
XX
```

PN WO9523225-A2.
XX 31-AUG-1995.
XX 23-FEB-1995; 95WO-IB000156.
XX 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 16-AUG-1994; 94US-00291932.
PR 17-AUG-1994; 94US-00291433.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX (RIBO-) RIBOZYME PHARM INC.
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Belgelman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozyms having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX Claim 2; Page 175; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1007
AAT52138/c

AT52138 standard; RNA; 15 BP.
AAT52138;
25-MAR-2003 (revised)
25-MAR-1997 (first entry)
Human ICAM hammerhead ribozyme target sequence (nt. position 2911).
Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
intercellular adhesion molecule; rel A; tumour necrosis factor;
TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
translocation; chronic myelogenous leukaemia; CML; cancer;
Philadelphia chromosome; inflammation; autoimmune disease;
atherosclerosis; myocardial infarction; stroke; restenosis;
transplant rejection; rheumatoid arthritis; psoriasis;
myocardial ischaemia; Kawasaki disease; septic shock; HIV;
human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
ss.
Homo sapiens.
WO9523225-A2.
31-AUG-1995.
23-FEB-1995; 95WO-IB000156.
23-FEB-1994; 94US-00201109.
29-MAR-1994; 94US-00218934.
04-APR-1994; 94US-00222795.
07-APR-1994; 94US-00224483.
15-APR-1994; 94US-00227958.
15-APR-1994; 94US-00228041.
18-MAY-1994; 94US-00245736.
06-JUL-1994; 94US-00271280.
16-AUG-1994; 94US-00291932.
16-AUG-1994; 94US-00291433.
17-AUG-1994; 94US-00292620.
19-AUG-1994; 94US-00293520.
02-SEP-1994; 94US-00300000.
08-SEP-1994; 94US-00303039.
23-SEP-1994; 94US-00311486.
23-SEP-1994; 94US-00311749.
28-SEP-1994; 94US-00314397.
03-OCT-1994; 94US-00316771.
07-OCT-1994; 94US-00319492.
11-OCT-1994; 94US-00321993.
04-NOV-1994; 94US-00334847.
10-NOV-1994; 94US-00337608.
28-NOV-1994; 94US-00345516.
16-DEC-1994; 94US-00357577.
23-DEC-1994; 94US-00363233.
30-JAN-1995; 95US-00380734.
(RIBO-) RIBOZYME PHARM INC.
Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
Modak A, Pavco P, Belgelman L, Sullivan SM, Sweedler D, Thompson JD;
Tracz D, Usman N, Wincott FE, Woolf T;
WPI; 1995-351090/45.
Ribozyms having modified bases and methods for producing them - for use
in inhibiting disease related genes.
Claim 2; Page 175; 407pp; English.
The present sequence represents a preferred target sequence for an
enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
nucleotide base position indicated in the DE line. Regions of the mRNA
that do not form secondary folding structures and that contain potential
hammerhead and hairpin ribozyme cleavage sites were identified by
computer analysis. Ribozymes directed against these mRNA sequences were
designed and synthesised with modifications that improve their nuclease
resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
inhibit ICAM-1 expression, making them useful for reducing transplant
rejection and alleviating symptoms in patients with rheumatoid arthritis,
asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
correct PI field.)
Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1007
AAT52138/c

CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICM-1 target sequences and thereby
 CC inhibit ICM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)

XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
 SQ Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1008

AAV01604
 ID AAV01604 standard; DNA; 15 BP.

XX AC AAV01604;

XX 25-MAR-2003 (revised)

DT 31-MAR-1998 (first entry)

XX Oligonucleotide containing phosphoramidate linkages.

XX phosphoramidate linkage; solid phase synthesis; ss.

OS Synthetic.

XX FH Key Location/Qualifiers

FT misc_feature 1..15

FT /*tag= a

FT /note= "these residues have N3'->P5' phosphoramidate linkages"

XX PN WO97311009-A1.

XX PD 28-AUG-1997.

XX PF 14-JUN-1996; 96WO-US010418.

XX PR 21-FEB-1996; 96US-00603566.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;
 PI Schultz RG;

XX DR WPI; 1997-435080/40.

XX Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
 PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
 PT phosphoramidite then oxidation, useful as research, diagnostic and
 PT therapeutic agents.

XX PS Disclosure; Page 28; 60pp; English.

XX A new method is provided for the synthesis of oligonucleotides having N3'
 CC ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
 CC protected amino nucleoside to a solid support; (b) deprotecting the 3'-
 CC amino; (c) reacting with a 3'-protected aminonucleoside-5'-
 CC phosphoramidite monomer to form an internucleoside N3'-> P5'
 CC phosphoramidite link; (d) oxidising this link to phosphoramidate; and
 CC optionally repeating steps (b)-(d) until the required oligonucleotide is
 CC completed. This method provides better yields with lower reagent
 CC consumption than known processes, and can be operated on a large scale.

CC The obtained oligos, containing phosphoramidate linkages, have favourable
 CC binding properties, nuclease resistance and solubility, and are useful as
 CC research, diagnostic and therapeutic agents. The present sequence is an
 CC example of an oligonucleotide in which N3'->P5' phosphoramidate linkages
 CC have been introduced by the new method. (Updated on 25-MAR-2003 to
 CC correct PR field.)

SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 1 AAAAAAAAAAAAAA 15

RESULT 1009

AAV01603/c

ID AAV01603 standard; DNA; 15 BP.

XX AC AAV01603;

XX 25-MAR-2003 (revised)

DT 31-MAR-1998 (first entry)

XX Oligonucleotide containing phosphoramidate linkages.

XX phosphoramidate linkage; solid phase synthesis; ss.

OS Synthetic.

XX FH Key Location/Qualifiers

FT misc_feature 1..15

FT /*tag= a

FT /note= "these residues have N3'->P5' phosphoramidate linkages"

XX PN WO97311009-A1.

XX PD 28-AUG-1997.

XX PF 14-JUN-1996; 96WO-US010418.

XX PR 21-FEB-1996; 96US-00603566.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Hirschbein BL, Fearon KL, Gryaznov SM, Mccurdy SN, Nelson JS;
 PI Schultz RG;

XX DR WPI; 1997-435080/40.

XX Synthesis of N3' to P5' phosphoramidate oligo:nucleotide - by reacting
 PT immobilised 3'-amino nucleotide with new amino:nucleoside 5'-
 PT phosphoramidite then oxidation, useful as research, diagnostic and
 PT therapeutic agents.

XX PS Disclosure; Page 28; 60pp; English.

XX A new method is provided for the synthesis of oligonucleotides having N3'
 CC ->P5' phosphoramidate linkages. The method comprises (a) attaching a 3'-
 CC protected amino nucleoside to a solid support; (b) deprotecting the 3'-
 CC amino; (c) reacting with a 3'-protected aminonucleoside-5'-
 CC phosphoramidite monomer to form an internucleoside N3'-> P5'
 CC phosphoramidite link; (d) oxidising this link to phosphoramidate; and
 CC optionally repeating steps (b)-(d) until the required oligonucleotide is
 CC completed. This method provides better yields with lower reagent
 CC consumption than known processes, and can be operated on a large scale.
 CC The obtained oligos, containing phosphoramidate linkages, have favourable
 CC binding properties, nuclease resistance and solubility, and are useful as
 CC research, diagnostic and therapeutic agents. The present sequence is an

CC example of an oligonucleotide in which N3'-->P5' phosphoramidate linkages
 CC have been introduced by the new method. (Updated on 25-MAR-2003 to
 CC correct PR field.)

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAA 1750
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1010
 AAV07431/c
 ID AAV07431 standard; DNA; 15 BP.
 XX AC AAV07431;
 XX DT 27-OCT-1998 (first entry)
 XX DE Synthetic peptide-labeled oligonucleotide primer.
 XX KW oligonucleotide; peptide; conjugate; release tag compound;
 XX KW mass spectrometry; detection; identification; diagnosis; primer; ss.
 XX OS Synthetic.
 XX PN W09826095-A1.
 XX PD 18-JUN-1998.
 XX PF 10-DEC-1997; 97WO-US022639.
 XX PR 10-DEC-1996; 96US-0033037P.
 XX PR 16-MAY-1997; 97US-0046719P.
 XX PA (GENE-) GENETRACE SYSTEMS INC.
 XX PI Montforte JA, Becker CH, Pollart DJ, Shaler TA;
 XX DR WPI; 1998-348547/30.
 XX PT New release tag compounds for detecting target molecule(s) - comprising a
 PT reactive group, a release group and a releasable non-volatile mass label
 PT detectable by mass spectrometry.
 XX PS Example 3; Page 92; 170pp; English.

CC The sequence is that of an oligonucleotide primer which was produced as
 CC part of an oligonucleotide peptide conjugate as an example of a release
 CC tag compound (RTC). These comprise a reactive group, a release group and
 CC a non-volatile mass label comprising a synthetic polymer or biopolymer
 CC detectable by mass spectrometry. The RTCs can be used as probes for the
 CC detection of TMs. They can be used for e.g. identification of gene
 CC sequences, identification of non-coding nucleotide sequences,
 CC identification of mutations within a gene or protein sequence, detection
 CC of metals, detection of toxins, detection of receptors on an organism or
 CC a cell, characterisation of antibody-antigen interactions, enzyme-
 CC substrate interactions and characterisation of ligand interactions.
 CC Multiplex applications include multiple pathogen diagnostics, multigene
 CC genetic polymorphism screening, single nucleotide polymorphism (SNP)
 CC genotyping, clone and gene mapping, and gene expression analysis. The
 CC RTCs permit the ready detection of releasable mass labels by mass
 CC spectroscopy. The releasable mass labels permit the multiplexing of tens,
 CC hundreds and perhaps even thousands of different mass labels that can be
 CC used to uniquely identify each desired target

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAA 1750
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1011
 AAT86675/c
 ID AAT86675 standard; DNA; 15 BP.
 XX AC AAT86675;
 XX DT 04-JUN-1998 (first entry)
 XX DE Oligonucleotide linked to polyacrylamide.
 XX KW Capillary affinity gel electrophoresis; separation; polymer-gel;
 XX KW polyacrylamide; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT modified_base 1
 FT /*tag= a
 FT /note= "Thymine at 5' end attached to a polyacrylamide
 FT gel via a linking group"

XX PN W09745721-A1.
 XX PD 04-DEC-1997.
 XX PF 23-MAY-1997; 97WO-EP002647.
 XX PR 24-MAY-1996; 96CH-00001320.
 XX PA (NOVS) NOVARTIS AG.
 XX PI Muscate A, Paulus A, Matt F;
 XX DR WPI; 1998-041763/04.
 XX PT Separation of electrically charged target molecules - by capillary
 PT affinity gel electrophoresis using polymer-gel to which receptors for
 PT target molecules are bound.
 XX PS Example A1; Page 22; 41pp; English.

CC This sequence represents an oligonucleotide receptor molecule covalently
 CC bound to a polyacrylamide gel via a linking group. The invention relates
 CC to selective separation of electrically charged target molecules in an
 CC analytical mixture. It comprises capillary affinity gel electrophoresis
 CC using a capillary tube which is at least partly filled with a polymer
 CC gel. Receptors for target molecules are covalently bound to the polymer.
 CC An electric field of at least 50 volts/cm is applied. The capillary tube
 CC is charged with the analytical mixture. In a first separation stage, the
 CC target molecules in the mixture are bound to the receptors and the
 CC remaining components are eluted, optionally whilst splitting open. In a
 CC second stage, the elution conditions are changed, optionally in stages,
 CC so that the affinity of the target molecules for the receptor is
 CC eliminated and the target molecules are eluted and detected, optionally
 CC whilst splitting open. The process is useful for selective separation
 CC and/or determination of charged organic compounds, such as
 CC oligonucleotides, peptides or carbohydrates. It may be used, e.g. for
 CC isolation of specific proteins and DNA molecules, purification of
 CC antibodies, analysis of antisense compounds or screening for enzyme
 CC inhibitors. The process achieves higher resolution and selectivity than
 CC prior art processes, especially in the case of complex biological
 CC analytical mixtures. It has high sensitivity, even with small amounts of
 CC samples. The derivatised polymers may be synthesised specifically using
 CC standard methods

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 1012

AAT86605/c
ID AAT86605 standard; DNA; 15 BP.

XX AC AAT86605;

XX DT 04-JUN-1998 (first entry)

XX DE Oligonucleotide separated by capillary affinity gel electrophoresis.

XX KW Capillary affinity gel electrophoresis; separation; polymer-gel;
XX KW polyacrylamide; ss.

XX OS Synthetic.

XX PN WO9745721-A1.

XX PD 04-DEC-1997.

XX PF 23-MAY-1997; 97WO-BF002647.

XX PR 24-MAY-1996; 96CH-00001320.

XX PA (NOVS) NOVARTIS AG.

XX PI Muscate A, Paulus A, Natt F;

XX DR WPI; 1998-041763/04.

XX PT Separation of electrically charged target molecules - by capillary
XX PT affinity gel electrophoresis using polymer-gel to which receptors for
XX PT target molecules are bound.

XX Example D3; Page 25; 41pp; English.

XX PS A mixture of oligonucleotides (AAT86604-7) were separated by a new
XX CC process using capillary affinity gel electrophoresis. The invention
XX CC relates to selective separation of electrically charged target molecules
XX CC in an analytical mixture. It comprises capillary affinity gel
XX CC electrophoresis using a capillary tube which is at least partly filled
XX CC with a polymer gel. Receptors for target molecules are covalently bound
XX CC to the polymer. An electric field of at least 50 volts/cm is applied. The
XX CC capillary tube is charged with the analytical mixture. In a first
XX CC separation stage, the target molecules in the mixture are bound to the
XX CC receptors and the remaining components are eluted, optionally whilst
XX CC splitting open. In a second stage, the elution conditions are changed,
XX CC optionally in stages, so that the affinity of the target molecules for
XX CC the receptor is eliminated and the target molecules are eluted and
XX CC detected, optionally whilst splitting open. The process is useful for
XX CC selective separation and/or determination of charged organic compounds,
XX CC such as oligonucleotides, peptides or carbohydrates. It may be used, e.g.
XX CC for isolation of specific proteins and DNA molecules, purification of
XX CC antibodies, analysis of antisense compounds or screening for enzyme
XX CC inhibitors. The process achieves higher resolution and selectivity than
XX CC prior art processes, especially in the case of complex biological
XX CC analytical mixtures. It has high sensitivity, even with small amounts of
XX CC samples. The derivatised polymers may be synthesised specifically using
XX CC standard methods

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 1013

AAX00787/c

ID AAX00787 standard; DNA; 15 BP.

XX AC AAX00787;

XX DT 13-APR-1999 (first entry)

XX DE N3-P5 phosphoramidate oligonucleotide #3.

XX KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT misc_difference 1..15

XX FT /tag= a

XX FT /note= "contains internucleotide N3-P5 phosphoramidate
internucleotide linkages"

XX PN US5859233-A.

XX PD 12-JAN-1999.

XX PF 20-DEC-1996; 96US-00771789.

XX PR 21-FEB-1996; 96US-00603566.

XX PR 14-JUN-1996; 96US-00663918.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Gryaznov SM, Nelson JS, Mccurdy SN, Hirschbein BL, Schultz RG;
XX PI Fearon KL;

XX DR WPI; 1999-120007/10.

XX PT New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
XX PT the synthesis of oligo-nucleotide(s).

XX PS Example 10; Col 33; 34pp; English.

XX CC This sequence represents an example of an oligonucleotide containing
XX CC novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
XX CC sequence is generated synthetically by using an amine-exchange reaction
XX CC of phosphoramidites in which a deprotected 3'-amino group of an
XX CC oligonucleotide chain is exchanged for the amino portion of a 5'-
XX CC phosphoramidite with a protected 3' amino group. The resulting
XX CC phosphoramidite internucleotide linkage is oxidised to form a stable
XX CC protected phosphoramidate linkage

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
DB 15 AAAAAAAAAAAAAA 1

RESULT 1014

AAX00788

ID AAX00788 standard; DNA; 15 BP.

XX

AC AAX00788;
DT 13-APR-1999 (first entry)
DE N3-P5 phosphoramidate oligonucleotide #4.
KW Oligonucleotide; phosphoramidate; phosphoramidite; nucleoside; ss.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT misc_difference 1..15
FT /tag= a
FT /note= "contains internucleotide N3-P5 phosphoramidate
internucleotide linkages"
XX
PN US5859233-A.
PD 12-JAN-1999.
XX
PF 20-DEC-1996; 96US-00771789.
XX
PR 21-FEB-1996; 96US-00603566.
PR 14-JUN-1996; 96US-00663918.
XX
PA (LYNX-) LYNX THERAPEUTICS INC.
XX
PI Gryaznov SN, Nelson JS, Mccurdy SN, Hirschbein BL, Schultz RG;
PI Fearon KL;
XX
DR WPI; 1999-120007/10.
XX
XX New 3'-protected-amino-nucleoside-5'-phosphoramidite monomers - used in
PT the synthesis of oligo-nucleotide(s).
XX
PS Example 10; Col 33; 34pp; English.
XX
CC This sequence represents an example of an oligonucleotide containing
CC novel 3'-amino-5'-phosphoramidite nucleoside of the invention. The
CC sequence is generated synthetically by using an amine-exchange reaction
CC of phosphoramidites in which a deprotected 3'-amino group of an
CC oligonucleotide chain is exchanged for the amino portion of a 5'-
CC phosphoramidite with a protected 3' amino group. The resulting
CC phosphoramidite internucleotide linkage is oxidised to form a stable
CC protected phosphoramidate linkage
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 1015
AAZ61854/c
ID AAZ61854 standard; RNA; 15 BP.
XX
AC AAZ61854;
XX
DT 28-MAR-2000 (first entry)
XX
DE HCV 3' non core region substrate for Hammerhead ribozyme HCV.3-118.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX

PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Blatt L, Mswiggen JA, Roberts E, Pavco PA, Macejak D;
XX WPI; 2000-062023/05.
XX
PT Novel ribozymes for the treatment of diseases and conditions related to
hepatitis C infection.
XX
PS Claim 1; Page 49; 123pp; English.
XX
CC The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence in the 3' non-core region. The
CC HCV sequence was screened for optimal ribozyme target sites using a
CC computer folding algorithm and regions of the mRNA which did not form
CC secondary folding structures and contained potential ribozyme cleavage
CC sites were identified. Ribozymes were synthesised to target these sites
CC and their activities optimised by either varying the length of the
CC binding arms or by modification to prevent degradation by nucleases. The
CC ribozymes of the invention inhibit gene expression and/or viral
CC replication, and are used to treat diseases associated with Hepatitis C
CC virus (HCV) infection, e.g. cirrhosis, liver failure and hepatocellular
CC carcinoma. The ribozymes may be used in combination with interferon to
CC treat HCV infection, other infectious diseases, autoimmune diseases, and
CC cancer
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1016
AAZ64910/c
ID AAZ64910 standard; RNA; 15 BP.
XX
AC AAZ64910;
XX
DT 28-MAR-2000 (first entry)
XX
DE Substrate for HH ribozyme HCV.3-118 which cleaves HCV at nt. 9418.
XX
KW Enzymatic nucleic acid; hammerhead ribozyme; virus replication; cleavage;
KW cirrhosis; liver failure; hepatocellular carcinoma; interferon; cancer;
KW autoimmune disease; ss.
XX
OS Hepatitis C virus.
XX
PN WO9955847-A2.
XX
PD 04-NOV-1999.
XX
PF 26-APR-1999; 99WO-US009027.
XX
PR 27-APR-1998; 98US-0083217P.
PR 18-SEP-1998; 98US-0100842P.
XX

```

PR 25-FEB-1999; 99US-00257608.
PR 23-MAR-1999; 99US-00274553.
PA (RIBO-) RIBOZYME PHARM INC.
PI Blatt L, Mcswiggen JA, Roberts E, Pavco PA, Macejak D;
DR WPI; 2000-062023/05.
XX
XX Novel ribozymes for the treatment of diseases and conditions related to
PT hepatitis C infection.
PS Claim 1; Page 102; 123pp; English.
XX
XX The present sequence represents the preferred target sequence of an
CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
CC the Hepatitis C virus (HCV) RNA sequence at the base position given in
CC the descriptor line. The HCV sequence was screened for optimal ribozyme
CC target sites using a computer folding algorithm and regions of the mRNA
CC which did not form secondary folding structures and contained potential
CC ribozyme cleavage sites were identified. Ribozymes were synthesized to
CC target these sites and their activities optimised by either varying the
CC length of the binding arms or by modification to prevent degradation by
CC nucleases. The ribozymes of the invention inhibit gene expression and/or
CC viral replication, and are used to treat diseases associated with
CC Hepatitis C virus (HCV) infection, e.g. cirrhosis, liver failure and
CC hepatocellular carcinoma. The ribozymes may be used in combination with
CC interferon to treat HCV infection, other infectious diseases, autoimmune
CC diseases, and cancer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1
RESULT 1017
AAA46502/c
ID AAA46502 standard; cDNA; 15 BP.
XX
AC AAA46502;
XX
XX 04-SEP-2000 (first entry)
XX
XX PCR primer used to amplify DNA encoding an endo-beta-mannanase.
XX
XX Hydrolysis; polysaccharide; mannan; coffee; endo-beta-mannanase;
KW PCR primer; ss.
XX
XX Coffea arabica.
XX
XX WO200028046-A1.
XX
XX 18-MAY-2000.
XX
XX 28-OCT-1999; 99WO-EP008314.
XX
XX 11-NOV-1998; 98EP-00203742.
XX
XX (NEST ) SOC PROD NESTLE SA.
XX
XX Marraccini P, Rogers J;
XX
XX WPI; 2000-399535/34.
XX
XX New DNA encoding endo-beta-mannanase from coffee, used e.g. in
PT pharmaceutical, cosmetic or food compositions to hydrolyze polymannans.
XX
PS Disclosure; Page 32; 41pp; French.
XX
XX PCR primers AAA46501-02 were used to amplify DNA encoding an endo-beta-
CC mannanase enzyme, which is involved in the hydrolysis of polysaccharides
CC that consist of molecules of mannan, either simple or branched, linked
CC together by beta(1-4) bonds. The mannanase polynucleotide sequence is
CC used for in vivo modification of the coffee endo-beta-mannanase gene. It
CC is also used to produce transgenic plant cells (especially coffee cells)
CC which have modified properties of mannan polysaccharide, and thus altered
CC flavour or structure. The enzyme is used for modification, degradation or
CC synthesis of mannan polysaccharides in vitro, particularly to treat
CC coffee beans to increase the percentage of dry matter extraction, and
CC thus reduce the quantity of sediment
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1
RESULT 1018
AAA75048/c
ID AAA75048 standard; DNA; 15 BP.
XX
AC AAA75048;
XX
XX 15-JAN-2001 (first entry)
XX
XX Primer used to reverse transcribe human RNA.
XX
XX Human; heparanase; gene therapy; tumour; inflammation; autoimmunity;
KW heparin-binding growth factor; cytokine; neurodegenerative plaque;
KW wound healing; infection; burn; angiogenesis; restenosis;
KW atherosclerosis; inflammation; neurodegenerative disease;
KW Gerstmann-Straussler Syndrome; Creutzfeldt-Jakob disease; primer; ss.
XX
XX Homo sapiens.
XX
XX WO200052178-A1.
XX
XX 08-SEP-2000.
XX
XX 14-FEB-2000; 2000WO-US003542.
XX
XX 01-MAR-1999; 99US-00258892.
XX
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA (FRIE/) FRIEDMAN M M.
XX
XX Pecker I, Vlodaysky I, Feinstein E;
XX
XX WPI; 2000-579289/54.
XX
XX New polynucleotides encoding a polypeptide having heparanase activity,
PT useful in wound healing and in gene therapy, particularly in treating
PT tumor, inflammation, autoimmunity, neurodegenerative diseases.
XX
XX Disclosure; Page 44; 152pp; English.
XX
XX The present primer was used to reverse transcribe human RNA, from which a
CC cDNA sequence encoding a protein with heparanase catalytic activity was
CC amplified. The heparanase (hpa) polynucleotide is useful in gene therapy,
CC particularly in treating tumour, inflammation or autoimmunity.
CC Particularly, the polynucleotide is useful in modulating the
CC bioavailability of heparin-binding growth factors, cellular responses to
CC heparin-binding growth factors (e.g. bFGF) and cytokines (e.g.
CC interleukin (IL)-8), cell interaction with plasma lipoproteins, cellular

```

CC susceptibility to certain viral and some bacterial and protozoa
CC infections, or disintegration of neurodegenerative plaques. The
CC polynucleotide is also useful in wound healing (e.g. thermal, chemical or
CC radiation burns), and in the treatment of angiogenesis, restenosis,
CC atherosclerosis, inflammation, neurodegenerative diseases (Gerstmann-
CC Strausler Syndrome or Creutzfeldt-Jakob disease), and some viral,
CC bacterial or protozoa infections
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1019
AAA07792/C
ID AAA07792 standard; DNA; 15 BP.
XX
AC AAA07792;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-e.
XX
Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleonome, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
The invention provides modified nucleonome of specified formula and
CC their pharmaceutically acceptable salts. The nucleonome are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC infections, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleonome exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair

CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1020
AAA07794/C
ID AAA07794 standard; DNA; 15 BP.
XX
AC AAA07794;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-g.
XX
Nucleonome; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleonome, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.
XX
The invention provides modified nucleonome of specified formula and
CC their pharmaceutically acceptable salts. The nucleonome are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC infections, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleonome exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form

CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA0788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 1021
AAA07828/C
ID AAA07828 standard; DNA; 15 BP.
XX
AC AAA07828;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of a strand of triplex oligomer 15.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; triplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 30; 42pp; English.

CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07820-834 represent sequences forming triplex oligomers

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 1022
AAA07790/C
ID AAA07790 standard; DNA; 15 BP.
XX
AC AAA07790;
XX
DT 23-JUN-2000 (first entry)
XX
DE Nucleic acid sequence of ODN-c.
XX
KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX
OS Synthetic.
XX
PN WO200011013-A1.
XX
PD 02-MAR-2000.
XX
PF 20-AUG-1999; 99WO-US019029.
XX
PR 22-AUG-1998; 98US-0097712P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Gold B;
XX
DR WPI; 2000-246530/21.
XX
PT Modified nucleomonomers, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX
PS Disclosure; Page 20; 42pp; English.

CC The invention provides modified nucleomonomers of specified formula and
CC their pharmaceutically acceptable salts. The nucleomonomers are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences

XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1023

AAA07789/C

ID AAA07789 standard; DNA; 15 BP.

XX AC AAA07789;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-b.

XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

XX KW viral infection; inflammatory response; cellular proliferation;

XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX FN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US019029.

XX PR 22-AUG-1998; 98US-0097712P.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

XX DR WPI; 2000-246530/21.

XX PT Modified nucleomonomers, used in physiologically stable, non-toxic

XX PT oligomers used to inhibit expression of nucleic acids and in gene

XX PT regulation, antisense technology and diagnostics.

XX PS Disclosure; Page 20; 42pp; English.

XX CC The invention provides modified nucleomonomers of specified formula and

XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as

XX CC monomers in oligomers, which are used in pharmaceutical compositions to

XX CC inhibit expression of nucleic acid molecules including DNA and RNA in

XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-

XX CC infected cells. They are used in oligomers for gene regulation, antisense

XX CC technology, diagnostic applications to detect target sequences in

XX CC biological samples such as those containing pathogenic bacteria, fungi

XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or

XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion

XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and

XX CC interleukins associated with pathological conditions such as inflammatory

XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral

XX CC infections and bacterial infections (see AAA07786 for details of other

XX CC uses for which the oligomers are suitable for). Oligomers comprising the

XX CC target nucleic acid sequences, are physiologically stable, non-toxic and

XX CC able to penetrate into cells while maintaining stringent base pair

XX CC fidelity for target DNA sequences. The oligomers demonstrate significant

XX CC single- or double-stranded target nucleic acid binding activity to form

XX CC duplexes, triplexes or other forms of stable association. Sequences

XX CC AAA07788-803 represent oligonucleotides forming a third strand along with

XX CC the duplex sequences

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;

XX Query Match 0.9%; Score 15; DB 1; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 5.6e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 5.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 1024

AAA07795/C

ID AAA07795 standard; DNA; 15 BP.

XX AC AAA07795;

XX DT 23-JUN-2000 (first entry)

XX DE Nucleic acid sequence of ODN-h.

XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;

XX KW viral infection; inflammatory response; cellular proliferation;

XX KW psoriasis; duplex; ss.

XX OS Synthetic.

XX FN WO200011013-A1.

XX PD 02-MAR-2000.

XX PF 20-AUG-1999; 99WO-US019029.

XX PR 22-AUG-1998; 98US-0097712P.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Gold B;

XX DR WPI; 2000-246530/21.

XX PT Modified nucleomonomers, used in physiologically stable, non-toxic

XX PT oligomers used to inhibit expression of nucleic acids and in gene

XX PT regulation, antisense technology and diagnostics.

XX PS Disclosure; Page 20; 42pp; English.

XX CC The invention provides modified nucleomonomers of specified formula and

XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as

XX CC monomers in oligomers, which are used in pharmaceutical compositions to

XX CC inhibit expression of nucleic acid molecules including DNA and RNA in

XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-

XX CC infected cells. They are used in oligomers for gene regulation, antisense

XX CC technology, diagnostic applications to detect target sequences in

XX CC biological samples such as those containing pathogenic bacteria, fungi

XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or

XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion

XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and

XX CC interleukins associated with pathological conditions such as inflammatory

XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral

XX CC infections and bacterial infections (see AAA07786 for details of other

XX CC uses for which the oligomers are suitable for). Oligomers comprising the

XX CC target nucleic acid sequences, are physiologically stable, non-toxic and

XX CC able to penetrate into cells while maintaining stringent base pair

XX CC fidelity for target DNA sequences. The oligomers demonstrate significant

XX CC single- or double-stranded target nucleic acid binding activity to form

XX CC duplexes, triplexes or other forms of stable association. Sequences

XX CC AAA07788-803 represent oligonucleotides forming a third strand along with

XX CC the duplex sequences

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;

XX Query Match 0.9%; Score 15; DB 1; Length 15;

XX Best Local Similarity 100.0%; Pred. No. 5.6e+02;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 15 AAAAAAAAAAAAAA 1

RESULT 1025
 AAA07797/c
 ID AAA07797 standard; DNA; 15 BP.
 XX
 AC AAA07797;
 XX
 DT 23-JUN-2000 (first entry)
 XX
 DE Nucleic acid sequence of ODN-j.
 XX
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX
 OS Synthetic.
 XX
 PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-US019029.
 XX
 PR 22-AUG-1998; 98US-0097712P.
 XX
 PA (UYNE-) UNIV NEBRASKA.
 XX
 PI Gold B;
 XX
 DR WPI; 2000-246530/21.
 XX
 PT Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.
 XX
 PS Disclosure; Page 20; 42pp; English.
 XX
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 15 AAAAAAAAAAAAAA 1

DB 15 AAAAAAAAAAAAAA 1
 |||||
 RESULT 1026
 AAA07799/c
 ID AAA07799 standard; DNA; 15 BP.
 XX
 AC AAA07799;
 XX
 DT 23-JUN-2000 (first entry)
 XX
 DE Nucleic acid sequence of ODN-1.
 XX
 KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 XX
 OS Synthetic.
 XX
 PN WO200011013-A1.
 XX
 PD 02-MAR-2000.
 XX
 PF 20-AUG-1999; 99WO-US019029.
 XX
 PR 22-AUG-1998; 98US-0097712P.
 XX
 PA (UYNE-) UNIV NEBRASKA.
 XX
 PI Gold B;
 XX
 DR WPI; 2000-246530/21.
 XX
 PT Modified nucleomonomers, used in physiologically stable, non-toxic
 PT oligomers used to inhibit expression of nucleic acids and in gene
 PT regulation, antisense technology and diagnostics.
 XX
 PS Disclosure; Page 20; 42pp; English.
 XX
 CC The invention provides modified nucleomonomers of specified formula and
 CC their pharmaceutically acceptable salts. The nucleomonomers are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 15 AAAAAAAAAAAAAA 1


```
XX AC AAA07831;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of a strand of triplex oligomer 16.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; triplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US019029.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX PS Disclosure; Page 30; 42pp; English.
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC infections, cardiovascular disorders, immune reactions, cancer, viral
XX CC conditions for which the oligomers are suitable for). Oligomers comprising the
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07820-834 represent sequences forming triplex oligomers
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 1 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1031
AAA07831/c
ID AAA07803 standard; DNA; 15 BP.
XX AC AAA07803;
XX AC AAA07803;
XX DT 23-JUN-2000 (first entry)
XX DT
```

```
DT 23-JUN-2000 (first entry)
XX Nucleic acid sequence of ODN-p.
XX KW Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US019029.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX PS Disclosure; Page 20; 42pp; English.
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC infections, cardiovascular disorders, immune reactions, cancer, viral
XX CC conditions for which the oligomers are suitable for). Oligomers comprising the
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1031
AAA07834/c
ID AAA07834 standard; DNA; 15 BP.
XX AC AAA07834;
XX DT 23-JUN-2000 (first entry)
XX DT
```


DE Nucleic acid sequence of a strand of triplex oligomer 17.
 KW Nucleonome; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; triplex; ss.
 XX Synthetic.
 OS
 XX WO200011013-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 20-AUG-1999; 99WO-US019029.
 XX
 XX 22-AUG-1998; 98US-0097712P.
 PF
 XX (UYNE-) UNIV NEBRASKA.
 PR
 XX Gold B;
 PA
 XX WPI; 2000-246530/21.
 PI
 XX Modified nucleonome, used in physiologically stable, non-toxic
 DR oligomers used to inhibit expression of nucleic acids and in gene
 XX regulation, antisense technology and diagnostics.
 XX Disclosure; Page 30; 42pp; English.
 PS
 XX The invention provides modified nucleonome of specified formula and
 CC their pharmaceutically acceptable salts. The nucleonome are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections, and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleonome exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07820-834 represent sequences forming triplex oligomers
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db | | | | | | | | | | | | | | | |
 15 AAAAAAAAAAAAAA 1
 RESULT 1032
 AAA07796/c
 ID AAA07796 standard; DNA; 15 BP.
 AC AAA07796;
 XX
 XX 23-JUN-2000 (first entry)
 DT
 XX Nucleic acid sequence of ODN-1.
 DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; triplex; ss.

KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.
 OS Synthetic.
 XX WO200011013-A1.
 PN
 XX 02-MAR-2000.
 PD
 XX 20-AUG-1999; 99WO-US019029.
 XX
 XX 22-AUG-1998; 98US-0097712P.
 PF
 XX (UYNE-) UNIV NEBRASKA.
 PR
 XX Gold B;
 PA
 XX WPI; 2000-246530/21.
 PI
 XX Modified nucleonome, used in physiologically stable, non-toxic
 DR oligomers used to inhibit expression of nucleic acids and in gene
 XX regulation, antisense technology and diagnostics.
 XX Disclosure; Page 20; 42pp; English.
 PS
 XX The invention provides modified nucleonome of specified formula and
 CC their pharmaceutically acceptable salts. The nucleonome are used as
 CC monomers in oligomers, which are used in pharmaceutical compositions to
 CC inhibit expression of nucleic acid molecules including DNA and RNA in
 CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
 CC infected cells. They are used in oligomers for gene regulation, antisense
 CC technology, diagnostic applications to detect target sequences in
 CC biological samples such as those containing pathogenic bacteria, fungi
 CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
 CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
 CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
 CC interleukins associated with pathological conditions such as inflammatory
 CC conditions, cardiovascular disorders, immune reactions, cancer, viral
 CC infections, and bacterial infections (see AAA07786 for details of other
 CC uses for which the oligomers are suitable for). Oligomers comprising the
 CC nucleonome exhibit increased duplex DNA stability when hybridizing to
 CC target nucleic acid sequences, are physiologically stable, non-toxic and
 CC able to penetrate into cells while maintaining stringent base pair
 CC fidelity for target DNA sequences. The oligomers demonstrate significant
 CC single- or double-stranded target nucleic acid binding activity to form
 CC duplexes, triplexes or other forms of stable association. Sequences
 CC AAA07788-803 represent oligonucleotides forming a third strand along with
 CC the duplex sequences
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db | | | | | | | | | | | | | | | |
 15 AAAAAAAAAAAAAA 1
 RESULT 1033
 AAA07800/c
 ID AAA07800 standard; DNA; 15 BP.
 AC AAA07800;
 XX
 XX 23-JUN-2000 (first entry)
 DT
 XX Nucleic acid sequence of ODN-m.
 DE Nucleonome; cancer; gene regulation; antisense technology; leukemia;
 KW viral infection; inflammatory response; cellular proliferation;
 KW psoriasis; duplex; ss.

```
XX OS Synthetic.
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US019029.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX PS Disclosure; Page 20; 42pp; English.
XX CC The invention provides modified nucleomoners of specified formula and
CC their pharmaceutically acceptable salts. The nucleomoners are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 2 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1034
AAA07793/c
ID AAA07793 standard; DNA; 15 BP.
XX AC AAA07793;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-f.
XX KW Nucleomoner; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX OS Synthetic.
```

```
XX PN WO200011013-A1.
XX PD 02-MAR-2000.
XX PF 20-AUG-1999; 99WO-US019029.
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX DR WPI; 2000-246530/21.
XX PT Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX PS Disclosure; Page 20; 42pp; English.
XX CC The invention provides modified nucleomoners of specified formula and
CC their pharmaceutically acceptable salts. The nucleomoners are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1035
AAA07798/c
ID AAA07798 standard; DNA; 15 BP.
XX AC AAA07798;
XX DT 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-k.
XX KW Nucleomoner; cancer; gene regulation; antisense technology; leukemia;
XX viral infection; inflammatory response; cellular proliferation;
XX psoriasis; duplex; ss.
XX OS Synthetic.
XX PN WO200011013-A1.
```

```

XX 02-MAR-2000.
XX 20-AUG-1999; 99WO-US019029.
XX 22-AUG-1998; 98US-0097712P.
XX (UTNE-) UNIV NEBRASKA.
XX Gold B;
XX WPI; 2000-246530/21.
XX Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX Disclosure; Page 20; 42pp; English.
XX The invention provides modified nucleomoners of specified formula and
CC their pharmaceutically acceptable salts. The nucleomoners are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, cytokines, oncogenes, growth factors and
CC molecules, receptor molecules, hormones, serum proteins, adhesion
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1036
AAA07788/c
ID AAA07788 standard; DNA; 15 BP.
XX AAA07788;
XX 23-JUN-2000 (first entry)
XX Nucleic acid sequence of ODN-a.
DE Nucleomoner; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX Synthetic.
XX OS
XX WO200011013-A1.
XX 02-MAR-2000.
XX 02-MAR-2000.

```

```

XX 20-AUG-1999; 99WO-US019029.
XX 22-AUG-1998; 98US-0097712P.
XX (UTNE-) UNIV NEBRASKA.
XX Gold B;
XX WPI; 2000-246530/21.
XX Modified nucleomoners, used in physiologically stable, non-toxic
PT oligomers used to inhibit expression of nucleic acids and in gene
PT regulation, antisense technology and diagnostics.
XX Disclosure; Page 20; 42pp; English.
XX The invention provides modified nucleomoners of specified formula and
CC their pharmaceutically acceptable salts. The nucleomoners are used as
CC monomers in oligomers, which are used in pharmaceutical compositions to
CC inhibit expression of nucleic acid molecules including DNA and RNA in
CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
CC infected cells. They are used in oligomers for gene regulation, antisense
CC technology, diagnostic applications to detect target sequences in
CC biological samples such as those containing pathogenic bacteria, fungi
CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
CC encoded RNAs that encode enzymes, cytokines, oncogenes, growth factors and
CC molecules, receptor molecules, hormones, serum proteins, adhesion
CC interleukins associated with pathological conditions such as inflammatory
CC conditions, cardiovascular disorders, immune reactions, cancer, viral
CC infections and bacterial infections (see AAA07786 for details of other
CC uses for which the oligomers are suitable for). Oligomers comprising the
CC nucleomoners exhibit increased duplex DNA stability when hybridizing to
CC target nucleic acid sequences, are physiologically stable, non-toxic and
CC able to penetrate into cells while maintaining stringent base pair
CC fidelity for target DNA sequences. The oligomers demonstrate significant
CC single- or double-stranded target nucleic acid binding activity to form
CC duplexes, triplexes or other forms of stable association. Sequences
CC AAA07788-803 represent oligonucleotides forming a third strand along with
CC the duplex sequences
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1037
AAA07791/c
ID AAA07791 standard; DNA; 15 BP.
XX AAA07791;
XX 23-JUN-2000 (first entry)
XX Nucleic acid sequence of ODN-d.
DE Nucleomoner; cancer; gene regulation; antisense technology; leukemia;
KW viral infection; inflammatory response; cellular proliferation;
KW psoriasis; duplex; ss.
XX Synthetic.
XX OS
XX WO200011013-A1.
XX 02-MAR-2000.
XX 20-AUG-1999; 99WO-US019029.

```

```
XX PR 22-AUG-1998; 98US-0097712P.
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX PI WPI; 2000-246530/21.
XX DR Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX PS Disclosure; Page 20; 42pp; English.
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral
XX CC infections and bacterial infections (see AAA07786 for details of other
XX CC uses for which the oligomers are suitable for). Oligomers comprising the
XX CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX CC the duplex sequences
XX CC Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;
XX CC Query Match 0.9%; Score 15; DB 1; Length 15;
XX CC Best Local Similarity 100.0%; Pred. No. 5.6e+02;
XX CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAA 1750
XX DB 15 AAAAAAAAAAAAAA 1
XX RESULT 1038
XX AAA07801/c
XX ID AAA07801 standard; DNA; 15 BP.
XX AC AAA07801;
XX XX 23-JUN-2000 (first entry)
XX DE Nucleic acid sequence of ODN-n.
XX XX Nucleomonomer; cancer; gene regulation; antisense technology; leukemia;
XX KW viral infection; inflammatory response; cellular proliferation;
XX KW psoriasis; duplex; ss.
XX OS Synthetic.
XX XX WO200011013-A1.
XX PN 02-MAR-2000.
XX PD 20-AUG-1999; 99WO-US019029.
XX PF 22-AUG-1998; 98US-0097712P.
XX PR
```

```
XX PA (UYNE-) UNIV NEBRASKA.
XX PI Gold B;
XX PI WPI; 2000-246530/21.
XX DR Modified nucleomonomers, used in physiologically stable, non-toxic
XX PT oligomers used to inhibit expression of nucleic acids and in gene
XX PT regulation, antisense technology and diagnostics.
XX PS Disclosure; Page 20; 42pp; English.
XX CC The invention provides modified nucleomonomers of specified formula and
XX CC their pharmaceutically acceptable salts. The nucleomonomers are used as
XX CC monomers in oligomers, which are used in pharmaceutical compositions to
XX CC inhibit expression of nucleic acid molecules including DNA and RNA in
XX CC cells such as bacterial, fungal, yeast, mammalian, cancer and virally-
XX CC infected cells. They are used in oligomers for gene regulation, antisense
XX CC technology, diagnostic applications to detect target sequences in
XX CC biological samples such as those containing pathogenic bacteria, fungi
XX CC and viruses, oncogenes, growth hormones and enzymes, to target genes or
XX CC encoded RNAs that encode enzymes, hormones, serum proteins, adhesion
XX CC molecules, receptor molecules, cytokines, oncogenes, growth factors and
XX CC interleukins associated with pathological conditions such as inflammatory
XX CC conditions, cardiovascular disorders, immune reactions, cancer, viral
XX CC infections and bacterial infections (see AAA07786 for details of other
XX CC uses for which the oligomers are suitable for). Oligomers comprising the
XX CC nucleomonomers exhibit increased duplex DNA stability when hybridizing to
XX CC target nucleic acid sequences, are physiologically stable, non-toxic and
XX CC able to penetrate into cells while maintaining stringent base pair
XX CC fidelity for target DNA sequences. The oligomers demonstrate significant
XX CC single- or double-stranded target nucleic acid binding activity to form
XX CC duplexes, triplexes or other forms of stable association. Sequences
XX CC AAA07788-803 represent oligonucleotides forming a third strand along with
XX CC the duplex sequences
XX CC Sequence 15 BP; 0 A; 0 C; 0 G; 11 T; 4 U; 0 Other;
XX CC Query Match 0.9%; Score 15; DB 1; Length 15;
XX CC Best Local Similarity 100.0%; Pred. No. 5.6e+02;
XX CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1736 AAAAAAAAAAAAAA 1750
XX DB 15 AAAAAAAAAAAAAA 1
XX RESULT 1039
XX AAA62350/c
XX ID AAA62350 standard; DNA; 15 BP.
XX AC AAA62350;
XX XX 06-NOV-2000 (first entry)
XX DE Oligonucleotide #2 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
XX DE Conformationally-locked oligonucleotide; antisense inhibitor;
XX KW bicyclic sugar nucleoside analogue; gene probe; ds.
XX OS Synthetic.
XX XX Key Location/Qualifiers
XX FT modified_base 7 /tag= a
XX FT /mod_base= OTHER
XX FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX FT modified_base 9 /tag= b
XX FT /mod_base= OTHER
XX FT /note= "3'-C-amino-5'(S)-C,3'-N-ethanothymidine"
XX FT
```

```

PN      US6083482-A.
XX
XX
XX      PD      04-JUL-2000.
XX
XX      PF      11-MAY-1999; 99US-00309742.
XX
XX      PR      11-MAY-1999; 99US-00309742.
XX
XX      PA      (ICNC ) ICN PHARM INC.
XX
XX      PI      Wang G;
XX
XX      DR      WPI; 2000-451496/39.
XX
XX      PT      New conformationally restricted 3',5'-bridged nucleosides and
XX      PT      oligonucleotides useful as antisense therapeutics or as gene-specific
XX      PT      diagnostics.
XX
XX      PS      Example 20; Col 16; 10pp; English.
XX
XX      CC      The present sequence is an oligonucleotide containing 3'-C-amino-5'(S)-
XX      CC      C,3'-N-ethanethymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX      CC      the sequence were incorporated by phosphoramidite chemistry using a DNA
XX      CC      synthesizer. Bicyclic sugar nucleosides are conformationally restricted
XX      CC      3',5'-bridged nucleosides which can be used as building blocks for
XX      CC      oligonucleotides. Oligonucleotides can be produced that have certain,
XX      CC      desired, geometrical shapes and entropy advantages. They may have
XX      CC      superior hybridisation to DNA and RNA, and excellent biological
XX      CC      stability. The conformationally-modified oligonucleotides may be useful
XX      CC      as antisense inhibitors of gene expression or as gene probes, and may
XX      CC      therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX      SQ      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 1040
AAAG62347/C
ID      AAA62347 standard; DNA; 15 BP.
XX
XX      AC      AAAG62347;
XX
XX      DT      06-NOV-2000 (first entry)
XX
XX      DE      Oligonucleotide #3 containing 3'-C-amino-5'(R)-C,3'-N-ethanethymidine.
XX      KW      Conformationally-locked oligonucleotide; antisense inhibitor;
XX      KW      bicyclic sugar nucleoside analogue; gene probe; ds.
XX      OS      Synthetic.
XX
XX      FH      Key      Location/Qualifiers
XX      FT      modified_base 1
XX      FT      /*tag= a
XX      FT      /mod_base= OTHER
XX      FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
XX      FT      modified_base 3
XX      FT      /*tag= b
XX      FT      /mod_base= OTHER
XX      FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
XX      FT      modified_base 5
XX      FT      /*tag= c
XX      FT      /mod_base= OTHER
XX      FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
XX      FT      modified_base 9
XX      FT      /*tag= d

```

```

FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
FT      modified_base 11
FT      /*tag= e
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
FT      modified_base 13
FT      /*tag= f
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
FT      modified_base 15
FT      /*tag= g
FT      /mod_base= OTHER
FT      /note= "3'-C-amino-5'(R)-C,3'-N-ethanethymidine"
XX
XX      US6083482-A.
XX
XX      PD      04-JUL-2000.
XX
XX      PF      11-MAY-1999; 99US-00309742.
XX
XX      PR      11-MAY-1999; 99US-00309742.
XX
XX      PA      (ICNC ) ICN PHARM INC.
XX
XX      PI      Wang G;
XX
XX      DR      WPI; 2000-451496/39.
XX
XX      PT      New conformationally restricted 3',5'-bridged nucleosides and
XX      PT      oligonucleotides useful as antisense therapeutics or as gene-specific
XX      PT      diagnostics.
XX
XX      PS      Example 20; Col 15; 10pp; English.
XX
XX      CC      The present sequence is an oligonucleotide containing 3'-C-amino-5'(R)-
XX      CC      C,3'-N-ethanethymidine, a bicyclic-sugar nucleoside. All nucleotides in
XX      CC      the sequence were incorporated by phosphoramidite chemistry using a DNA
XX      CC      synthesizer. Bicyclic sugar nucleosides are conformationally restricted
XX      CC      3',5'-bridged nucleosides which can be used as building blocks for
XX      CC      oligonucleotides. Oligonucleotides can be produced that have certain,
XX      CC      desired, geometrical shapes and entropy advantages. They may have
XX      CC      superior hybridisation to DNA and RNA, and excellent biological
XX      CC      stability. The conformationally-modified oligonucleotides may be useful
XX      CC      as antisense inhibitors of gene expression or as gene probes, and may
XX      CC      therefore be used in antisense therapeutics or gene-specific diagnostics
XX
XX      SQ      Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match      0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAAAAAAAAAA 1750
Db      15 AAAAAAAAAAAAAA 1

RESULT 1041
AAAG62348/C
ID      AAA62348 standard; DNA; 15 BP.
XX
XX      AC      AAAG62348;
XX
XX      DT      06-NOV-2000 (first entry)
XX
XX      DE      Oligonucleotide #4 containing 3'-C-amino-5'(R)-C,3'-N-ethanethymidine.
XX      KW      Conformationally-locked oligonucleotide; antisense inhibitor;
XX      KW      bicyclic sugar nucleoside analogue; gene probe; ds.
XX      OS      Synthetic.
XX

```

Key	Location/Qualifiers
modified_base 7	/*tag= a
FT	/mod_base= OTHER
FT	/note= "3'-C-amino-5' (R) -C, 3'-3'-N-ethanothymidine"
modified_base 9	/*tag= b
FT	/mod_base= OTHER
FT	/note= "3'-C-amino-5' (R) -C, 3'-3'-N-ethanothymidine"
XX	
PN	US6083482-A.
XX	
PD	04-JUL-2000.
XX	
PF	11-MAY-1999; 99US-00309742.
XX	
PR	11-MAY-1999; 99US-00309742.
XX	
PA	(ICNC) ICN PHARM INC.
XX	
PI	Wang G;
XX	
DR	WPI; 2000-451496/39.
XX	
PT	New conformationally restricted 3',5'-bridged nucleosides and oligonucleotides useful as antisense therapeutics or as gene-specific diagnostics.
PT	
XX	
XX	Example 20; Col 15; 10pp; English.
XX	
CC	The present sequence is an oligonucleotide containing 3'-C-amino-5' (R) -C,3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesizer. Bicyclic sugar nucleosides are conformationally restricted 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics
XX	
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
	Query Match 0.9%; Score 15; DB 1; Length 15;
	Best Local Similarity 100.0%; Pred. No. 5.6e+02;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	1736 AAAAAAAAAAAAAA 1750
Db	15 AAAAAAAAAAAAAA 1
RESULT 1042	
AAH20308/c	
ID	AAH20308 standard; DNA; 15 Bp.
XX	
AC	AAH20308;
XX	
DT	31-JUL-2001 (first entry)
XX	
DE	Oligo dT15 EDTA labelled probe.
XX	
XW	Hybridisation probe; DNA cleavage; double-helix; oncogene; ss.
XX	
OS	Synthetic.
XX	
Key	Location/Qualifiers
FT	1
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "Optionally thymidine has EDTA covalently attached at C-5"

	modified_base	5	/tag= b /mod_base= OTHER /note= "Optionally thymidine has EDTA covalently attached at C-5"
	modified_base	8	/tag= c /mod_base= OTHER /note= "Optionally thymidine has EDTA covalently attached at C-5"
XX	US2001002314-A1.		
PN			
XX			
PD	31-MAY-2001.		
XX			
PB	04-AUG-1998;	98US-00128732.	
XX			
PR	30-OCT-1987;	87US-00115922.	
PR	16-NOV-1990;	90US-00614205.	
PR	12-NOV-1993;	93US-00152250.	
XX			
PA	(FLEH-) FLEHR HOHBACH TEST ALBRITTON & HERBERT.		
XX	Dervan PB, Moser HE;		
FI			
XX			
DR	WPI; 2001-342909/36.		
XX			
PT	New hybridization probe for specific triplex formation with large double helices, useful e.g. for site-specific diagnostic cleavage, contains attached functional residue.		
FT			
XX			
PS	Example 1; Fig 3B; 20pp; English.		
CC	This invention relates to hybridisation probes which target a specific sequence within a large double-helical nucleic acid. The probe is complementary to the target sequence and contains at least one nucleotide with an attached molecule that is able to cleave double-helical DNA e.g. EDTA-Fe(II) (ethylenediaminetetraacetic acid-iron complex). The probes where the attached molecule is a label or compound that alters gene expression, are used for specific detection and/or cleavage of double-stranded DNA, e.g. for diagnosis, for treatment of disease (particularly caused by viruses, genetic defects or oncogenes), for chromosomal analysis, and for the isolation and mapping of genes. The present sequence represents probe of the invention used in an example illustrating how the probe binds to and cleaves double stranded DNA		
SQ	Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;		
	Query Match	0.9%; Score 15; DB 1; Length 15;	
	. Best Local Similarity	100.0%; Pred. No. 5.6e+02;	
	Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	1736 AAAAAAAAAAAAAAA 1750		
DB	15 AAAAAAAAAAAAAAA 1		
RESULT 1043			
AFF3082/C			
ID	AFF30882 standard; DNA; 15 BP.		
XX			
AC	AFF30882;		
XX			
DT	09-JUN-2001 (first entry)		
XX	Oligonucleotide portion of ODN-MGB-LF conjugate.		
DE			
XX	ODN-MGB-LF; oligonucleotide; minor groove binder; latent fluorophore;		
KW	hybridisation; detection; fluorescence; probe; ss.		
OS	Synthetic.		
XX			
FN	WO200131063-A1.		

```

XX PD 03-MAY-2001.
XX PF 26-OCT-2000; 2000WO-US029786.
XX PR 26-OCT-1999; 99US-00428236.
XX PA (EPOC-) EPOCH BIOSCIENCES INC.
XX PI Dempcy RO, Afonina IA, Vermeulen NMJ;
XX PI WPI; 2001-328656/34.
XX DR
XX PT Conjugate of oligonucleotide, minor groove binder and latent fluorophore,
XX PT useful for detecting specific nucleic acids, e.g. for single-nucleotide
XX PT mismatch discrimination.
XX PS Disclosure; Page 58; 105pp; English.
XX CC The present sequence is that of the oligonucleotide (ODN) component of an
XX CC ODN-MGB (minor groove binder)-LF (latent fluorophore) conjugate of the
XX CC invention. MGBs bind in a non-intercalating manner to the minor groove of
XX CC non-single-stranded DNA, RNA or their hybrids, while a LF binds similarly
XX CC but in an intercalating manner, or lies in the minor groove, or is
XX CC oriented in some other way to the DNA molecule by MGB, such that it
XX CC becomes fluorescent (or its fluorescent properties change detectably).
XX CC The conjugates are used as hybridisation probes and amplification primers
XX CC for fluorescent detection of specifically hybridising sequences, for
XX CC analysis or diagnosis, especially (real-time) PCR, for single-nucleotide
XX CC mismatch discrimination, target or signal amplification, array-based
XX CC assays and sequencing, including detection of double-stranded DNA by
XX CC triplex formation. Many different targets can be detected a single
XX CC reaction vessel. The present ODN-MGB-LF conjugate was used to demonstrate
XX CC hybridisation-triggered fluorescence. Upon hybridisation to the
XX CC complementary target sequence there was an increase in fluorescence
XX CC yield, measured as the ratio of the fluorescence emitted by the hybrid
XX CC between the ODN-MGB-LF conjugate and its target sequence to the
XX CC fluorescence emitted by unhybridised (i.e. single-stranded) ODN-MGB-LF,
XX CC of 8.3
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1044
AAH20511/C
ID AAH20511 standard; DNA; 15 BP.
AC AAH20511;
XX 31-JUL-2001 (first entry)
XX Oligonucleotide b) for solid phase synthesis of oligonucleotides.
XX Cross-linked vinyl acetate copolymer carrier material; AIDS treatment;
XX phosphorothioate; solid phase synthesis; modified oligonucleotide;
XX clinical diagnostic; cancer treatment; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..14
XX /tag= a
XX /mod_base= OTHER
XX /note= "Phosphorothioate deoxynucleotides"
XX

```

```

PN DE10051726-A1.
XX 10-MAY-2001.
XX PF 18-OCT-2000; 2000DE-01051726.
XX PR 30-OCT-1999; 99DE-01052376.
XX PA (MERE ) MERCK PATENT GMBH.
XX PI Seliger H, Sobkowski M, Hinz M;
XX PI WPI; 2001-336414/36.
XX DR
XX PT Intermediate for oligonucleotide synthesis comprises partially hydrolysed
XX PT cross-linked vinyl acetate copolymer loaded with nucleotide derivative.
XX PS Example 2; Page 5; 8pp; German.
XX CC This invention describes a novel chemical product comprising a partially
XX CC hydrolysed cross-linked vinyl acetate copolymer carrier material loaded
XX CC with nucleotide derivative(s). The product is an intermediate for the
XX CC large (gram) scale solid phase synthesis of modified oligonucleotides
XX CC useful e.g. as clinical diagnostics and therapeutics, e.g. for the
XX CC treatment of AIDS and cancers. The presence of the partially hydrolysed
XX CC copolymer facilitates the synthesis of larger amounts of oligonucleotides
XX CC compared with the use of Merckogel (RTM; macroporous polyvinyl acetate)
XX CC described in Nucleic Acid Res. Sympos. Ser. 31, p. 153, 1994.
XX CC Oligonucleotides are obtained in very good quality and high yields. Also,
XX CC the nucleosides do not display the reduced activity seen in some prior
XX CC art procedures, less carrier material, reagents and solvent are required.
XX CC Further, the carrier material is biodegradable and thus does not present
XX CC disposal problems. It also swells uniformly in a range of solvents, which
XX CC obviates expansion or contraction during use or solvent exchange.
XX CC AAH20510-AAH20513 represent oligonucleotides containing modified
XX CC deoxynucleotides which are used to illustrate the method of the invention
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1045
AAF49041/C
ID AAF49041 standard; DNA; 15 BP.
XX AAF49041;
XX 30-MAR-2001 (first entry)
XX IGF-I oligonucleotide #1.
XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
XX skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
XX growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
XX hyperneovascular condition; hyperplasia; kidney disease;
XX neovascular condition of the retina; ss.
XX Homo sapiens.
XX OS
XX WO200078341-A1.
XX 28-DEC-2000.
XX

```

```

PF 21-JUN-2000; 2000NO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
XX WPI; 2001-041421/05.
DR
XX
XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional), and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
XX Example 8; Page 60; 201pp; English.
PS
XX
XX The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC 45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, seborrheoa, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
XX Sequence 15 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 0 Other;
SQ
    Query Match          0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.6e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAATAAAAAAAAAA 1749
DB 15 CAATAAAAAAAAAA 1

RESULT 1046
AAH49243/c
ID AAH49243 standard; DNA; 15 BP.
XX
XX AC AAH49243;
XX
XX 26-NOV-2001 (first entry)
XX
XX DE PNA-forming oligonucleotide #7.
XX
KW Polyamide-oligonucleotide derivative; anticancer; antiproliferative;
KW antiviral; hepatotropic; vasotropic; antisense inhibition; ribozyme;
KW integrin; cell-cell adhesion; cancer; restenosis; stability; PNA;
KW peptide nucleic acid; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH modified_base 9 /*tag= a
FT /*mod_base= OTHER
FT /*note= "t-but"
FT modified_base 15 /*tag= b
FT /*mod_base= OTHER
FT /*note= "t-hex"
XX
XX EP1113021-A2.
XX

```

```

PD 04-JUL-2001.
XX
XX 08-MAR-1995; 2001EP-00104012.
XX
XX 14-MAR-1994; 94DE-04408528.
PR 08-MAR-1995; 95EP-00103332.
XX
XX (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
XX Uhlmann E, Breipohl G;
XX
XX WPI; 2001-591267/67.
DR
XX
XX New DNA-peptide nucleic acid chimeras, useful e.g. as antisense agents
PT for treating e.g. cancer, also as diagnostic probes and primers.
XX
XX Example 26; Page 40; 54pp; German.
XX
XX This invention describes novel polyamide-oligonucleotide derivatives (I)
CC and their physiologically acceptable salts of formula F((DNA)-Li)q(PNA-
CC Li)r(DNA-Li)s(PNA)t xF', where q, r, s, t = 0 or 1, with the sum of
CC two or more adjacent letters at least 2; x = 1-20; DNA = nucleic acid
CC (such as DNA or RNA or their known derivatives); Li = covalent linkage
CC between DNA and PNA, i.e. a bond or a residue containing at least one
CC atom of carbon, nitrogen, oxygen or sulfur; PNA = polyamide structure
CC containing at least one nucleobase different from thymine; and F, F' =
CC end groups and/or are connected through a covalent bond. The products of
CC the invention have anticancer, antiproliferative, antiviral, hepatotropic
CC and vasotropic activity and can be used for the inhibition of gene
CC expression by antisense, ribozyme, sense, or triple-helix methods, or by
CC binding to proteins (aptamers). (I) are used for treating diseases caused
CC by viruses (human immune deficiency, herpes simplex, influenza, vesicular
CC stomatitis, hepatitis B or papilloma), or mediated by integrins or cell-
CC cell adhesion reactions, for treating cancer, or for inhibiting
CC restenosis, particularly as antisense reagents. They are also useful in
CC heterogeneous or homogeneous assays, as primers or probes, particularly
CC where the target is amplified before being detected by hybridization, for
CC diagnosis of genetic, malignant or pathogen-related diseases. (I) retain
CC the increased affinity for complementary strands and better stability in
CC serum, associated with conventional peptide nucleic acids (PNA), but lack
CC the disadvantages, i.e. have improved cellular uptake, do not aggregate
CC in aqueous solution, and have reduced affinity for purification
CC materials, reduced cytotoxicity, better sequence specificity. They are
CC more active than either DNA or PNA oligomers. When used as probes, (I)
CC show different responses to base-pair mismatches in the DNA and PNA-
CC segments, allowing better discrimination between pathogenic and non-
CC pathogenic conditions such as the transition from proto-oncogene to
CC oncogene, also, when used as primers, with the PNA segment at the 5'-end,
CC they produce amplicons resistant to 5'-exonuclease, allowing this enzyme
CC to be used to eliminate RNA or DNA primers. The DNA component allows
CC additional reactions not possible with PNA alone, e.g. 3'-tailing and (I)
CC may be incorporated into a gene. AAH49208-AAH49264 represent
CC oligonucleotides used to illustrate the method of the invention
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
SQ
    Query Match          0.9%; Score 15; DB 1; Length 15;
    Best Local Similarity 100.0%; Pred. No. 5.6e+02;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAAAAA 1

RESULT 1047
ABL40743/c
ID ABL40743 standard; DNA; 15 BP.
XX
XX AC ABL40743;
XX
XX 03-JUL-2002 (first entry)
XX
XX

```


DE Chicken heparanase (hpa) cDNA cloning oligo dT(15) primer.
XX Heparanase; catalytic; cytostatic; antiviral; antibacterial; enzyme;
KW anti-protozoan; neuroprotective; heparin; hpa; chicken; PCR primer; ss.
XX Gallus gallus.
OS
XX US2002034810-A1.
PN
PD 21-MAR-2002.
XX
XX 16-AUG-2001; 2001US-00930218.
PF
XX
XX 20-SEP-2000; 2000US-00666390.
PR
XX (INSI-) INSIGHT STRATEGY & MARKETING LTD.
PA
XX Goldshmidt O, Pecker I, Vlodavsky I, Michal I, Zcharia E;
PI
XX WPI; 2002-338926/37.
DR
XX Nucleic acid encoding avian and reptile heparanase polypeptide is useful
XX to treat various heparin-related disorders and the signal peptide is
PT useful in production of membrane-targeted or secreted recombinant
PT proteins.
XX
XX Disclosure; Page 13; 39pp; English.
PS
XX The invention relates to an isolated avian and reptile nucleic acid,
XX encoding a polypeptide with heparanase catalytic activity. The signal
CC peptide of the nucleic acid can be used to express membrane-associated or
CC secreted proteins in heterologous expression systems. The encoded
CC polypeptides can be used to prevent tumour angiogenesis, metastasis and
CC invasion, and to intervene with pathologies associated with impaired
CC heparin-binding growth factors, cellular responses to heparin-binding
CC growth factors and cytokines, cell interaction with plasma lipoproteins,
CC cellular susceptibility to viral, protozoa and bacterial infections or
CC disintegration of neurodegenerative plaques. The present sequence
CC represents a chicken heparanase (hpa) cDNA cloning oligo dT(15) primer
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db |||||||||||
15 AAAAAAAAAAAAAA 1
RESULT 1048
ABA97403/C
ID ABA97403 standard; DNA; 15 BP.
AC
XX ABA97403;
XX
XX 18-JUN-2002 (first entry)
DT
XX
DE Nucleotide sequence of oligomer # 10 used to compare mismatches.
XX
XX Protein nucleic acid molecule; PNA; ds.
KW
XX Synthetic.
OS
XX WO2000168673-A1.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 13-MAR-2001; 2001WO-US008111.
PF
XX
XX 14-MAR-2000; 2000US-0189190P.
PR
XX 30-NOV-2000; 2000US-0250334P.
PR

XX (ACTI-) ACTIVE MOTIF.
PA
XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
PI Chakmakchcheau O, Buryakova A, Choob M, Hondorp K;
XX
XX WPI; 2002-041177/05.
DR
XX Oligonucleotides analogs useful in detection, separation and purification
XX of nucleic acid molecules, comprise monomers, dimers and oligomers.
PT
XX
XX Example 20; Page 123; 197pp; English.
PS
XX This invention relates to oligonucleotide analogues comprising a protein
XX nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adaptors and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC nucleic acid molecules with greater affinity than DNA or RNA
CC concentration. The compounds are relatively simple to synthesize and are
CC used in a wide variety of applications. This sequence represents a DNA
CC oligomer which is used to represent the effect of single base mismatches
CC on oligonucleotides
XX
SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750
Db |||||||||||
15 AAAAAAAAAAAAAA 1
RESULT 1049
AAL49453
ID AAL49453 standard; DNA; 15 BP.
XX
XX AAL49453;
AC
XX
XX 14-NOV-2002 (first entry)
DT
XX
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 1.
XX
XX Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..15
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 15-FEB-2002; 2002WO-EF001651.
PF
XX
XX 16-FEB-2001; 2001DE-01007317.
PR
XX
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA
XX

PI Kahmann S, Mueller O;
XX WPI; 2002-674959/72.
DR P-PSDB; AAO19054.
XX
PT Detecting mutations in nucleic acid, useful for diagnosis and
PT characterization of tumors, by amplification, in vitro transcription and
PT translation, then protein detection.
PS Claim 11; Fig 5; 62pp; German.
XX
CC The present invention relates to a method of detecting mutations in a
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC amplicon, in vitro transcription and translation of this amplicon, and
CC detection of the translated protein. The primers used for amplification
CC are designed to produce an amplicon that is translatable and allows
CC differentiation between translation products of wild-type and mutated
CC nucleic acids. The method is used to detect mutations in tumour
CC suppressor genes, for (early) diagnosis, monitoring and characterisation
CC of tumours (especially of bladder and intestines) and in the germ line
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC is used to detect or verify the reading frame of a nucleic acid cloned in
CC it, and to determine the suitability of detectable peptides for analysis
CC and/or purification of a recombinant protein, expressed from a sequence
CC cloned in the vector. The present sequence encodes a tag peptide and was
CC used in the invention
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 1050
AAL49455
ID AAL49455 standard; DNA; 15 BP.
AC AAL49455;
XX
XX 14-NOV-2002 (first entry)
DT
DE Mutation detection method tag peptide coding sequence SEQ ID NO: 3.
XX
XX Mutation detection; primer; mutant; tag; tumour suppressor gene;
KW protein production; cancer; ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..15
FT /*tag= a
FT /product= "tag peptide"
FT /partial
FT /note= "no start or stop"
XX
XX WO200266675-A2.
PN
XX
XX 29-AUG-2002.
PD
XX
XX 15-FEB-2002; 2002WO-EP001651.
PF
XX
XX 16-FEB-2001; 2001DE-01007317.
PR
XX
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PA
PI Kahmann S, Mueller O;
XX
XX WPI; 2002-674959/72.
DR

DR P-PSDB; AAO19056.
XX
XX Detecting mutations in nucleic acid, useful for diagnosis and
PT characterization of tumors, by amplification, in vitro transcription and
PT translation, then protein detection.
XX
XX Claim 11; Fig 5; 62pp; German.
PS
XX
CC The present invention relates to a method of detecting mutations in a
CC nucleic acid by amplifying the nucleic acid to produce a double-stranded
CC amplicon, in vitro transcription and translation of this amplicon, and
CC detection of the translated protein. The primers used for amplification
CC are designed to produce an amplicon that is translatable and allows
CC differentiation between translation products of wild-type and mutated
CC nucleic acids. The method is used to detect mutations in tumour
CC suppressor genes, for (early) diagnosis, monitoring and characterisation
CC of tumours (especially of bladder and intestines) and in the germ line
CC (using nucleic acids from embryos or blood cells). A new multi-tag vector
CC is used to detect or verify the reading frame of a nucleic acid cloned in
CC it, and to determine the suitability of detectable peptides for analysis
CC and/or purification of a recombinant protein, expressed from a sequence
CC cloned in the vector. The present sequence encodes a tag peptide and was
CC used in the invention
XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 1 AAAAAAAAAAAAAA 15
RESULT 1051
AAD29506/c
ID AAD29506 standard; DNA; 15 BP.
XX
AC AAD29506;
XX
XX 17-MAY-2002 (first entry)
DT
DE Primer used for the expression of adipocytes in human preadipose cells.
XX
XX Pre-adipose cell line; white adipocyte; food ingredient; obesity; lipid;
KW diabetes; cardiovascular disease; reverse transcription; RT-PCR primer;
KW ss.
XX
OS Unidentified.
XX
XX WO200206450-A1.
PN
XX
XX 24-JAN-2002.
PD
XX
XX 13-JUL-2001; 2001WO-EP008165.
PF
XX
XX 18-JUL-2000; 2000EP-00115489.
PR
XX
XX (NEST) SOC PROD NESTLE SA.
PA
XX
XX Darimont C, Mace K, Pfeifer A;
PI
XX
XX WPI; 2002-189539/24.
DR
XX
XX New human pre-adipose cell line capable of differentiating to adipose
PT cells, useful in developing drug, food ingredients, and supplements
PT against obesity, diabetes and cardiovascular diseases.
XX
XX Example 5; Page 10; 30pp; English.
PS
XX
XX The present invention relates to new human pre-adipose cell lines capable
CC to differentiate to white adipose cells, exhibiting essentially the same

CC cellular properties of normal white adipose cells. The human pre-adipose
 CC cell lines are useful for the identification of substances controlling
 CC the regulation of lipid uptake and release by human white adipocytes, and
 CC substances controlling the differentiation of preadipocytes into mature
 CC adipocytes. They are useful for screening compounds capable to regulate
 CC the secretion of any metabolites or hormones from human white adipocytes.
 CC Sequences of the invention are useful for developing drugs, food
 CC ingredients and supplements against obesity, diabetes and cardio-
 CC vascular diseases. The present DNA sequence is a reverse transcription
 CC (RT)-PCR primer which is used for the expression of adipocytes in
 CC differentiated immortalised human preadipose cells. This primer is used
 CC in the exemplification of the invention

XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 SQ Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

Qy 1736 AAAAAAAAAAAAAA 1750
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1052
 AAD22531
 ID AAD22531 standard; RNA; 15 BP.
 XX AC AAD22531;
 XX 29-AUG-2003 (revised)
 DT 07-AUG-2003 (revised)
 DT 12-FEB-2002 (first entry)
 XX XX
 DE Retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment.
 XX RNase inhibitor; anti-HIV; cytostatic; hepatotropic; antiinflammatory;
 KW hepatitis; oncogene; cancer; transcription; translation; leukaemia virus;
 KW herpetic virus; human immunodeficiency virus; retroviral; DNP-poly [A];
 KW poly-2'-O-(2,4-dinitrophenyl)-poly [A]; viral reverse transcriptase; ss.
 XX unidentifed retrovirus.
 OS Unidentified.
 XX US6291438-B1.
 XX 18-SEP-2001.
 XX 06-OCT-1998; 98US-00167375.
 XX 24-FEB-1993; 93US-00022055.
 PR 23-FEB-1994; 94US-00200650.
 PR 22-FEB-1996; 96US-00604871.
 XX (WANG/) WANG J H.
 XX Wang JH;
 XX WPI; 2002-009339/01.
 XX Derivatized antisense oligoribonucleotide useful to inhibit e.g. viral
 PT reverse transcriptase comprises at the 2'-O position of the
 PT oligoribonucleotide, a hydrophobic carrier reagent containing a poly
 PT substituted phenyl compound.
 XX Example 3; Col 24; 56pp; English.
 XX The invention relates to derivatised antisense oligoribonucleotides with
 CC enhanced membrane permeability and stability. The derivatised antisense
 CC oligoribonucleotide complementary to a sequence of nucleotides found in a
 CC virus or a cell is useful for inhibiting e.g., viral reverse
 CC transcriptase. Derivatized antisense oligoribonucleotide is conjugated at
 CC the 2'-O position with a hydrophobic carrier reagent containing a poly

CC substituted phenyl compound. The derivatised oligoribonucleotides are
 CC used to decrease the expression of oncogenes and thereby decrease the
 CC expression of cancer cells which rely upon oncogene expression for their
 CC phenotypic and pathological properties. The oligoribonucleotides are also
 CC used for increasing the effectiveness of antisense oligonucleotide
 CC targeted to a gene associated with a disease or a condition in an
 CC animal. To alter gene transcription and/or translation for any gene or
 CC gene segment responsible for expression, to inhibit viral reverse
 CC transcriptase, to inhibit the expression of leukaemia virus, hepatitis
 CC virus, oncogenes and human immunodeficiency virus. The present sequence
 CC is retroviral reverse transcriptase inhibitor DNP-poly [A] RNA fragment
 CC which is used in the treatment of moloney murine leukaemia virus (MuLV)
 CC in mammals. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-
 CC AUG-2003 to standardise OS field)

XX Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 SQ Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

Qy 1736 AAAAAAAAAAAAAA 1750
 Db 1 AAAAAAAAAAAAAA 15

RESULT 1053
 ABQ82140
 ID ABQ82140 standard; DNA; 15 BP.
 XX AC ABQ82140;
 XX 11-DEC-2002 (first entry)
 DT XX
 DE Acceptor vector pHELLSGATE 4 nucleotide sequence SEQ ID NO:23.
 XX Chimeric nucleic acid construct; recombinational cloning; silencing;
 KW recombination site; double stranded RNA; plant; ds.
 XX Synthetic.
 OS WO200259294-A1.
 XX 01-AUG-2002.
 XX 24-JAN-2002; 2002WO-AU000073.
 XX 26-JAN-2001; 2001US-0264067P.
 PR 29-NOV-2001; 2001US-0333743P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX Wesley S, Waterhouse P, Helliwell C;
 XX WPI; 2002-682669/73.
 XX New vectors comprising operably linked DNA fragments having an origin of
 PT replication, a selectable marker and a chimeric DNA construct, useful for
 PT silencing target nucleic acids and for producing large amounts of double-
 PT stranded RNA.
 XX Claim 14; Page 74; 104pp; English.
 XX The present invention describes a vector (i) comprising operably linked
 CC DNA fragments having: (a) origin of replication allowing replication in a
 CC recipient cell, preferably in bacteria such as Escherichia coli; (b)
 CC selectable marker region capable of being expressed in the recipient cell
 CC ; and (c) a chimeric DNA construct comprising: (i) promoter or promoter
 CC region capable of being recognized by RNA polymerases of a eukaryotic
 CC cell or by prokaryotic RNA polymerase; (ii) first, second, third and
 CC fourth recombination sites; (iii) 3' transcription terminating and
 CC polyadenylation region functional in the eukaryotic cell. The first and
 CC fourth recombination sites, or the second and third recombination sites

CC are capable of reacting with a same recombination site, and preferably
CC are identical. The first and second recombination sites, or the third and
CC fourth recombination sites, do not recombine with each other or with a
CC same recombination site. The vector is useful for producing large amounts
CC of double-stranded RNA which can be used for silencing target nucleic
CC acid sequences. The vectors can also be used to convert a DNA fragment
CC into an inverted repeat structure. Plants transformed with a vector from
CC the present invention can be used in a conventional breeding scheme to
CC produce more plants with the same characteristics or to introduce a
CC chimeric gene for reduction of the phenotypic expression of nucleic
CC acids. The present sequence represents an acceptor vector nucleotide
CC sequence from the present invention

XX
SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 1 AAAAAAAAAAAAAA 15

RESULT 1054
ABX00240/C
ID ABX00240 standard; RNA; 15 BP.

XX AC ABX00240;

XX DT 23-DEC-2002 (first entry)

DE Hepatitis C virus substrate #22 for HCV hammerhead ribozyme #22.

XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX OS Hepatitis C virus.

XX PN US2002082225-A1.

XX PD 27-JUN-2002.

XX PF 23-MAR-1999; 99US-00274553.

XX PR 23-MAR-1999; 99US-00274553.

XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PA (ROBE/) ROBERTS B.

PA (PVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;

XX WPI; 2002-617759/66.

XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.

XX PS Claim 1; Page 21; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of

CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
CC a condition associated with HCV infection in conjunction with one or more
CC other drug therapies, particularly type I interferon, especially
CC interferon alpha, beta or gamma or consensus interferon. The present
CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
CC Some of the sequence data for this patent did not form part of the
CC printed specification. The complete sequence data for this patent was
CC obtained in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/paipdIDentry.html

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
|||||
Db 15 AAAAAAAAAAAAAA 1

RESULT 1055

ABX03406/C

ID ABX03406 standard; RNA; 15 BP.

XX AC ABX03406;

XX DT 24-DEC-2002 (first entry)

XX DE Hepatitis C virus substrate #1319 for HCV hammerhead ribozyme #1319.

XX Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virucide;
KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
KW type I interferon; interferon alpha; interferon beta; cytostatic;
KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
KW substrate; hammerhead ribozyme; HH ribozyme; ss.

XX OS Hepatitis C virus.

XX PN US2002082225-A1.

XX PD 27-JUN-2002.

XX PF 23-MAR-1999; 99US-00274553.

XX PR 23-MAR-1999; 99US-00274553.

XX (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J A.

PA (ROBE/) ROBERTS B.

PA (PVC/) PAVCO P A.

PA (MACE/) MACEJACK D.

XX PI Blatt L, Mcswiggen JA, Roberts B, Pavco PA, Macejack D;

XX WPI; 2002-617759/66.

XX New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
PT replication and are useful to treat hepatitis C virus infections and
PT cirrhosis, liver failure or hepatocellular carcinoma.

XX PS Claim 1; Page 64; 80pp; English.

XX The present invention relates to enzymatic nucleic acids which
CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
CC (HP) motif where the binding arms comprise sequences complementary to one
CC of the substrate sequences defined in the specification. The HCV
CC ribozymes are useful for modulating the expression and/or replication of
CC HCV. They can be used to treat cirrhosis, liver failure and/or
CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating

CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a substrate for a HCV hammerhead (HH) ribozyme. Note:
 CC Some of the sequence data for this patent did not form part of the
 CC printed specification. The complete sequence data for this patent was
 CC obtained in electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipubIDentry.html
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 0 T; 15 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 1056
 ABL57064/C
 ID ABL57064 standard; DNA; 15 BP.
 XX
 AC ABL57064;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Hydrazide precursor phosphoramidite oligonucleotide O35.
 XX
 KW Macromolecule; hydrazide; immobilisation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..15
 FT /*tag= b
 FT /note= "phosphoramidite linkage"
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Diethyl 5-(((2-cyanoethoxy) (diisopropylamino)
 FT phosphanyloxy)methyl)isophthalate, synthetic branching
 FT amidite"
 FT 15
 FT modified_base 15
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "3' Cy3 dye"
 FT
 FN WO200214558-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-US041663.
 XX
 PR 11-AUG-2000; 2000WO-US022205.
 XX
 PA (NANO-) NANOGEN INC.
 XX
 PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;
 XX
 DR WPI; 2002-404476/43.
 XX
 PT Compound for binding macromolecule to substrate surface or conjugation
 PT targets, contains phosphorous containing reactive group, hydrazide
 PT protecting group and benzene ring, and has predefined formula.
 XX
 PS Example 4; Page 44; 120pp; English.
 XX
 CC The present sequence is of a hydrazine treated hydrazide precursor
 CC phosphoramidite 15-mer, designated oligo O35, which was produced in an
 CC example from the invention and which includes a synthetic branching

CC amidite compound. The invention describes an improved process for
 CC immobilisation of macromolecules including DNA, RNA, peptide nucleic
 CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
 CC multiple reactive sites, to a substrate surface or other conjugation
 CC target. It also describes the preparation of oligos containing one or
 CC more hydrazides, which can be used for conjugation to surface binding
 CC moieties, or for other conjugation reactions. The process is useful e.g.
 CC in nucleic acid hybridisation based assays, DNA chip technology and
 CC biosensor applications
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1
 RESULT 1057
 ABL57054/C
 ID ABL57054 standard; DNA; 15 BP.
 XX
 AC ABL57054;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Hydrazide phosphoramidite oligonucleotide O9.
 XX
 KW Macromolecule; hydrazide; immobilisation; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..15
 FT /*tag= b
 FT /note= "phosphoramidite linkage"
 FT modified_base 1
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "6-((2-cyanoethoxy) (diisopropylamino)
 FT phosphanyloxy)-N'-tritylhexanohydrazide"
 FT 15
 FT modified_base 15
 FT /*tag= c
 FT /mod_base= OTHER
 FT /note= "3' Cy3 dye"
 FT
 FN WO200214558-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 10-AUG-2001; 2001WO-US041663.
 XX
 PR 11-AUG-2000; 2000WO-US022205.
 XX
 PA (NANO-) NANOGEN INC.
 XX
 PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
 PI Havens JR, Onofrey TJ, Greef CH, Wang D;
 XX
 DR WPI; 2002-404476/43.
 XX
 PT Compound for binding macromolecule to substrate surface or conjugation
 PT targets, contains phosphorous containing reactive group, hydrazide
 PT protecting group and benzene ring, and has predefined formula.
 XX
 PS Example 2; Page 40; 120pp; English.
 XX
 CC The present sequence is of a trityl deprotected hydrazide phosphoramidite
 CC 15-mer, designated oligo O9, which was produced in an example from the
 CC invention. The invention describes an improved process for immobilisation
 CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
 CC RNA and peptides, especially macromolecules containing multiple reactive
 CC sites, to a substrate surface or other conjugation target. It also
 CC describes the preparation of oligos containing one or more hydrazides,

CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred.No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

RESULT 1058
ABL57063/C
ID ABL57063 standard; DNA; 15 BP.

XX	22-JUL-2002 (first entry)
DT	
XX	
DE	Hydrazide precursor phosphoramidite oligonucleotide O39.
XX	
XX	Macromolecule; hydrazide; immobilisation; ss.
KW	

more hydrazides, which can be used for conjugation to surface binding moieties, or for other conjugation reactions. The process is useful e.g. in nucleic acid hybridisation based assays, DNA chip technology and biosensor applications

```

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match          0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

RESULT 1059
ABL57066/c
ID ABL57066 standard; DNA; 15 BP.

XX	22-JUL-2002 (first entry)
DT	
XX	
DE	Amino-C6-modified and Cy3 labeled T15 oligonucleotide.
XX	
KW	Macromolecule; hydrazide; immobilisation; ss.

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1060
ABL57059/c
ID ABL57059 standard; DNA; 15 BP.
XX AC ABL57059;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide O33.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.

XX FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "4-(2-cyanoethyl)-(diisopropylamino)
FT phosphanyloxymethyl)-benzoic acid methyl ester"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3, Cy3 dye"

XX WO200214558-A2.
XX 21-FEB-2002.
XX 10-AUG-2001; 2001WO-US041663.
XX 11-AUG-2000; 2000WO-US022205.
XX (NANO-) NANOGEN INC.
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX Example 3; Page 43; 120pp; English.

XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O33, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1061
ABL57061/c
ID ABL57061 standard; DNA; 15 BP.
XX AC ABL57061;
XX DT 22-JUL-2002 (first entry)
XX DE Hydrazide precursor phosphoramidite oligonucleotide O37.
XX KW Macromolecule; hydrazide; immobilisation; ss.
XX OS Synthetic.

XX FH Key Location/Qualifiers
FT modified_base 1..15
FT /*tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /*tag= a
FT /mod_base= OTHER
FT /note= "1,3-Bis-(3',5'-bis(ethyloxycarbonyl)
FT phenylcarbonylamido)-2-((2',-cyanoethyloxy)
FT (diisopropylamino)-phosphanyloxy)-propane"
FT modified_base 15
FT /*tag= c
FT /mod_base= OTHER
FT /note= "3, Cy3 dye"

XX WO200214558-A2.
XX 21-FEB-2002.
XX 10-AUG-2001; 2001WO-US041663.
XX 11-AUG-2000; 2000WO-US022205.
XX (NANO-) NANOGEN INC.
XX Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
XX Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.
XX Compound for binding macromolecule to substrate surface or conjugation
XX targets, contains phosphorous containing reactive group, hydrazide
XX protecting group and benzene ring, and has predefined formula.
XX Example 3; Page 43; 120pp; English.

XX The present sequence is of a hydrazine treated hydrazide precursor
XX phosphoramidite 15-mer, designated oligo O37, which was produced in an
XX example from the invention. The invention describes an improved process
XX for immobilisation of macromolecules including DNA, RNA, peptide nucleic
XX acids, pyranosyl-RNA and peptides, especially macromolecules containing
XX multiple reactive sites, to a substrate surface or other conjugation
XX target. It also describes the preparation of oligos containing one or
XX more hydrazides, which can be used for conjugation to surface binding
XX moieties, or for other conjugation reactions. The process is useful e.g.
XX in nucleic acid hybridisation based assays, DNA chip technology and
XX biosensor applications

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 1

RESULT 1062
ABLS7056/c
ID ABL57056 standard; DNA; 15 BP.

XX AC ABL57056;

XX DT 22-JUL-2002 (first entry)

XX DE Hydrazide phosphoramidite oligonucleotide O31.

XX KW Macromolecule; hydrazide; immobilisation; ss.

XX OS Synthetic.

PH Key Location/Qualifiers
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "6-((2Cyanooethoxy)(diisopropylamino)
FT phosphanyloxy)-N'-tritylhexanohydrazide"
FT modified_base 15
FT /tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"

XX WO200214558-A2.

XX PD 21-FEB-2002.

XX PF 10-AUG-2001; 2001WO-US041663.

XX PR 11-AUG-2000; 2000WO-US022205.

XX PA (NANO-) NANOGEN INC.

XX PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.

XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.

PS Example 2; Page 40; 120pp; English.

XX The present sequence is of a trityl deprotected hydrazide phosphoramidite
CC 15-mer, designated oligo O31, which was produced in an example from the
CC invention. The invention describes an improved process for immobilisation
CC of macromolecules including DNA, RNA, peptide nucleic acids, pyranosyl-
CC RNA and peptides, especially macromolecules containing multiple reactive
CC sites, to a substrate surface or other conjugation target. It also
CC describes the preparation of oligos containing one or more hydrazides,
CC which can be used for conjugation to surface binding moieties, or for
CC other conjugation reactions. The process is useful e.g. in nucleic acid
CC hybridisation based assays, DNA chip technology and biosensor
CC applications

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 1

RESULT 1063
ABLS7060/c
ID ABL57060 standard; DNA; 15 BP.

XX AC ABL57060;

XX DT 22-JUL-2002 (first entry)

XX DE Hydrazide precursor phosphoramidite oligonucleotide O34.

XX KW Macromolecule; hydrazide; immobilisation; ss.

XX OS Synthetic.

PH Key Location/Qualifiers
FT modified_base 1..15
FT /tag= b
FT /note= "phosphoramidite linkage"
FT modified_base 1
FT /tag= a
FT /mod_base= OTHER
FT /note= "Diethyl 5-((2-cyanoethoxy)(diisopropylamino)
FT phosphanyloxy)methyl)isophthalate"
FT modified_base 15
FT /tag= c
FT /mod_base= OTHER
FT /note= "3' Cy3 dye"

XX WO200214558-A2.

XX PD 21-FEB-2002.

XX PF 10-AUG-2001; 2001WO-US041663.

XX PR 11-AUG-2000; 2000WO-US022205.

XX PA (NANO-) NANOGEN INC.

XX PI Raddatz S, Mueller-Ibeler J, Schweitzer M, Bruecher C, Windhab N;
PI Havens JR, Onofrey TJ, Greef CH, Wang D;
XX WPI; 2002-404476/43.

XX Compound for binding macromolecule to substrate surface or conjugation
PT targets, contains phosphorous containing reactive group, hydrazide
PT protecting group and benzene ring, and has predefined formula.

PS Example 3; Page 43; 120pp; English.

XX The present sequence is of a hydrazine treated hydrazide precursor
CC phosphoramidite 15-mer, designated oligo O34, which was produced in an
CC example from the invention. The invention describes an improved process
CC for immobilisation of macromolecules including DNA, RNA, peptide nucleic
CC acids, pyranosyl-RNA and peptides, especially macromolecules containing
CC multiple reactive sites, to a substrate surface or other conjugation
CC target. It also describes the preparation of oligos containing one or
CC more hydrazides, which can be used for conjugation to surface binding
CC moieties, or for other conjugation reactions. The process is useful e.g.
CC in nucleic acid hybridisation based assays, DNA chip technology and
CC biosensor applications

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1064

ABK98141/c
 ID ABK98141 standard; DNA; 15 BP.

XX AC ABK98141;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #26.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.

XX PS Example 1; Fig 3B; 108pp; English.

XX CC The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic bacteria or viruses for
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 15 AAAAAAAAAAAAAA 1

RESULT 1065

ABK98184/c
 ID ABK98184 standard; DNA; 15 BP.

XX AC ABK98184;

XX DT 07-OCT-2002 (first entry)

XX DE Triple helix forming associated oligonucleotide #48.

XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
 KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
 KW pathogenic bacteria; virus; replication; virulence; cancer;
 KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.

XX OS Synthetic.

XX PN US6403302-B1.

XX PD 11-JUN-2002.

XX PF 16-DEC-1993; 93US-00168920.

XX PR 17-SEP-1992; 92US-00946976.

XX PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX PI Dervan PB, Beal PA;

XX DR WPI; 2002-536030/57.

XX PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
 PT oligonucleotide which binds in parallel and antiparallel orientation,
 PT respectively, for targeting sequences on alternate strands of DHNA to
 PT control gene expression.

XX PS Example 7; Fig 24A; 108pp; English.

XX CC The present invention relates to methods and oligonucleotides for forming
 CC a triple-helix comprising a double helical nucleic acid comprising first
 CC and second substantially complementary strands, and an oligonucleotide
 CC bound to a purine-rich target sequence within the double helical nucleic
 CC acid, where the oligonucleotide binds in a parallel and antiparallel
 CC orientation, respectively, to target sequences on alternate strands of
 CC the double helical nucleic acid. The method has therapeutic applications,
 CC where gene expression is controlled by selective triple-helix formation
 CC within expression regulatory sequences of a target gene. The
 CC oligonucleotides can be used to form triple-helices, and are useful to
 CC detect the presence or absence of specific sequences within genomic DNA
 CC for diagnostic and therapeutic purposes. The oligonucleotides can be
 CC selected to specifically bind to pathogenic bacteria or viruses for
 CC specific sequences required by pathogenic bacteria or viruses for
 CC replication or virulence, reducing their pathogenicity. Alternatively,
 CC the oligonucleotide can be chosen to target a unique sequence of the
 CC pathogen which is not found in the genome of pathogen's host. The
 CC oligonucleotides can be used in cancer treatment by way of triple-helix
 CC suppression of specific oncogenes including those of endogenous or viral
 CC origin. Such therapeutic oligonucleotides are capable of forming triple-
 CC helices with such sequences in cancerous cells containing the activated
 CC oncogene, so preferentially killing or repressing the cancer causing
 CC cell. The present sequence represents an oligonucleotide used in the
 CC methods of the present invention

XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 1

RESULT 1066
ABZ37501/C
ID ABZ37501 standard; DNA; 15 BP.
XX AC ABZ37501;
XX DT 18-FEB-2003 (first entry)
XX DE Oligonucleotide SEQ ID NO:622.
XX KW Library; cleavage; display; diverse family; ss.
XX OS Synthetic.
XX PN WO200283872-A2.
XX PD 24-OCT-2002.
XX PF 17-APR-2002; 2002WO-US012405.
XX PR 17-APR-2001; 2001US-00837306.
XX PR 24-OCT-2001; 2001US-0000516.
XX PR 25-OCT-2001; 2001US-00045674.
XX PA (LADN/) LADNER R C.
XX PA (COHE/) COHEN E H.
XX PA (NASTR/) NASTRI H G.
XX PA (ROOK/) ROOKEY K L.
XX PA (HOET/) HOET R.
XX PA (HOOG/) HOOGBOOM H R J M.
XX PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
XX PI Hoogenboom HRJW;
XX DR WPI; 2003-093015/08.
XX PT Cleaving single-stranded nucleic acid sequences at a desired location by
XX PT contacting the nucleic acid with an single strand oligonucleotide
XX PT complementary to a nucleic acid region where cleavage is desired.
XX PS Disclosure; Page 481; 485pp; English.

CC The present invention describes a method for cleaving single-stranded
CC nucleic acid sequences at a desired location. Also described: (1) methods
CC for displaying or expressing a member of a diverse family of peptides,
CC polypeptides or proteins on the surface of a genetic package and
CC collectively displaying at least a part of the diversity of the family,
CC where the displayed or expressed peptide, polypeptide or protein is
CC encoded at least in part by a nucleic acid that has been cleaved at a
CC desired location; (2) a method for preparing single-stranded nucleic
CC acids; (3) a method for preparing a library comprising a collection of
CC genetic packages that display a member of a diverse family of peptides,
CC polypeptides or proteins and that collectively display at least a portion
CC of the family; (4) a vector comprising a DNA sequence encoding an
CC antibody variable region linked to a version of PIII anchor which does
CC not mediate infection of phage particles, and wild-type gene III; (5) a
CC method for producing a population or a library of immunoglobulin genes;
CC and (6) a library of immunoglobulins that comprise members having at
CC least one variable domain in which at least one of CDR1 and CDR2 contain
CC synthetic diversity and CDR3 diversity is captured from B cells. The
CC method is useful for cleaving single-stranded nucleic acid sequences at a
CC desired location, which can be subsequently used to produce libraries or

CC genetic packages that display and/or express a diverse family of
CC peptides, polypeptides or proteins. ABZ36912 to ABZ37510 and ABZ55464 to
CC ABZ55499 represent sequences used in the exemplification of the present
CC invention
XX Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
| | | | | | | | | | | | | | | |
Db 15 AAAAAAAAAAAAAA 1

RESULT 1067
ABV74142
ID ABV74142 standard; DNA; 15 BP.
XX AC ABV74142;
XX DT 23-JAN-2003 (first entry)
XX DE 5' End of cDNA library clone.
XX KW G-protein coupled receptor; odourant; receptor; olfaction; array;
XX KW microarray; anosmia; attractant; aromatic; pesticide; ss.
XX OS Synthetic.
XX PN WO200277200-A2.
XX PD 03-OCT-2002.
XX PF 26-MAR-2002; 2002WO-US009559.
XX PR 27-MAR-2001; 2001US-0279168P.
XX PR 31-JAN-2002; 2002US-035392P.
XX PA (INSC-) INSCENT INC.
XX PI Woods D, Dimitratos S;
XX PI WPI; 2003-029930/02.
XX PT Identifying nucleic acid encoding novel sex-linked-tissue-linked
XX PT receptors, useful for isolating odourant binding proteins or pesticide
XX PT alternatives, by analyzing sequences from a male- and female-specific
XX PT nucleic acid library.
XX PS Disclosure; Fig 5; 83pp; English.

CC The present sequence is that of the 5' end of a cDNA clone isolated from
CC a cDNA library e.g. a mosquito antenna library. A clone was isolated
CC using a method designed to rapidly array and normalize a complex cDNA
CC library obtained from a target species. Clones are arrayed into multi-
CC well plates. Each well contains 16 oligonucleotides (see ABV74137) with a
CC 5' polylinker, a poly-T run capable of binding cDNAs by their poly-A tail
CC and a unique 3' sequence, which allows an anchored oligonucleotide in
CC each well to selectively hybridise only to those cDNA clones with a
CC complementary 5' end. The unique 3' key sequences are designed to give a
CC comprehensive level of degeneracy since they are diverse and numerous
CC enough to ensure that every possible cDNA sequence can be bound by an
CC individual, specific oligonucleotide in a single well. The cDNA library
CC is heated to denature the clones into single stranded DNA, and an aliquot
CC is added to every well. The anchored oligonucleotide serves as the 3',
CC primer in PCR, and the common 5' region present in every cDNA clone
CC serves as the 5' priming site. Denaturing and washing leave anchored cDNA
CC in each well. The library is now arrayed and normalised. The method was
CC used to identify and isolate clones encoding G-protein coupled receptors,
CC especially odourant receptors, and active effectors involved in the
CC olfactory pathway of invertebrates and vertebrates, e.g. odourant binding

CC proteins, or other olfactory or neuronal proteins. The identified
 CC receptors and proteins are useful for identifying compounds that reduce a
 CC target animal's sensitivity to odours, for manufacturing compounds or
 CC devices that mask odours, or trapping invertebrates with odourants.
 CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
 CC with desirable effects on specific species, for the development of pest
 CC monitoring systems or non-toxic, species-specific pesticide alternatives,
 CC for controlling insect feeding and breeding behaviour, detecting the
 CC presence of small air-borne molecules, etc
 XX
 SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 1 AAAAAAAAAAAAAA 15
 |||||
 RESULT 1068
 ABV74141/c
 ID ABV74141 standard; DNA; 15 BP.
 XX
 AC ABV74141;
 XX
 DT 23-JAN-2003 (first entry)
 XX
 DE Oligonucleotide used in cDNA library array.
 XX
 KW G-protein coupled receptor; odourant; receptor; olfaction; array;
 KW microarray; anosmia; attractant; aromatic; pesticide; PCR; primer; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1 /*tag= a
 FT /mod_base= OTHER
 FT /note= "5' polylinker"
 XX
 FN WO20027200-A2.
 XX
 XX 03-OCT-2002.
 XX
 PF 26-MAR-2002; 2002WO-US009559.
 XX
 PR 27-MAR-2001; 2001US-0279168P.
 PR 31-JAN-2002; 2002US-035392P.
 XX
 PA (INSC-) INSCENT INC.
 XX
 PI Woods D, Dimitratos S;
 XX
 DR WPI; 2003-029930/02.
 XX
 FT Identifying nucleic acid encoding novel sex-linked-tissue-linked
 FT receptors, useful for isolating odourant binding proteins or pesticide
 FT alternatives, by analyzing sequences from a male- and female-specific
 FT nucleic acid library.
 XX
 PS Disclosure; Fig 5; 83pp; English.
 XX
 CC The present sequence is that of a poly-T oligonucleotide used in a method
 CC designed to rapidly array and normalize a complex cDNA library obtained
 CC from a target species. Clones are arrayed into multi-well plates. Each
 CC well contains 16 oligonucleotides with a 5' polylinker, a poly-T run
 CC capable of binding cDNAs by their poly-A tail and a unique 3' sequence,
 CC which allows an anchored oligonucleotide in each well to selectively
 CC hybridise only to those cDNA clones with a complementary 5' end. The
 CC unique 3' key sequences are designed to give a comprehensive level of
 CC degeneracy since they are diverse and numerous enough to ensure that

CC every possible cDNA sequence can be bound by an individual, specific
 CC oligonucleotide in a single well. The cDNA library is heated to denature
 CC the clones into single stranded DNA, and an aliquot is added to every
 CC well. The anchored oligonucleotide serves as the 3' primer in PCR, and
 CC the common 5' region present in every cDNA clone serves as the 5' priming
 CC site. Denaturing and washing leave anchored cDNA in each well. The
 CC library is now arrayed and normalised. The method was used to identify
 CC and isolate clones encoding G-protein coupled receptors, especially
 CC odourant receptors, and active effectors involved in the olfactory
 CC pathway of invertebrates and vertebrates, e.g. odourant binding proteins,
 CC or other olfactory or neuronal proteins. The identified receptors and
 CC proteins are useful for identifying compounds that reduce a target
 CC animal's sensitivity to odours, for manufacturing compounds or devices
 CC that mask odours, or trapping invertebrates with odourants.
 CC Semiochemicals (e.g. aromatics or pheromone mimetics) can be developed
 CC with desirable effects on specific species, for the development of pest
 CC monitoring systems or non-toxic, species-specific pesticide alternatives,
 CC for controlling insect feeding and breeding behaviour, detecting the
 CC presence of small air-borne molecules, etc
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 15 AAAAAAAAAAAAAA 1
 |||||
 RESULT 1069
 ABV75865/c
 ID ABV75865 standard; DNA; 15 BP.
 XX
 AC ABV75865;
 XX
 DT 05-FEB-2003 (first entry)
 XX
 DE Oligonucleotide T15-Q-CDPI3.
 XX
 KW Deprotection; phosphoramidite; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..15
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "phosphoramidite linkage"
 FT modified_base 15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "3' Q-CDPI3"
 XX
 FN WO200272864-A2.
 XX
 XX 19-SEP-2002.
 XX
 PF 04-MAR-2002; 2002WO-US006739.
 XX
 PR 08-MAR-2001; 2001US-0274309P.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Nelson J;
 XX
 DR WPI; 2003-046740/04.
 XX
 FT New oligonucleotide deprotection reagent useful for deprotecting
 FT oligonucleotide comprises an active methylene compound and an amine
 FT reagent.
 XX

PS Example 2; Page 25; 46pp; English.

XX The present invention provides a method for deprotection of an

CC oligonucleotide. This involves reacting a protected oligonucleotide,

CC which is preferably covalently attached to a solid support through a

CC linkage, with a deprotection reagent comprising an active methylene

CC compound and an amine reagent. The process and reagent minimise side-

CC reactions leading to certain impurities that contaminate synthetic

CC oligonucleotides. The present sequence is a T15 phosphoramidite

CC oligonucleotide having a quencher moiety (Q) and minor groove binder

CC (CDP13) at the 3' end, which was synthesised in an example of the

CC invention. This protected oligonucleotide was treated either with 15%

CC ethanolic ammonia or with 3% diethylmalonate (DEM) dissolved in 15%

CC ethanolic ammonia for 2 hours at 55 degrees C. HPLC analysis showed that

CC deprotection without DEM yielded a complex mixture of products containing

CC only 26.5% of the desired product. When DEM was used, 76.8% of the

CC desired product was obtained

XX

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.6e+02; Indels 0;

Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 15 AAAAAAAAAAAAAA 1

RESULT 1070

ADA14836

ID ADA14836 standard; DNA; 15 BP.

AC ADA14836;

XX

DT 06-NOV-2003 (first entry)

XX

DE Hairpin target sequence, #1, used in an example of the invention.

XX

KW Hairpin sensor; hairpin loop; complementary probe; inverse repeat arm;

KW quenchable fluorescing agent; microarray; semiconductor; nanocrystal;

KW rhodamine B-labelled dye; detection; gold support; ss.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc_binding 1..15

FT /tag= a

FT /bound_moiety= "Hairpin oligonucleotide #1"

FT /note= "Forms a double-stranded region with the hairpin

FT oligonucleotide shown in example 2"

XX

PN US2003013109-A1.

XX

PD 16-JAN-2003.

XX

PF 21-JUN-2002; 2002US-00176055.

XX

PR 21-JUN-2001; 2001US-0299460P.

XX

PA (BALL/) BALLINGER C T.

PA (LOCA/) LOCASCIO M.

PA (LAND/) LANDRY D P.

XX

PI Ballinger CT, Locascio M, Landry DP;

XX

DR WPI; 2003-596312/56.

XX

XX

PT Hairpin sensor useful for detecting a target nucleotide sequence in a

PT sample, comprises a hairpin loop assembly including a complementary probe

PT and a quenchable fluorescing agent.

XX

PS Example 2; Page 11; 16pp; English.

XX The invention discloses a hairpin sensor comprising a hairpin loop

CC assembly including a complementary probe positioned between a first

CC inverse repeat arm and a second inverse repeat arm, and a quenchable

CC fluorescing agent joined, directly or indirectly, to the end of the

CC second inverse repeat arm of the hairpin loop assembly opposite the

CC complementary probe. Also claimed is a microarray comprising the hairpin

CC sensor, where the end of the first inverse repeat arm opposite the

CC complementary probe is bound, directly or indirectly, to a support, a kit

CC for detecting a target nucleotide sequence in a sample comprising the

CC hairpin sensor, and a support, and a hairpin sensor system, in which the

CC particle is conductive or semi-conductive, including at least one of the

CC above hairpin sensor assemblies. The hairpin sensor further comprises a

CC functional group joined to the end of the first inverse repeat arm

CC opposite the complementary probe, or first spacer opposite the first

CC inverse repeat arm, the functional group selected from amino, carboxyl,

CC thiol and hydroxyl. Further, the sensor comprises a ligand positioned

CC between the second inverse repeat arm and the quenchable fluorescing

CC agent, where the ligand is selected from mercapto, hydroxyl, amino,

CC nitrile and carboxyl, carboxylic acid, organic acid and amino acid. The

CC quenchable fluorescing agent which comprises a semiconductor nanocrystal

CC or rhodamine B-labelled dye. Within the microarray the support is capable

CC of accepting a charge. At least one hairpin sensor comprises two or more

CC hairpin sensors. The two or more hairpin sensors include complementary

CC probes that are the same or different and respective quenchable

CC fluorescing agents that are the same or different. The two or more

CC hairpin sensors are arranged in a spatially-defined pattern. The sensor

CC and system are useful for detecting a target nucleotide sequence in a

CC sample. Further, the method involves identifying the target nucleotide

CC sequence by the location of the complementary probe to which the target

CC nucleotide sequence binds. The two or more hairpin sensors include

CC complementary probes or quenchable fluorescing agents, that are

CC different. The sequence presented is the hairpin oligonucleotide target

CC sequence, #1, used in an example of the invention.

XX

SQ Sequence 15 BP; 15 A; 0 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.6e+02; Indels 0;

Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

Db 1 AAAAAAAAAAAAAA 15

RESULT 1071

ADB68520/c

ID ADB68520 standard; DNA; 15 BP.

XX

AC ADB68520;

XX

DT 04-DEC-2003 (first entry)

XX

DE Single-base mismatch oligonucleotide SEQ ID 10 DNA.

XX

KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;

KW gene expression; respiration; secretion; signalling;

KW ion-channel activity; cell motility; developmental phenotype;

KW tumour regression; single-base mismatch; ss;

KW phosphono-peptide nucleic acid; pPNA.

OS Synthetic.

XX

FN WO2003068798-A2.

XX

PD 21-AUG-2003.

XX

PF 07-FEB-2003; 2003WO-US003904.

XX

PR 09-FEB-2002; 2002US-00072975.

XX

PA (ACTI-) ACTIVE MOTIF.
 XX
 PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
 XX
 DR WPI; 2003-689653/65.
 XX
 XX
 XX Method of inhibiting expression of genes or RNA transcripts, useful for
 PT therapy and determining effects of genes, by administering oligomers
 PT containing hydroxyproline nucleic acid.
 XX
 XX Example 20; Page 234; 240pp; English.
 PS
 XX The invention relates to a novel method of inhibiting the expression of
 CC one or more genes or RNA transcripts by administering at least one
 CC oligonucleotide analogue that includes at least one hydroxyproline
 CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The
 CC oligonucleotides of the invention may be used to monitor properties
 CC including gene expression, respiration, secretion, signalling, ion-
 CC channel activity, cell motility, developmental phenotype and tumour
 CC regression. Furthermore, they may be utilised to determine the effects of
 CC particular genes, as antisense or homologous recombination constructs
 CC e.g. for creating animal models of disease and finally, for increasing
 CC the activity of some enzymes, such as polymerases. The current sequence
 CC is that of the single-base mismatch oligonucleotide SEQ ID 10 DNA of the
 CC invention. This sequence may also comprise a peptide nucleic acid (PNA),
 CC a phosphono-PNA (pPNA) or a HypNA.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db |||||||
 15 AAAAAAAAAAAAAA 1
 RESULT 1072
 ADC18592/c
 ID ADC18592 standard; DNA; 15 BP.
 XX
 AC ADC18592;
 XX
 XX 18-DEC-2003 (first entry)
 XX
 XX Annealing control primer Oligo-dT15 SEQ ID NO:54.
 DE
 XX annealing control primer; ACP; annealing specificity;
 KW nucleic acid amplification; hybridisation; DNA fingerprinting;
 KW genomic DNA; RNA fingerprint; primer; ss.
 XX
 XX Synthetic.
 OS
 XX WO2003050305-A1.
 PN
 XX 19-JUN-2003.
 PD
 XX 19-SEP-2002; 2002WO-KR001781.
 PF
 XX 08-DEC-2001; 2001WO-KR002133.
 PR
 XX 01-MAY-2002; 2002WO-KR000816.
 XX
 XX (SEEG-) SEEGENE INC.
 PA
 XX Chun J;
 FI
 XX WPI; 2003-627256/59.
 DR
 XX
 XX Annealing control primer to improve annealing specificity in nucleic acid
 PT amplification, has region complementary to target; arbitrary nucleotide
 PT sequence, regulator with universal base/non-discriminatory base analog.
 XX

PS Example 2; SEQ ID NO 54; 190pp; English.
 XX
 XX The present invention describes an annealing control primer (ACP) (I) for
 CC improving the annealing specificity in nucleic acid amplification. (I)
 CC has a 3'-end portion with a nucleotide sequence complementary to a site
 CC on a template nucleic acid for hybridisation, a 5'-end portion having a
 CC pre-selected arbitrary nucleotide sequence, and a regulator portion
 CC between the 3' and 5'-end portions, comprising a universal or non-
 CC discriminatory base analogue, where the regulator portion is capable of
 CC regulating an annealing portion of the primer in association with
 CC annealing temperature. (I) is useful for improving annealing specificity
 CC in nucleic acid amplification. (I) is useful for amplifying a nucleic
 CC acid sequence from a DNA or a mixture of nucleic acids, for selectively
 CC amplifying a target nucleic acid sequence from a DNA, and for selectively
 CC amplifying a target nucleic acid sequence from a mRNA, by reverse
 CC transcribing the mRNA and performing an amplification reaction using (I).
 CC (I) is also useful for detecting DNA complementary to differentially
 CC expressed mRNA in two or more nucleic acid samples, by reverse
 CC transcribing the mRNA and performing an amplification reaction using (I).
 CC (I) is also useful for rapidly amplifying a target cDNA fragment
 CC comprising a cDNA region corresponding to the 3'-end or 5'-end region of
 CC an mRNA, for amplifying a population of full-length double-stranded cDNAs
 CC complementary to mRNAs, and amplifying 5'-enriched double-stranded cDNAs
 CC complementary to mRNAs. (I) is also useful for amplifying more than one
 CC target nucleotide sequence simultaneously using more than one pair of
 CC primers in the same reaction, where the primers are derived from (I), for
 CC producing a DNA fingerprint of genomic DNA (gDNA), for producing a RNA
 CC fingerprint of an mRNA sample, identifying conserved homology segments in
 CC a multigene family from an mRNA sample, and for identifying conserved
 CC homology segments in a multigene family from gDNA. (I) is also useful for
 CC identifying a nucleotide variation in a target nucleic acid, and for
 CC mutagenesis in a target nucleic acid. The present sequence represents a
 CC primer which is used in the exemplification of the present invention.
 XX
 SQ Sequence 15 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db |||||||
 15 AAAAAAAAAAAAAA 1
 RESULT 1073
 AAX18365/c
 ID AAX18365 standard; DNA; 16 BP.
 XX
 AC AAX18365;
 XX
 XX 11-MAY-1999 (first entry)
 XX
 XX RT-PCR primer of the invention SEQ ID 6.
 DE
 XX RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 KW
 XX Synthetic.
 OS
 XX JF11032765-A.
 PN
 XX 09-FEB-1999.
 PD
 XX 18-JUL-1997; 97JP-00208312.
 PF
 XX 18-JUL-1997; 97JP-00208312.
 PR
 XX (TAKI) TAKARA SHUZO CO LTD.
 PA
 XX WPI; 1999-183822/16.
 DR
 XX Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 PT

XX Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

SEQ

Query Match 0.9%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1749

DB 15 CAAAAAAAAAAAAA 1

RESULT 1074

AX18366/c

ID AAX18366 standard; DNA; 16 BP.

XX

AC AAX18366;

DT 11-MAY-1999 (first entry)

XX

DE RT-PCR primer of the invention SEQ ID 7.

XX

RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

XX JP11032765-A.

PN 09-FEB-1999.

PD

PF 18-JUL-1997; 97JP-00208312.

PP

PR 18-JUL-1997; 97JP-00208312.

XX (TAKI) TAKARA SHUZO CO LTD.

PA

WIPI; 1999-183822/16.

DR

PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.

PT

PS Disclosure; Page 10; 19pp; Japanese.

XX

CC This sequence represents a primer of the invention. The invention relates

CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta

CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or

CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =

CC natural number indicating the repetition of alpha; beta, delta = V or N;

CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or

CC thymine; gamma = thymine; k = natural number of 3 or over indicating the

CC repetition of gamma, in which thymine expressed by gamma is composed of

CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new

CC sequences allow for reproductive and highly efficient analysis of gene

CC sequences

XX Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

SEQ

Query Match 0.9%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

DB 15 CAAAAAAAAAAAAA 1

RESULT 1075

ABL57075

ID ABL57075 standard; DNA; 16 BP.

XX

AC ABL57075;

DT 22-JUL-2002 (first entry)

XX

DE Molecular beacon target sequence.

XX

Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc_binding 1..16

FT /tag= a

FT /bound_moiety= "Molecular beacon"

FT /note= "forms double-stranded region with bases 5-21 of

FT sequence in ABL57069"

XX

PN WO200218951-A2.

PD 07-MAR-2002.

PF 29-AUG-2001; 2001WO-US041941.

PP

PR 29-AUG-2000; 2000US-0228728P.

PR 30-MAR-2001; 2001US-0280350P.

XX (UYRQ) UNIV ROCKEFELLER.

PA

PI Dubertret B, Calame M, Libchaber A;

XX

WIPI; 2002-404569/43.

DR

PT Sensitively detecting proximity changes in a system that utilizes an

PT interacting fluorophore and quencher, for high sensitivity applications,

PT involves utilizing a metal surface as quencher.

XX

PS Example 3; Page 30; 62pp; English.

XX

CC The present sequence is that of a perfectly matched target sequence for a

CC molecular beacon comprising an oligonucleotide probe (see ABL57069)

CC covalently attached at the 3' end to fluorescent dye and at the 5' end to

CC a nanoparticle. In the native state, the probe forms a hairpin

CC conformation with hybridised termini. The proximity of the fluorophore

CC and quencher (gold nanoparticle) in the molecular beacon results in

CC little or no detectable fluorescence. Upon hybridisation of the central

CC complementary stretch of the probe to a target sequence, such as the

CC present sequence, the hairpin undergoes a conformational change resulting

CC in an increase in fluorescence, the extent of which is proportional to

CC the amount of target sequence present. Single mismatches can be detected.

CC The invention relates generally to the use of metal surface quenchers

CC such as particles or films for high sensitivity applications in, for

CC example, detection and diagnostic systems

XX

Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

SEQ

Query Match 0.9%; Score 15; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 5.9e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750

```
Db      |||||
        2 AAAAAAAAAAAAAA 16

RESULT 1076
AAD57845
ID AAD57845 standard; DNA; 16 BP.
XX
AC AAD57845;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target oligonucleotide #2 used in nonlinear optical technique.
XX
KW Nonlinear optical technique; screening; ss.
XX
OS Unidentified.
XX
PN WO2003064991-A2.
XX
PD 07-AUG-2003.
XX
PF 17-JUL-2002; 2002WO-US022681.
XX
PR 17-JUL-2001; 2001US-0306040P.
XX
PR 23-OCT-2001; 2001US-0347821P.
XX
PR 06-FEB-2002; 2002US-0354668P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
DR WPI; 2003-646172/61.
XX
PT Screening candidate binding partner(s) for binding to test molecule by
PT applying external force field to sample in homogeneous phase, and
PT illuminating sample with light beam(s) at fundamental frequencies, and
PT measuring physical properties.
XX
PS Disclosure; Fig 20-B; 146pp; English.
XX
CC The present invention relates to a method for detecting interactions
CC between biological components using a nonlinear optical technique. The
CC invention is used for screening candidate binding partner(s) for binding
CC to test molecule. It can also be used to detect changes in orientation or
CC conformation of the probe and/or target. The present sequence is a target
CC oligonucleotide used in nonlinear optical technique
XX
SQ Sequence 16 BP; 15 A; 0 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 2 AAAAAAAAAAAAAA 16

RESULT 1077
ADB68508/c
ID ADB68508 standard; DNA; 16 BP.
XX
AC ADB68508;
XX
DT 04-DEC-2003 (first entry)
XX
DE PNA-HypNA hybridisation oligomer.
XX
KW hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
KW gene expression; respiration; secretion; signalling;
KW ion-channel activity; cell motility; developmental phenotype;
KW tumour regression; hybridisation; ss; serine nucleic acid; SerNA;
```

```
KW phosphono-peptide nucleic acid; pPNA.
XX Synthetic.
OS
FH Key modified_base 16 Location/Qualifiers
FT /*tag= a
FT /mod_base= OTHER
FT /note= "OTHER = P (phosphono PNA monomer with phenyl
FT group attached to terminal phosphate"
XX
PN WO2003068798-A2.
XX
PD 21-AUG-2003.
XX
PF 07-FEB-2003; 2003WO-US003904.
XX
PR 09-FEB-2002; 2002US-00072975.
XX
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
XX WPI; 2003-689653/65.
XX
DR Method of inhibiting expression of genes or RNA transcripts, useful for
XX therapy and determining effects of genes, by administering oligomers
XX containing hydroxyproline nucleic acid.
XX
PS Example 17; Page 148; 240pp; English.
XX
CC The invention relates to a novel method of inhibiting the expression of
CC one or more genes or RNA transcripts by administering at least one
CC oligonucleotide analogue that includes at least one hydroxyproline
CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The
CC oligonucleotides of the invention may be used to monitor properties
CC including gene expression, respiration, secretion, signalling, ion-
CC channel activity, cell motility, developmental phenotype and tumour
CC regression. Furthermore, they may be utilised to determine the effects of
CC particular genes, as antisense or homologous recombination constructs
CC e.g. for creating animal models of disease and finally, for increasing
CC the activity of some enzymes, such as polymerases. The current sequence
CC is that of the PNA-HypNA hybridisation oligomer of the invention. This
CC sequence may also comprise phosphono-PNA (pPNA) and serine nucleic acid
CC (SerNA) components.
XX
SQ Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;

Query Match 0.9%; Score 15; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1078
AAT53444/c
ID AAT53444 standard; RNA; 17 BP.
XX
AC AAT53444;
XX
DT 25-MAR-2003 (revised)
DT 27-MAR-1997 (first entry)
XX
DE Rat ICAM hammerhead ribozyme target sequence (nt. position 510).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
```

KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
OS Rattus rattus.
XX
PN W0952323225-A2.
XX
XX
PD 31-AUG-1995.
XX
XX
PF 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 18-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Dorenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
DR
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 201; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were
CC designed and synthesised with modifications that improve their nuclease
CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
CC inhibit ICAM-1 expression, making them useful for reducing transplant
CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 17 BP; 2 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 CCCACGGAGCAGCAC 271
Db 15 CCCACGGAGCAGCAC 1
RESULT 1079
AA69799/c
ID AAX69799 standard; RNA; 17 BP.
XX
AC AAX69799;
XX
XX 28-JUL-1999 (first entry)
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1094.
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN W09715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
PR 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (CHIR) CHIRON CORP.
XX
PI Pavco P, McSwiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 79; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 17 AAAAAAAAAAAAAA 3
RESULT 1080
AA69802/c
ID AAX69802 standard; RNA; 17 BP.
XX

XX WPI; 1998-333259/29.
XX Protein from leukocytes and DNA encoding it - useful as reagents for
PT diagnosing and treating IGA nephropathy.
XX
XX Example 2; Page 33; 41pp; Japanese.
XX PCR primers AAV37933-39 are used in the course of the invention. The
CC specification describes a novel protein isolated from leukocytes of
CC patients with IGA nephropathy. Oligonucleotides based on the DNA sequence
CC encoding this protein are useful as reagents for diagnosing and treating
CC IGA nephropathy
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1083
AAV49503/c
ID AAV49503 standard; cDNA to mRNA; 17 BP.
AC AAV49503;
XX
DT 18-NOV-1998 (first entry)
XX Human eosinophil cell activator HVC002 primer #1.
DE
XX Eosinophil cell activator; treatment; diagnosis; malignant tumour;
KW parasitic infection; allergic inflammation; eosinophilic pneumonia;
KW rapid onset eosinophilia; autoimmune disease; gene therapy; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9824817-A1.
XX
PD 11-JUN-1998.
XX
PF 05-DEC-1997; 97WO-JP004470.
XX
PR 05-DEC-1996; 96JP-00325762.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Yoshisue H, Saito A, Nakagawa S, Kuga T, Shinkai A, Koike M;
PI Nishi T;
XX
DR WPI; 1998-333261/29.
XX
PT DNA and encoded protein which activates eosinophil cells - for treatment
PT of cancer, parasite infection, autoimmune disease and allergic
PT inflammation.
XX
PS Example 1; Page 64; 92pp; Japanese.
XX
CC AAV49503-V49507 are primers used in the isolation of a human eosinophil
CC cell activator. This protein and antibodies generated from the protein
CC can be used for treatment and diagnosis of malignant tumours, parasitic
CC infections, allergic inflammation, eosinophilic pneumonia, rapid onset
CC eosinophilia, and autoimmune diseases. DNA can be used for diagnosis, and
CC the antisense DNA in gene therapy of these disorders. The protein can be
CC used for screening of potential agonists or antagonists of its activity
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1084
AAA30179/c
ID AAA30179 standard; DNA; 17 BP.
XX
AC AAA30179;
XX
DT 16-AUG-2000 (first entry)
XX
DE PCR primer GT15A used in pollenosis associated gene identification.
XX
KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
KW IGE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200020575-A1.
XX
PD 13-APR-2000.
XX
PF 06-OCT-1999; 99WO-JP005506.
XX
PR 06-OCT-1998; 98JP-00284610.
XX
PA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Lu N, Ogawa K;
XX
DR WPI; 2000-317712/27.
XX
PT Gene highly expressed in patients with high cedar pollen-specific IGE
PT levels, useful for diagnosing pollenosis, and screening candidate
PT compounds for pollenosis treatment.
XX
PS Example 6; Page 38; 44pp; Japanese.
XX
CC This sequence represents a PCR primer used in the identification of a
CC human pollenosis associated gene. The gene is highly expressed in
CC individuals with high pollen-specific immunoglobulin E (IGE) levels. The
CC invention relates to the nucleotide sequence encoding the pollenosis
CC associated protein, diagnosing pollenosis and screening candidate
CC compounds for treating pollenosis. The gene can be used in diagnosing
CC pollenosis, particularly cedar pollenosis, and screening candidate
CC compounds for pollenosis treatment
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1085
AAA30180/c
ID AAA30180 standard; DNA; 17 BP.
XX
AC AAA30180;
XX
DT 16-AUG-2000 (first entry)
XX

DE PCR primer GT15C used in pollenosis associated gene identification.
 KW Pollenosis-associated protein; high pollen-specific immunoglobulin E;
 KW IgE; diagnose; cedar pollenosis; treatment; human; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO200020575-A1.
 PN
 XX 13-APR-2000.
 PD
 XX 06-OCT-1999; 99WO-JP005506.
 XX
 XX 06-OCT-1998; 98JP-00284610.
 PR
 XX (GENO-) GENOX RES INC.
 PA
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Lu N, Ogawa K;
 PI
 XX WPI; 2000-317712/27.
 DR
 XX Gene highly expressed in patients with high cedar pollen-specific IgE
 PT levels, useful for diagnosing pollenosis, and screening candidate
 PT compounds for pollenosis treatment.
 XX
 XX Example 6; Page 38; 44pp; Japanese.
 PS
 XX This sequence represents a PCR primer used in the identification of a
 CC human pollenosis associated gene. The gene is highly expressed in
 CC individuals with high pollen-specific immunoglobulin E (IgE) levels. The
 CC invention relates to the nucleotide sequence encoding the pollenosis
 CC associated protein, diagnosing pollenosis and screening candidate
 CC compounds for treating pollenosis. The gene can be used in diagnosing
 CC pollenosis, particularly cedar pollenosis, and screening candidate
 CC compounds for pollenosis treatment
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 1086
 AAX82722/c
 ID AAX82722 standard; DNA; 17 BP.
 AC AAX82722;
 XX
 XX 10-NOV-2000 (first entry)
 DT Human IGA nephropathy-associated cDNA primer #63.
 DE IGA nephropathy-associated protein; diagnosis; treatment; antisense;
 XX human; primer; ss.
 KW Homo sapiens.
 XX
 XX WO9963085-A1.
 PN
 XX 09-DEC-1999.
 PD
 XX 28-MAY-1999; 99WO-JP002855.
 XX
 XX 02-JUN-1998; 98JP-00152603.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 PI Sawada S, Takei M, Shibata K, Furuya A;
 PI
 XX WPI; 2000-097328/08.
 DR
 XX DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins.
 XX
 XX Claim 3; Page 169; 180pp; Japanese.
 PS
 XX This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy
 CC incorporating the antisense sequences; the treatment of IGA nephropathy
 CC using the antisense sequences for mRNA inhibition; proteins associated
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
 CC antibodies recognizing these proteins; the production of the proteins by
 CC culture of host cells transformed with DNA encoding them; diagnostic
 CC reagents for IGA nephropathy containing the antibodies; and compositions
 CC for the treatment of IGA nephropathy which contain the antibodies. The
 CC products of the invention can be used for the diagnosis and treatment of
 CC IGA nephropathy. This sequence represents a primer used in the isolation
 CC and identification of the human IGA nephropathy-associated proteins
 CC described in the method of the invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 1087
 AAX82720/c
 ID AAX82720 standard; DNA; 17 BP.
 AC AAX82720;
 XX
 XX 10-NOV-2000 (first entry)
 DT Human IGA nephropathy-associated cDNA primer #61.
 DE IGA nephropathy-associated protein; diagnosis; treatment; antisense;
 XX human; primer; ss.
 KW Homo sapiens.
 XX
 XX WO9963085-A1.
 PN
 XX 09-DEC-1999.
 PD
 XX 28-MAY-1999; 99WO-JP002855.
 XX
 XX 02-JUN-1998; 98JP-00152603.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 PI Sawada S, Takei M, Shibata K, Furuya A;
 PI
 XX WPI; 2000-097328/08.
 DR
 XX DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins.
 XX
 XX Claim 3; Page 169; 180pp; Japanese.
 PS
 XX This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to

PI Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 PI Sawada S, Takei M, Shibata K, Furuya A;
 DR WPI; 2000-097328/08.
 XX
 XX DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins.
 XX
 XX Claim 3; Page 170; 180pp; Japanese.
 PS
 XX This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to
 CC them. Independent claims cover diagnostic reagents for IGA nephropathy
 CC incorporating the antisense sequences; the treatment of IGA nephropathy
 CC using the antisense sequences for mRNA inhibition; proteins associated
 CC with IGA nephropathy, containing sequences encoded by the DNA sequences;
 CC antibodies recognizing these proteins; the production of the proteins by
 CC culture of host cells transformed with DNA encoding them; diagnostic
 CC reagents for IGA nephropathy containing the antibodies; and compositions
 CC for the treatment of IGA nephropathy which contain the antibodies. The
 CC products of the invention can be used for the diagnosis and treatment of
 CC IGA nephropathy. This sequence represents a primer used in the isolation
 CC and identification of the human IGA nephropathy-associated proteins
 CC described in the method of the invention
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db |||||
 16 AAAAAAAAAAAAAA 2
 RESULT 1087
 AAX82720/c
 ID AAX82720 standard; DNA; 17 BP.
 AC AAX82720;
 XX
 XX 10-NOV-2000 (first entry)
 DT Human IGA nephropathy-associated cDNA primer #61.
 DE IGA nephropathy-associated protein; diagnosis; treatment; antisense;
 XX human; primer; ss.
 KW Homo sapiens.
 XX
 XX WO9963085-A1.
 PN
 XX 09-DEC-1999.
 PD
 XX 28-MAY-1999; 99WO-JP002855.
 XX
 XX 02-JUN-1998; 98JP-00152603.
 PR (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 XX Ishiwata T, Sakurada M, Kawabata A, Nakagawa S, Nishi T, Kuga T;
 PI Sawada S, Takei M, Shibata K, Furuya A;
 PI
 XX WPI; 2000-097328/08.
 DR
 XX DNA sequences preferentially expressed in IGA nephropathy patients,
 PT proteins encoded by them, and antibodies to those proteins.
 XX
 XX Claim 3; Page 169; 180pp; Japanese.
 PS
 XX This invention describes novel DNA sequences preferentially expressed in
 CC IGA nephropathy patients, and DNA sequences stringently hybridizing to

CC them. Independent claims cover diagnostic reagents for Iga nephropathy
CC incorporating the antisense sequences; the treatment of Iga nephropathy
CC using the antisense sequences for mRNA inhibition; proteins associated
CC with Iga nephropathy, containing sequences encoded by the DNA sequences;
CC antibodies recognizing these proteins; the production of the proteins by
CC culture of host cells transfected with DNA encoding them; diagnostic
CC reagents for Iga nephropathy containing the antibodies; and compositions
CC for the treatment of Iga nephropathy which contain the antibodies. The
CC products of the invention can be used for the diagnosis and treatment of
CC Iga nephropathy. This sequence represents a primer used in the isolation
CC and identification of the human Iga nephropathy-associated proteins
CC described in the method of the invention

XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 1088

AAZ89372/c
ID AAZ89372 standard; DNA; 17 BP.

XX AC AAZ89372;

XX DT 15-JUN-2000 (first entry)

XX DE RNA detecting primer #2.

XX KW Amplification; detection; gene expression; primer; ss.

XX OS Unidentified.

XX PN DE19840731-A1.

XX PD 09-MAR-2000.

XX PF 07-SEP-1998; 98DE-01040731.

XX PR 07-SEP-1998; 98DE-01040731.

XX PA (HMR1) HOECHST MARION ROUSSEL DEUT GMBH.

XX DR WPI; 2000-257789/23.

XX PT Analysis of RNA samples, useful for detection of differential gene
XX expression uses two differently labeled primers.

XX PS Disclosure; Page 10; 10pp; German.

XX CC This invention describes a novel method for analysis of an RNA sample
CC which comprises amplifying cDNA with first and second differently labeled
CC primers and analysis of the amplified labeled cDNA. The method is useful
CC for analyzing differential gene expression, for identifying and/or
CC characterizing pharmacological activities or for identifying target
CC genes. The use of different primer combinations allow more cDNAs to be
CC amplified. The method also provides a more detailed analysis than prior
CC art methods. This sequence represents a primer used to illustrate the
CC method of the invention

XX SQ Sequence 17 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 2 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||

Db 15 AAAAAAAAAAAAAA 1

RESULT 1089

AAZ36739/c
ID AAZ36739 standard; DNA; 17 BP.

XX AC AAZ36739;

XX DT 13-MAR-2000 (first entry)

XX DE Anchored oligo(dT) primer AT15A used for modified differential display.

XX KW Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
KW differentially expressed nucleic acid; disease state; cancer;
KW autoimmune disease; infectious disease; aging; developmental disorder;
KW proliferative disorder; neurological disorder; toxicity; primer;
KW treatment resistance; differential expression; drug discovery;
KW growth factor; epidermal growth factor; radiation; stress; pathogen; ss.

XX OS Synthetic.

XX PN WO9955913-A2.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-US009119.

XX PR 27-APR-1998; 98US-0083331P.

XX PR 27-AUG-1998; 98US-0098070P.

XX PR 04-FEB-1999; 99US-0118624P.

XX PA (KIMM-) KIMMEL CANCER CENT SIDNEY.

XX PI McClelland M, Welsh J, Trenkle T;

XX DR WPI; 2000-086388/07.

XX PT Measuring expression of low abundance reduced complexity target nucleic
XX acid molecules.

XX PS Example 3; Page 91; 187pp; English.

XX CC AAZ36739-41 represent oligo(dT) primers used for modified differential
XX display, in the method of the invention. The specification describes a
XX method for measuring the level of two or more nucleic acid molecules in a
XX target. The method comprises contacting a probe with an arbitrarily or
XX statistically sampled target and detecting the amount of specific binding
XX of the target to the probe. The methods can be used to identify
XX differentially expressed nucleic acid molecules associated with disease
XX states, such as cancer, autoimmune disease, infectious disease, aging,
XX developmental disorder, proliferative disorder or neurological disorder.
XX Alternatively the methods can be used to assess the efficacy or toxicity
XX of or a resistance to a treatment. Also the methods can be used to
XX determine differential expression of nucleic acid molecules in response
XX to a stimulus, e.g. a chemical, drug or growth factor (especially
XX epidermal growth factor), radiation, stress or a pathogen. The methods
XX can also be used to determine co-regulated genes that can be potential
XX targets for drug discovery

XX SQ Sequence 17 BP; 2 A; 0 C; 0 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||

Db 16 AAAAAAAAAAAAAA 2

RESULT 1090

AAZ5448/c

ID AAA25448 standard; DNA; 17 BP.
 AC AAA25448;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1946.
 XX
 DE Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9954459-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 19-APR-1999; 99WO-US008547.
 XX
 PR 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Thompson JD, Beigelman L, McSwiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX
 XX WPI; 2000-013248/01.
 XX
 XX New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 PT
 XX
 XX Claim 77; Page 79; 148pp; English.
 PS
 CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphorodithioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A'), that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX
 XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 SQ
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 Db |||||||||||||
 17 AAAAAAAAAAAAAA 3
 RESULT 1091
 AAC64202/c
 ID AAC64202 standard; DNA; 17 BP.
 XX

AC AAC64202;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 373 isolation.
 XX
 KW Human; pollinosis-associated gene 373; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 OS Synthetic.
 XX
 PN WO200065046-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP002730.
 XX
 PR 27-APR-1999; 99JP-00120489.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 XX WPI; 2000-687339/67.
 DR
 XX Pollinosis-associated gene 373 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
 PT in diagnosis of allergic diseases and screening drug candidates.
 XX
 PS Example 6; Page 69; 80pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 373 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates also relates
 CC to the protein encoded by pollinosis gene 373; expression constructs and
 CC host cells comprising pollinosis-associated gene 373 nucleic acids;
 CC pollinosis-associated gene 373 primers and probes; antibodies against the
 CC protein encoded by the gene; methods of detection of pollinosis-
 CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
 CC diseases via the detection of pollinosis-associated gene 373 nucleic
 CC acids. The invention additionally encompasses methods of screening drug
 CC candidates for the treatment of allergic disease by measuring the
 CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
 CC T-cells in the presence of a test compound relative to a control.
 CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
 CC diseases and in the screening of drug candidates for the treatment of
 CC such diseases. The present sequence represents a PCR primer used in the
 CC isolation of human pollinosis-associated gene 373 cDNA
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 Db |||||||||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 1092
 AAC64203/c
 ID AAC64203 standard; DNA; 17 BP.
 XX
 AC AAC64203;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:4, used in human gene 373 isolation.

```
XX Human; pollinosis-associated gene 373; IGE; immunoglobulin E;
KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
KW drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
XX WO200065046-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002730.
XX
XX 27-APR-1999; 99JP-00120489.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687339/67.
XX
XX Pollinosis-associated gene 373 undergoing significantly low expression in
PT subjects with high cedar pollen-specific immunoglobulin-E levels, useful
PT in diagnosis of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 70; 80pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 373 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IGE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis gene 373; expression constructs and
CC host cells comprising pollinosis-associated gene 373 nucleic acids;
CC pollinosis-associated gene 373 primers and probes; antibodies against the
CC protein encoded by the gene; methods of detection of pollinosis-
CC associated gene 373 nucleic acids; and a method of diagnosis of allergic
CC diseases via the detection of pollinosis-associated gene 373 nucleic
CC acids. The invention additionally encompasses methods of screening drug
CC candidates for the treatment of allergic disease by measuring the
CC expression of pollinosis-associated gene 373 in pollen antigen-stimulated
CC T-cells in the presence of a test compound relative to a control.
CC Pollinosis-associated gene 373 is useful in the diagnosis of allergic
CC diseases and in the screening of drug candidates for the treatment of
CC such diseases. The present sequence represents a PCR primer used in the
CC isolation of human pollinosis-associated gene 373 cDNA
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1093
AAC64181/c
ID AAC64181 standard; DNA; 17 BP.
XX
XX AAC64181;
AC
XX 21-FEB-2001 (first entry)
DT
XX
XX PCR anchor primer, SEQ ID NO:2, used in human gene 419 isolation.
DE
XX
XX Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
```

```
XX Synthetic.
OS
XX WO200065045-A1.
PN
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002729.
XX
XX 27-APR-1999; 99JP-00120490.
XX
XX (GENO-) GENOX RES INC.
XX
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687338/67.
XX
XX Pollinosis-associated gene 419 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IGE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
XX Example 6; Page 49; 77pp; Japanese.
XX
XX The invention relates to the human pollinosis-associated gene 419 which
CC exhibits reduced expression in the T-cells of individuals with high cedar
CC pollen-specific IGE (immunoglobulin E) levels. The gene was isolated from
CC T-cells from individuals allergic to cedar pollen using the differential
CC display method. Pollinosis-associated gene 419 has homology with the gene
CC encoding human Fas-associated factor-1 (FAF-1). The invention also
CC relates to the protein encoded by pollinosis gene 419; expression
CC constructs and host cells comprising pollinosis- associated gene 419
CC nucleic acids; pollinosis-associated gene 419 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 419 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-
CC associated gene 419 nucleic acids. The invention additionally encompasses
CC methods of screening drug candidates for the treatment of allergic
CC disease by measuring the expression of pollinosis-associated gene 419 in
CC pollen antigen-stimulated T-cells in the presence of a test compound
CC relative to a control. Pollinosis-associated gene 419 is useful in the
CC diagnosis of allergic diseases and in the screening of drug candidates
CC for the treatment of such diseases. The present sequence represents a PCR
CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1094
AAC64182/c
ID AAC64182 standard; DNA; 17 BP.
XX
XX AAC64182;
AC
XX 21-FEB-2001 (first entry)
DT
XX
XX PCR anchor primer, SEQ ID NO:3, used in human gene 419 isolation.
DE
XX
XX Human; pollinosis-associated gene 419; FAF-1 homologue;
KW Fas-associated factor-1; IGE; immunoglobulin E; cedar pollen allergy;
KW T-cell; reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX
```

PN WO2000065045-A1.
 XX 02-NOV-2000.
 XX 26-APR-2000; 2000WO-JP002729.
 XX 27-APR-1999; 99JP-00120490.
 XX (GENO-) GENOX RES INC.
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687338/67.
 XX Pollinosis-associated gene 419 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX Example 6; Page 49; 77pp; Japanese.
 XX The invention relates to the human pollinosis-associated gene 419 which
 CC exhibits reduced expression in the T-cells of individuals with high cedar
 CC pollen-specific IgE (immunoglobulin E) levels. The gene was isolated from
 CC T-cells from individuals allergic to cedar pollen using the differential
 CC display method. Pollinosis-associated gene 419 has homology with the gene
 CC encoding human Fas-associated factor-1 (FAF-1). The invention also
 CC relates to the protein encoded by pollinosis gene 419; expression
 CC constructs and host cells comprising pollinosis-associated gene 419
 CC nucleic acids; pollinosis-associated gene 419 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 419 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-
 CC associated gene 419 nucleic acids. The invention additionally encompasses
 CC methods of screening drug candidates for the treatment of allergic
 CC disease by measuring the expression of pollinosis-associated gene 419 in
 CC pollen antigen-stimulated T-cells in the presence of a test compound
 CC relative to a control. Pollinosis-associated gene 419 is useful in the
 CC diagnosis of allergic diseases and in the screening of drug candidates
 CC for the treatment of such diseases. The present sequence represents a PCR
 CC primer used in the isolation of human pollinosis-associated gene 419 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 Db |||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 1095
 AAC64171/c
 ID AAC64171 standard; DNA; 17 BP.
 XX AAC64171;
 XX 21-FEB-2001 (first entry)
 XX PCR anchor primer, SEQ ID NO:2, used in human gene 513 isolation.
 XX Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO2000065049-A1.
 XX 02-NOV-2000.

PF 26-APR-2000; 2000WO-JP002733.
 XX 27-APR-1999; 99JP-00120491.
 XX (GENO-) GENOX RES INC.
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2000-687342/67.
 XX Pollinosis-associated gene 513 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX Example 6; Page 38; 46pp; Japanese.
 XX The invention relates to the human pollinosis-associated gene 513 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC detection of pollinosis-associated gene 513 nucleic acids; a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 513 nucleic acids; and methods of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 513
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 513 cDNA
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 Db |||||||
 16 AAAAAAAAAAAAAA 2
 RESULT 1096
 AAC64172/c
 ID AAC64172 standard; DNA; 17 BP.
 XX AAC64172;
 XX 21-FEB-2001 (first entry)
 XX PCR anchor primer, SEQ ID NO:3, used in human gene 513 isolation.
 XX Human; pollinosis-associated gene 513; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX Synthetic.
 OS
 XX WO2000065049-A1.
 XX 02-NOV-2000.
 XX 26-APR-2000; 2000WO-JP002733.
 XX 27-APR-1999; 99JP-00120491.
 XX (GENO-) GENOX RES INC.
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX

DR WPI; 2000-687342/67.
XX Pollinosis-associated gene 513 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX Example 6; Page 38; 46pp; Japanese.
XX The invention relates to the human pollinosis-associated gene 513 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates to methods of
CC detection of pollinosis-associated gene 513 nucleic acids; a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 513 nucleic acids; and methods of screening drug candidates for the
CC treatment of allergic disease by measuring the expression of pollinosis-
CC associated gene 513 in pollen antigen-stimulated T-cells in the presence
CC of a test compound relative to a control. Pollinosis-associated gene 513
CC is useful in the diagnosis of allergic diseases and in the screening of
CC drug candidates for the treatment of such diseases. The present sequence
CC represents a PCR primer used in the isolation of human pollinosis-
CC associated gene 513 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1097
AAC64161/c
ID AAC64161 standard; DNA; 17 BP.
XX AAC64161;
XX
XX
XX
XX 21-FEB-2001 (first entry)
XX PCR anchor primer, SEQ ID NO:2, used in human gene 581 isolation.
XX Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
XX cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX drug screening; allergic disease; PCR primer; ss.
XX Synthetic.
XX WO200065048-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002732.
XX
XX 27-APR-1999; 99JP-00120492.
XX (GENO-) GENOX RES INC.
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687341/67.
XX Pollinosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX Example 6; Page 39; 69pp; Japanese.
XX The invention relates to the human pollinosis-associated gene 581 which

CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression
CC constructs and host cells comprising pollinosis-associated gene 581
CC nucleic acids; pollinosis-associated gene 581 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 581 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 581 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 581 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 581 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1098
AAC64162/c
ID AAC64162 standard; DNA; 17 BP.
XX AAC64162;
XX
XX 21-FEB-2001 (first entry)
XX PCR anchor primer, SEQ ID NO:3, used in human gene 581 isolation.
XX Human; pollinosis-associated gene 581; IgE; immunoglobulin E;
XX cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
XX drug screening; allergic disease; PCR primer; ss.
XX Synthetic.
XX WO200065048-A1.
XX
XX 02-NOV-2000.
XX
XX 26-APR-2000; 2000WO-JP002732.
XX
XX 27-APR-1999; 99JP-00120492.
XX (GENO-) GENOX RES INC.
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX WPI; 2000-687341/67.
XX Pollinosis-associated gene 581 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX Example 6; Page 40; 69pp; Japanese.
XX The invention relates to the human pollinosis-associated gene 581 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. The invention also relates also relates
CC to the protein encoded by pollinosis-associated gene 581; to expression

CC constructs and host cells comprising pollinosis-associated gene 581
 CC nucleic acids; pollinosis-associated gene 581 primers and probes;
 CC antibodies against the protein encoded by the gene; methods of detection
 CC of pollinosis-associated gene 581 nucleic acids; and a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 581 nucleic acids. The invention additionally encompasses methods of
 CC screening drug candidates for the treatment of allergic disease by
 CC measuring the expression of pollinosis-associated gene 581 in pollen
 CC antigen-stimulated T-cells in the presence of a test compound relative to
 CC a control. Pollinosis-associated gene 581 is useful in the diagnosis of
 CC allergic diseases and in the screening of drug candidates for the
 CC treatment of such diseases. The present sequence represents a PCR primer
 CC used in the isolation of human pollinosis-associated gene 581 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1099
 AAC64213/C
 ID AAC64213 standard; DNA; 17 BP.
 XX
 AC AAC64213;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:2, used in human gene 627 isolation.
 XX
 KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065051-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP002735.
 XX
 PR 27-APR-1999; 99JP-00120493.
 XX
 PA (GENO-) GENOX RES INC.

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 DR WPI; 2000-687344/67.
 XX
 XX Pollinosis-associated gene 627 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX
 PS Example 6; Page 41; 51pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 627 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 627 nucleic acids; and a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 627

CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 627 cDNA
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 16 AAAAAAAAAAAAAA 2

RESULT 1100
 AAC64214/C
 ID AAC64214 standard; DNA; 17 BP.
 XX
 AC AAC64214;
 XX
 DT 21-FEB-2001 (first entry)
 XX
 DE PCR anchor primer, SEQ ID NO:3, used in human gene 627 isolation.
 XX
 KW Human; pollinosis-associated gene 627; IgE; immunoglobulin E;
 KW cedar pollen allergy; T-cell; reduced expression; detection; diagnosis;
 KW drug screening; allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 PN WO200065051-A1.
 XX
 PD 02-NOV-2000.
 XX
 PF 26-APR-2000; 2000WO-JP002735.
 XX
 PR 27-APR-1999; 99JP-00120493.
 XX
 PA (GENO-) GENOX RES INC.

PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX
 DR WPI; 2000-687344/67.
 XX
 XX Pollinosis-associated gene 627 undergoing significantly low expression in
 PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
 PT of allergic diseases and screening drug candidates.
 XX
 PS Example 6; Page 42; 51pp; Japanese.
 XX
 CC The invention relates to the human pollinosis-associated gene 627 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
 CC was isolated from T-cells from individuals allergic to cedar pollen using
 CC the differential display method. The invention also relates to methods of
 CC detection of pollinosis-associated gene 627 nucleic acids; a method of
 CC diagnosis of allergic diseases via the detection of pollinosis-associated
 CC gene 627 nucleic acids; and a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 627 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 627
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 627 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;

```
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
|||||

RESULT 1101
AAC64231/C
ID AAC64230 standard; DNA; 17 BP.
XX
AC AAC64231;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:3, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
|||||
```

```
QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
|||||

RESULT 1102
AAC64230/C
ID AAC64230 standard; DNA; 17 BP.
XX
AC AAC64230;
XX
DT 21-FEB-2001 (first entry)
XX
DE PCR anchor primer, SEQ ID NO:2, used in human gene 795 isolation.
XX
KW Human; pollinosis-associated gene 795; vimentin homologue; IgE;
KW immunoglobulin E; cedar pollen allergy; T-cell; reduced expression;
KW detection; diagnosis; drug screening; allergic disease; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO200065050-A1.
XX
PD 02-NOV-2000.
XX
PF 26-APR-2000; 2000WO-JP002734.
XX
PR 27-APR-1999; 99JP-00120494.
XX
PA (GENO-) GENOX RES INC.
PA (EISA) EISAI CO LTD.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
DR WPI; 2000-687343/67.
XX
PT Pollinosis-associated gene 795 undergoing significantly low expression in
PT subjects with high cedar pollen-specific IgE levels, useful in diagnosis
PT of allergic diseases and screening drug candidates.
XX
PS Page 45; Example 6; 73pp; Japanese.
XX
CC The invention relates to the human pollinosis-associated gene 795 which
CC exhibits significantly reduced expression in the T-cells of individuals
CC with high cedar pollen-specific IgE (immunoglobulin E) levels. The gene
CC was isolated from T-cells from individuals allergic to cedar pollen using
CC the differential display method. Pollinosis-associated gene 795 has
CC homology with the human vimentin gene. The invention also relates also
CC relates to the protein encoded by pollinosis gene 795; to expression
CC constructs and host cells comprising pollinosis-associated gene 795
CC nucleic acids; pollinosis-associated gene 795 primers and probes;
CC antibodies against the protein encoded by the gene; methods of detection
CC of pollinosis-associated gene 795 nucleic acids; and a method of
CC diagnosis of allergic diseases via the detection of pollinosis-associated
CC gene 795 nucleic acids. The invention additionally encompasses methods of
CC screening drug candidates for the treatment of allergic disease by
CC measuring the expression of pollinosis-associated gene 795 in pollen
CC antigen-stimulated T-cells in the presence of a test compound relative to
CC a control. Pollinosis-associated gene 795 is useful in the diagnosis of
CC allergic diseases and in the screening of drug candidates for the
CC treatment of such diseases. The present sequence represents a PCR primer
CC used in the isolation of human pollinosis-associated gene 795 cDNA
XX
SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
|||||
```

```

Db      16 AAAAAAAAAAAAAA 2
RESULT 1103
AAC92292/c
ID AAC92292 standard; DNA; 17 BP.
XX
XX AAC92292;
AC
DT 22-MAR-2001 (first entry)
XX
XX Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:2.
DE
XX Human pollinosis-associated gene 465; pollen scattering; allergy;
XX
KW Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO2000073439-A1.
PN
XX 07-DEC-2000.
PD
XX 18-MAY-2000; 2000WO-JP003191.
PF
XX 27-MAY-1999; 99JP-00148784.
PR
XX (GENO-) GENOX RES INC.
XX (EISA) EISAI CO LTD.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-061528/07.
DR
XX Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 43; 61pp; Japanese.
PS
XX The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
PS
XX The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
XX Query Match 0.9%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 6.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1104
AAC92293/c
ID AAC92293 standard; DNA; 17 BP.
XX
XX AAC92293;
AC
DT 22-MAR-2001 (first entry)
XX
XX Human pollinosis-associated gene 465 related PCR primer SEQ ID NO:3.
DE

```

```

XX Human; pollinosis-associated gene 465; pollen scattering; allergy;
KW allergic disease; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO2000073439-A1.
PN
XX 07-DEC-2000.
PD
XX 18-MAY-2000; 2000WO-JP003191.
PF
XX 27-MAY-1999; 99JP-00148784.
PR
XX (GENO-) GENOX RES INC.
XX (EISA) EISAI CO LTD.
PA
XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
PI Yokoi A;
XX
XX WPI; 2001-061528/07.
DR
XX Pollinosis-associated gene 465 undergoing significantly low expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
XX Example 6; Page 44; 61pp; Japanese.
PS
XX The present invention describes the human pollinosis-associated gene 465
CC which has a nucleic acid sequence of 3442 base pairs (bp), given in
CC (AAC92291), that undergoes significantly low expression in subjects after
CC pollen scattering, and is useful in the diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen. The gene is useful in
CC the diagnosis of allergic diseases and screening candidate compounds for
CC remedies capable of regulating the response of T cells to the stimulus by
CC an antigen. The present sequence represents a PCR primer which is used in
CC an example from the present invention
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
PS
XX Query Match 0.9%; Score 15; DB 1; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 6.1e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1105
AAC91720/c
ID AAC91720 standard; DNA; 17 BP.
XX
XX AAC91720;
AC
DT 27-MAR-2001 (first entry)
XX
XX PCR anchor primer, SEQ ID NO:3, used in human gene 787 isolation.
DE
XX Human; pollinosis-associated gene 787; pollen allergy; T-cell;
KW reduced expression; detection; diagnosis; drug screening;
KW allergic disease; PCR primer; ss.
XX
XX Synthetic.
OS
XX WO2000073440-A1.
PN
XX 07-DEC-2000.
PD
XX 18-MAY-2000; 2000WO-JP003192.
PF

```

XX 27-MAY-1999; 99JP-00148785.
 XX (GENO-) GENOX RES INC.
 PA (EISA) EISAI CO LTD.
 XX
 PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 XX Yokoi A;
 DR WPI; 2001-032159/04.
 XX
 PT Pollinosis-associated gene 787 undergoing significantly low expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 40; 54pp; Japanese.
 CC The invention relates to the human pollinosis-associated gene 787 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC after the pollen-scattering season, relative to expression levels in T-
 CC cells before the pollen-scattering season. The gene was isolated from T-
 CC cells from individuals allergic to pollen using the differential display
 CC method. The invention also relates to pollinosis-associated gene 787
 CC primers and probes; methods of detection of pollinosis-associated gene
 CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
 CC detection of pollinosis-associated gene 787 nucleic acids. The invention
 CC additionally encompasses a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 787
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 787 cDNA
 XX
 SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 1106
 AAC91719/c
 ID AAC91719 standard; DNA; 17 BP.
 XX
 AC AAC91719;
 XX
 XX 27-MAR-2001 (first entry)
 DE PCR anchor primer, SEQ ID NO:2, used in human gene 787 isolation.
 XX
 DE Human; pollinosis-associated gene 787; pollen allergy; T-cell;
 XX reduced expression; detection; diagnosis; drug screening;
 KW allergic disease; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO200073440-A1.
 PN 07-DEC-2000.
 XX
 XX 18-MAY-2000; 2000WO-JP003192.
 PF 27-MAY-1999; 99JP-00148785.
 XX
 PR (GENO-) GENOX RES INC.
 PA

PA (EISA) EISAI CO LTD.
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K, Takahashi E;
 PI Yokoi A;
 XX WPI; 2001-032159/04.
 DR
 XX Pollinosis-associated gene 787 undergoing significantly low expression in
 PT subjects after pollen scattering, useful in diagnosis of allergic
 PT diseases and screening candidate compounds to regulate response of T
 PT cells to antigen stimulus.
 XX
 PS Example 6; Page 40; 54pp; Japanese.
 CC The invention relates to the human pollinosis-associated gene 787 which
 CC exhibits significantly reduced expression in the T-cells of individuals
 CC after the pollen-scattering season, relative to expression levels in T-
 CC cells before the pollen-scattering season. The gene was isolated from T-
 CC cells from individuals allergic to pollen using the differential display
 CC method. The invention also relates to pollinosis-associated gene 787
 CC primers and probes; methods of detection of pollinosis-associated gene
 CC 787 nucleic acids; and a method of diagnosis of allergic diseases via the
 CC detection of pollinosis-associated gene 787 nucleic acids. The invention
 CC additionally encompasses a method of screening drug candidates for the
 CC treatment of allergic disease by measuring the expression of pollinosis-
 CC associated gene 787 in pollen antigen-stimulated T-cells in the presence
 CC of a test compound relative to a control. Pollinosis-associated gene 787
 CC is useful in the diagnosis of allergic diseases and in the screening of
 CC drug candidates for the treatment of such diseases. The present sequence
 CC represents a PCR primer used in the isolation of human pollinosis-
 CC associated gene 787 cDNA
 XX
 SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 1107
 AAC82875/c
 ID AAC82875 standard; DNA; 17 BP.
 XX
 AC AAC82875;
 XX
 XX 20-MAR-2001 (first entry)
 DE Human pollinosis-associated gene 441 primer #2.
 XX
 DE Pollinosis; pollinosis-associated gene 441; allergy; T cell;
 KW pollen scattering; antigen; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200073435-A1.
 PN 07-DEC-2000.
 XX
 XX 18-MAY-2000; 2000WO-JP003190.
 PF 27-MAY-1999; 99JP-00148783.
 XX
 PR (GENO-) GENOX RES INC.
 PA
 XX Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
 PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
 XX WPI; 2001-061526/07.
 DR

XX Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 35; 42pp; Japanese.
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1108
AAC82874/c
ID AAC82874 standard; DNA; 17 BP.
XX
AC AAC82874;
XX
DT 20-MAR-2001 (first entry)
XX
DE Human pollinosis-associated gene 441 primer #1.
XX
KW Pollinosis; pollinosis-associated gene 441; allergy; T cell;
KW pollen scattering; antigen; primer; ss.
OS Homo sapiens.
XX
XX WO200073435-A1.
XX
PD 07-DEC-2000.
XX
PF 18-MAY-2000; 2000WO-JP003130.
XX
PR 27-MAY-1999; 95JP-00148783.
XX
FA (GENO-) GENOX RES INC.
XX
PI Nagasu T, Sugita Y, Kashiwabara T, Oshida T, Obayashi M, Gunji S;
PI Obayashi I, Imai Y, Yoshida N, Ogawa K, Matsui K;
XX
DR WPI; 2001-061526/07.
XX
PT Pollinosis-associated gene 441 which undergoes lower expression in
PT subjects after pollen scattering, useful in diagnosis of allergic
PT diseases and screening candidate compounds to regulate response of T
PT cells to antigen stimulus.
XX
PS Example 6; Page 35; 42pp; Japanese.
XX
CC This invention describes a novel nucleic acid molecule comprising a
CC sequence (I) which undergoes significantly low expression in subjects
CC after pollen scattering, and is useful in diagnosis of allergic diseases
CC and screening candidate compounds for remedies capable of regulating the
CC response of T cells to the stimulus by an antigen
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1109
AAH47127/c
ID AAH47127 standard; DNA; 17 BP.
XX
AC AAH47127;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of primer GT15C.
XX
KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW PCR primer; ss.
OS Homo sapiens.
XX
XX WO200165259-A1.
XX
PD 07-SEP-2001.
XX
PF 23-FEB-2001; 2001WO-JP001372.
XX
PR 02-MAR-2000; 2000JP-00061832.
XX
PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
PI Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX
DR WPI; 2001-557789/62.
XX
PT Diagnosis of allergies including atopic dermatitis.
XX
PS Example 6; Page 66; 83pp; Japanese.
XX
CC The invention provides a method of diagnosis of allergies that involves:
CC assaying the levels of expression of genes B1001, B1466, B1072 or B1151
CC in T-cells; and comparing them with the level of expression in healthy T-
CC cells. The method is useful for diagnosing allergies, particularly atopic
CC dermatitis. The present sequence represents a PCR primer used for
CC analysis of the expression of the above genes
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2
RESULT 1110
AAH47126/c
ID AAH47126 standard; DNA; 17 BP.
XX
AC AAH47126;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of primer GT15A.
XX
KW B1001; B1466; B1072; B1151; T-cell; allergy; atopic dermatitis; human;
KW PCR primer; ss.
OS Homo sapiens.
XX

```

PN WO200165259-A1.
XX
PD
XX
XX 07-SEP-2001.
XX
XX 23-FEB-2001; 2001WO-JP001372.
XX
XX 02-MAR-2000; 2000JP-00061832.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX Nagasu T, Oshida T, Obayashi I, Matsui K, Saito H;
XX WPI; 2001-557789/62.
XX
XX Diagnosis of allergies including atopic dermatitis.
XX
XX Example 6; Page 65; 83pp; Japanese.
XX
XX The invention provides a method of diagnosis of allergies that involves:
XX assaying the levels of expression of genes B1001, B1466, B1072 or B1151
XX in T-cells; and comparing them with the level of expression in healthy T-
XX cells. The method is useful for diagnosing allergies, particularly atopic
XX dermatitis. The present sequence represents a PCR primer used for
XX analysis of the expression of the above genes
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1111
ID ABK49634/c
XX ABK49634 standard; DNA; 17 BP.
XX
XX ABK49634;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human Acetyltransferase-like protein 20-90-05 PCR primer GT15A.
XX
XX Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX differential display; eosinophil; antiallergic; atopic dermatitis; GT15A.
XX
XX Homo sapiens.
XX
XX WO200224903-A1.
XX
XX 28-MAR-2002.
XX
XX 21-SEP-2001; 2001WO-JP008246.
XX
XX 25-SEP-2000; 2000JP-00291318.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX (EISA) EISAI CO LTD.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX Takahashi E;
XX
XX WPI; 2002-315738/35.
XX
XX Examining allergic diseases by differential display of gene showing
XX different expression particularly increased expression in remission stage
XX in eosinophils of patients, also applicable in screening candidate
XX compounds for remedies.

```

```

XX
PS Example 1; Page 56; 72pp; Japanese.
XX
XX The invention relates to a method for examining allergic diseases
XX comprises determining the expression level of a gene containing, the
XX human cDNA appearing as ABK49633 which has homology with
XX acetyltransferases in the eosinophils of a patient and comparing the
XX expression level with that in the eosinophils of a healthy individual
XX (i.e. differential display). Also included are methods of screening for
XX candidate compounds which affect the expression level of the gene or the
XX activity of the protein encoded by the gene (including related proteins
XX and mutants), the use of probes based on the gene sequence in the
XX examination of allergic diseases, the use of reporter constructs in the
XX screening of candidate compounds, a vector containing a the transcription
XX -controlling region of the gene, cells transformed with the vector, an
XX antibody against the protein and a model animal for allergic diseases
XX which is a transgenic non-human vertebrate with lowering of expression
XX intensity of the gene in eosinophils. The method is examining allergic
XX diseases particularly atopic dermatitis which is also applicable in
XX screening candidate compounds for remedies. Such method can be performed
XX in high throughput, at low cost. The present sequence is a differential
XX display PCR primer for the cDNA encoding the human acetyltransferase-like
XX protein 20-90-05
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1111
ID ABK49635/c
XX ABK49635 standard; DNA; 17 BP.
XX
XX ABK49635;
XX
XX 15-JUL-2002 (first entry)
XX
XX Human Acetyltransferase-like protein 20-90-05 PCR primer GT15C.
XX
XX Human; ss; PCR; acetyltransferase; 20-90-05; allergic disease; primer;
XX differential display; eosinophil; antiallergic; atopic dermatitis; GT15C.
XX
XX Homo sapiens.
XX
XX WO200224903-A1.
XX
XX 28-MAR-2002.
XX
XX 21-SEP-2001; 2001WO-JP008246.
XX
XX 25-SEP-2000; 2000JP-00291318.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX (EISA) EISAI CO LTD.
XX
XX Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Tsujimoto G;
XX Takahashi E;
XX
XX WPI; 2002-315738/35.
XX
XX Examining allergic diseases by differential display of gene showing
XX different expression particularly increased expression in remission stage
XX in eosinophils of patients, also applicable in screening candidate
XX compounds for remedies.
XX
XX Example 1; Page 56; 72pp; Japanese.

```

XX The invention relates to a method for examining allergic diseases
CC comprises determining the expression level of a gene containing, the
CC human cDNA appearing as ABK49633 which has homology with
CC acetyltransferases in the eosinophils of a patient and comparing the
CC expression level with that in the eosinophils of a healthy individual
CC (i.e. differential display). Also included are methods of screening for
CC candidate compounds which affect the expression level of the gene or the
CC activity of the protein encoded by the gene (including related proteins
CC and mutants), the use of probes based on the gene sequence in the
CC examination of allergic diseases, the use of reporter constructs in the
CC screening of candidate compounds, a vector containing a the transcription
CC -controlling region of the gene, cells transformed with the vector, an
CC antibody against the protein and a model animal for allergic diseases
CC which is a transgenic non-human vertebrate with lowering of expression
CC intensity of the gene in eosinophils. The method is examining allergic
CC diseases particularly atopic dermatitis which is also applicable in
CC screening candidate compounds for remedies. Such method can be performed
CC in high throughput, at low cost. The present sequence is a differential
CC display PCR primer for the cDNA encoding the human acetyltransferase-like
CC protein 20-90-05
XX

SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db | | | | | | | | | | | | | | | | | |
16 AAAAAAAAAAAAAA 2

RESULT 1113
ABL59038/c
ID ABL59038 standard; DNA; 17 BP.
XX ABL59038;
AC
XX 20-AUG-2002 (first entry)
DT
XX Nucleotide sequence of PCR primer GT15A.
DE
XX Human; allergosis; eosinophil; PCR; primer; ss.

XX Homo sapiens.

XX JP2002095500-A.
XX 02-APR-2002;
XX 25-SEP-2000; 2000JP-00291316.
XX 25-SEP-2000; 2000JP-00291316.
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX WPI; 2002-439993/47.
XX

XX Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.

XX Example 1; Page 17; 20pp; Japanese.

XX The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergic diseases. The present sequence represents a PCR primer, which is used
CC in the course of the invention

XX

SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
XX Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db | | | | | | | | | | | | | | | | | |
16 AAAAAAAAAAAAAA 2

RESULT 1114
ABL59039/c
ID ABL59039 standard; DNA; 17 BP.
XX ABL59039;
AC
XX 20-AUG-2002 (first entry)
DT
XX Nucleotide sequence of PCR primer GT15C.
DE
XX Human; allergosis; eosinophil; PCR; primer; ss.

XX Homo sapiens.

XX JP2002095500-A.
XX 02-APR-2002.
XX 25-SEP-2000; 2000JP-00291316.
XX 25-SEP-2000; 2000JP-00291316.
XX (GENO-) GENOX SOYAKU KENKYUSHO KK.
XX (KOKU-) KOKURITSU SHONI BYOIN INCHO.
XX WPI; 2002-439993/47.
XX

XX Examining allergosis, involves measuring the expression levels of a
PT specific gene, and comparing it to the levels in the eosinophils of a
PT healthy control.

XX Example 1; Page 17; 20pp; Japanese.

XX The specification describes a method for examining allergosis. The method
CC comprises measuring the expression level of the gene given in ABL59037,
CC and comparing it with the expression level of the gene in the eosinophils
CC of a healthy person. The method is used for the examination of
CC allergic diseases. The present sequence represents a PCR primer, which is used
CC in the course of the invention

XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db | | | | | | | | | | | | | | | | | |
16 AAAAAAAAAAAAAA 2

RESULT 1115
ABL59039/c
ID ABL59039 standard; DNA; 17 BP.

XX ABL59039;

XX 15-AUG-2002 (first entry)

XX Human allergic disease related PCR primer SEQ ID NO: 18.

XX Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;

KW	primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200233069-A1.
XX	
PD	25-APR-2002.
XX	
XX	
PF	28-SEP-2001; 2001WO-JP008574.
XX	
PR	13-OCT-2000; 2000JP-00314093.
XX	
PA	(GENO-) GENOX RES INC.
PA	(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX	
PI	Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX	
DR	WPI, 2002-372311/40.
XX	
PT	Method for examining allergic diseases by differential display of
PT	seventeen genes showing different expression particularly significant
PT	increase in eosinophils in patients with mild atopic dermatitis, also
PT	applicable in screening compounds.
XX	
XX	
PS	Example 1; Page 109; 165pp; Japanese.
XX	
CC	The present invention relates to a method for examining allergic diseases
CC	which involves determining the expression level of a gene, having one of
CC	the 17 nucleotide sequences shown in ABN99812-ABN99828, in the
CC	eosinophils in a patient and comparing the expression level with that in
CC	the eosinophils of a healthy individual. The method can be used to
CC	examine allergic diseases, particularly atopic dermatitis, and its early
CC	diagnosis, which is also applicable in screening candidate compounds for
CC	remedies. The present sequence is a PCR primer described in the
CC	exemplification of the invention
XX	
SQ	Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
	Query Match 0.9%; Score 15; DB 1; Length 17;
	Best Local Similarity 100.0%; Pred. No. 6.1e+02; Gaps 0;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1736 AAAAAAAAAAAAAA 1750
Db	16 AAAAAAAAAAAAAA 2
RESULT 1116	
ABN99830/C	
ID	ABN99830 standard; DNA; 17 BP.
XX	
AC	ABN99830;
XX	
DT	
XX	15-AUG-2002 (first entry)
XX	
DE	Human allergic disease related PCR primer SEQ ID NO: 19.
XX	
KW	Human; allergy; atopic dermatitis; eosinophil; anti-allergic; PCR;
KW	primer; ss.
XX	
OS	Homo sapiens.
XX	
PN	W0200233069-A1.
XX	
PD	25-APR-2002.
XX	
PF	28-SEP-2001; 2001WO-JP008574.
XX	
PR	13-OCT-2000; 2000JP-00314093.
XX	
XX	
PA	(GENO-) GENOX RES INC.
PA	(NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX	

CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention

XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 1118
AAL49949/C

ID AAL49949 standard; DNA; 17 BP.

XX AC AAL49949;

XX DT 10-DEC-2002 (first entry)

XX DE Human B1153 expression in allergic disease related PCR primer GT15C.

XX KW Human; allergy; B1153; differential expression; antiallergic; asthma;
KW antiasthmatic; antiinflammatory; atopic skin inflammation; PCR; primer;
KW ss.

XX OS Unidentified.

XX PN WO200250269-A1.

XX PD 27-JUN-2002.

XX PF 21-DEC-2001; 2001WO-JP011286.

XX PR 21-DEC-2000; 2000JP-00389476.

XX PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.

XX PI Matsumoto Y, Imai Y, Oshida T, Sugita Y, Nagasu T, Tsujimoto G;
XX WPI; 2002-713252/77.

XX DR Examination of allergic diseases comprises detecting gene B1153 over-
XX expressed in T cells of allergy patients for diagnosis treatment and
XX investigation of atopic skin inflammation and asthma.

XX PS Example 6; Page 82; 102pp; Japanese.

XX CC The present invention relates to a method of examining allergic diseases
CC which comprises comparing the expression level of gene B1153 in allergy
CC patients with the expression level in healthy subjects. The method is
CC useful for the treatment, prevention, diagnosis and study of allergic
CC diseases including atopic skin inflammation and asthma. The present
CC sequence is a PCR primer described in the exemplification of the
CC invention

XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 1119
AAL47234/C

ID AAL47234 standard; DNA; 17 BP.

XX AC AAL47234;

XX DT 22-AUG-2002 (first entry)

XX DE Allergic disease examination method related anchor primer SEQ ID NO: 2.

XX KW Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
KW atopic dermatitis; human; PCR; primer; ss.

XX OS Unidentified.

XX PN WO200233122-A1.

XX PD 25-APR-2002.

XX PF 11-OCT-2001; 2001WO-JP008937.

XX PR 13-OCT-2000; 2000JP-00314093.

XX PA (GENO-) GENOX RES INC.
PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
PA (EISA) EISAI CO LTD.

XX PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
XX Takahashi E;
XX WPI; 2002-372313/40.

XX DR Method for examining allergic diseases by differential display of
XX intersectin 2 gene showing different expression particularly significant
XX increase in eosinophils in patients.

XX PS Example 1; Page 52; 90pp; Japanese.

XX CC The present invention relates to a method for examining allergic diseases
XX with intersectin 2 gene or a gene with equivalent function of intersectin
XX 2 as an indicator gene, which comprises determining the expression level
XX of the gene in the eosinophils in a patient, and comparing the expression
XX level with that in the eosinophils of a healthy individual. The method is
XX for examining allergic diseases, particularly atopic dermatitis, which is
XX also applicable in screening candidate compounds for remedies. The
XX present sequence is an anchor primer described in the exemplification of
XX the invention

XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
|||||
Db 16 AAAAAAAAAAAAAA 2

RESULT 1120
AAL47235/C

ID AAL47235 standard; DNA; 17 BP.

XX AC AAL47235;

XX DT 22-AUG-2002 (first entry)

XX DE Allergic disease examination method related anchor primer SEQ ID NO: 3.

XX KW Allergic disease; allergy; antiallergic; intersectin 2; eosinophil;
XX atopic dermatitis; human; PCR; primer; ss.

XX OS Unidentified.

XX PN WO200233122-A1.

XX PD 25-APR-2002.
XX PF 11-OCT-2001; 2001WO-JP008937.
XX PR 13-OCT-2000; 2000JP-00314093.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGS-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PA (EISA) EISAI CO LTD.
XX PI Sugita Y, Hashida R, Ogawa K, Obayashi M, Nagasu T, Saito H;
PI Takahashi E;
XX WPI; 2002-372313/40.
XX PT Method for examining allergic diseases by differential display of
PT intersectin 2 gene showing different expression particularly significant
PT increase in eosinophils in patients.
XX Example 1; Page 53; 90pp; Japanese.
XX The present invention relates to a method for examining allergic diseases
CC with intersectin 2 gene or a gene with equivalent function of intersectin
CC 2 as an indicator gene, which comprises determining the expression level
CC of the gene in the eosinophils in a patient, and comparing the expression
CC level with that in the eosinophils of a healthy individual. The method is
CC for examining allergic diseases, particularly atopic dermatitis, which is
CC also applicable in screening candidate compounds for remedies. The
CC present sequence is an anchor primer described in the exemplification of
CC the invention
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. NO. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1121
ID ABK18190
XX ABK18190 standard; RNA; 17 BP.
XX AC ABK18190;
XX 09-APR-2002 (first entry)
XX Human ERG hammerhead ribozyme target sequence, Seq ID No 837.
XX Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX Homo sapiens.
XX WO200188124-A2.
XX 22-NOV-2001.
XX 16-MAY-2001; 2001WO-US015866.
XX 16-MAY-2000; 2000US-00572021.

PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
PI Jarvis T; Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX WPI; 2002-082995/11.
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX Claim 4; Page 74; 149pp; English.
XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX Sequence 17 BP; 2 A; 13 C; 1 G; 0 T; 1 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. NO. 6.1e+02;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 271 CTCGAGCCCCCCCC 295
DB 1 CUCCAGCCCCCCCC 15
RESULT 1122
ABK18189
ID ABK18189 standard; RNA; 17 BP.
XX AC ABK18189;
XX 09-APR-2002 (first entry)
XX Human ERG hammerhead ribozyme target sequence, Seq ID No 836.
XX Human; hammerhead ribozyme; cytosolic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
XX Homo sapiens.
XX WO200188124-A2.

XX PD 22-NOV-2001.
 XX XX
 XX PD 16-MAY-2001; 2001WO-US015866.
 XX PF 16-MAY-2000; 2000US-00572021.
 XX PR (RIBO-) RIBOZYME PHARM INC.
 XX PA (GLAXO) GLAXO GROUP LTD.
 XX XX
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX XX WPI; 2002-082995/11.
 XX DR Novel polynucleotide which down regulates expression of Ets-related gene,
 XX PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 XX PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX XX
 XX PS Claim 4; Page 74; 149pp; English.
 XX XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX XX
 XX SQ Sequence 17 BP; 2 A; 13 C; 1 G; 0 T; 1 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 6.1e+02;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 271 CTCACGCCACCC 285
 |:|||||||
 Db 2 CUCCAGCCCCACCC 16
 RESULT 1123
 ABV90792/c
 ID ABV90792 standard; DNA; 17 BP.
 XX AC ABV90792;
 XX XX
 XX DT 23-DEC-2002 (first entry)
 XX XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1505.
 XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 XX KW gene therapy; transgenic; ss.
 XX OS Homo sapiens.
 XX XX

PN EPI239051-A2.
 XX XX
 XX PD 11-SEP-2002.
 XX XX
 XX PF 28-JAN-2002; 2002EP-00001165.
 XX XX
 XX PR 30-JAN-2001; 2001WO-US000663.
 XX PR 30-JAN-2001; 2001WO-US000664.
 XX PR 30-JAN-2001; 2001WO-US000665.
 XX PR 30-JAN-2001; 2001WO-US000666.
 XX PR 30-JAN-2001; 2001WO-US000667.
 XX PR 30-JAN-2001; 2001WO-US000668.
 XX PR 30-JAN-2001; 2001WO-US000669.
 XX PR 30-JAN-2001; 2001WO-US000670.
 XX PR 23-MAY-2001; 2001US-00864761.
 XX PR 10-OCT-2001; 2001US-0328205P.
 XX PA (AEOM-) AEOMICA INC.
 XX XX
 XX PI Shannon M;
 XX XX
 XX DR WPI; 2002-684061/74.
 XX XX
 XX PT Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
 XX PT -1, useful for treating disorders associated with decreased expression or
 XX PT activity of human POSHL1.
 XX XX
 XX PS Example 2; SEQ ID NO 1505; 60pp + Sequence Listing; English.
 XX XX
 CC The invention relates to an isolated SH3 domain (POSH)-like signalling
 CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
 CC acids (SI, ABB3999), a sequence having 65% sequence identity to (SI),
 CC (SI) having 95% deviations, especially conservative substitutions or a
 CC fragment of the sequences comprising at least 8 contiguous amino acids.
 CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
 CC adaptor protein that interacts with Rho family small GTPases as well as
 CC downstream components of the signal transduction pathway. (I) is useful
 CC for identifying a specific binding partner. (I) and nucleic acids (II)
 CC encoding (I) are useful for diagnosing, monitoring disease and treating
 CC caused by altered expression of human POSHL1 including diagnosing and
 CC treating cancer, they are useful in the development of vaccines and (II) is
 CC useful in gene therapy. (II) is useful for constructing microarrays which
 CC are useful for measuring and for surveying gene expression and creating
 CC transgenic non-human animals capable of producing the proteins. The
 CC present sequence is that of a scanning oligonucleotide useful in examples
 CC of the invention. Note: The present sequence did not form part of the
 CC printed specification, but is based on sequence information supplied to
 CC Derwent by the European Patent Office
 XX XX
 XX SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 897 GCCCCTGAGCCAGCC 911
 |:|||||||
 Db 15 GCCCCTGAGCCAGCC 1
 RESULT 1124
 ABV90790/c
 ID ABV90790 standard; DNA; 17 BP.
 XX AC ABV90790;
 XX XX
 XX DT 23-DEC-2002 (first entry)
 XX XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1503.
 XX KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
 XX KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
 XX KW gene therapy; transgenic; ss.

OS Homo sapiens.
PN EP1239051-A2.
XX 11-SEP-2002.
PD 28-JAN-2002; 2002EP-00001165.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
PA Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1503; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 2 A; 5 C; 8 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 897 GCCCTGTAGCCAGCC 911
DB 17 GCCCTGTAGCCAGCC 3
RESULT 1125
ABV90791/c
ID ABV90791 standard; DNA; 17 BP.
XX AC ABV90791;
XX 23-DEC-2002 (first entry)
XX DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1504.
XX

KW Human; POSHL1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
XX gene therapy; transgenic; ss.
OS Homo sapiens.
XX EP1239051-A2.
PN 11-SEP-2002.
PD 28-JAN-2002; 2002EP-00001165.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
PA Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1504; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC caused by altered expression of human POSHL1 including diagnosing and
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 1 A; 5 C; 9 G; 2 T; 0 U; 0 Other;
SQ Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 897 GCCCTGTAGCCAGCC 911
DB 16 GCCCTGTAGCCAGCC 2
RESULT 1126
ABK49757/c
ID ABK49757 standard; DNA; 17 BP.
XX AC ABK49757;
XX 15-JUL-2002 (first entry)
XX

```
XX DE Human atopic dermatitis cDNA related PCR primer GT15c.
XX KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
XX KM allergic disease; antiallergic; dermatological; GT15c.
XX OS Synthetic.
XX PN WO200226962-A1.
XX PD 04-APR-2002.
XX XX
XX PF 21-SEP-2001; 2001WO-JP008247.
XX PR 26-SEP-2000; 2000JP-00293021.
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX DR WPI; 2002-330097/36.
XX XX
XX XX Examining allergic diseases by differential display of genes showing
XX PT different expression particularly increase in remission stage in
XX PT eosinophils in patients.
XX XX
XX PS Example 1; Page 55; 74pp; Japanese.
XX CC This invention relates to gene sequences that are differentially
XX CC expressed in eosinophils from patients with atopic dermatitis in the
XX CC increment stage as compared with those in the remission stage. These
XX CC sequences are used in a novel method for examining allergic diseases
XX CC comprising determining the expression levels of these genes and comparing
XX CC the expression level with that in the eosinophils of a healthy
XX CC individual. The method of the invention may have antiallergic or
XX CC dermatological activities. The method can be used to diagnose allergic
XX CC diseases particularly atopic dermatitis, and may also be used to screen
XX CC candidate compounds for remedies. The method of the invention can be
XX CC performed in high throughput, at low cost. The present sequence
XX CC represents the GT15c PCR primer used to amplify the differentially
XX CC amplified atopic dermatitis related cDNA sequences of the invention
XX SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1127
ABK49756/c
ID ABK49756 standard; DNA; 17 BP.
XX AC ABK49756;
XX XX
XX DT 15-JUL-2002 (first entry)
XX DE
XX KW Human atopic dermatitis cDNA related PCR primer GT15a.
XX KW Atopic dermatitis; ss; differential display; primer; PCR; eosinophil;
XX KW allergic disease; antiallergic; dermatological; GT15a.
XX OS Synthetic.
XX OS WO200226962-A1.
XX PN
XX PD 04-APR-2002.
XX XX
```

```
PF 21-SEP-2001; 2001WO-JP008247.
XX
XX PR 26-SEP-2000; 2000JP-00293021.
XX
XX PA (GENO-) GENOX RES INC.
XX PA (NIGE-) JAPAN GEN NAT CHILDREN'S HOSPITAL.
XX
XX PI Sugita Y, Hashida R, Ogawa K, Fujishima T, Nagasu T, Saito H;
XX DR WPI; 2002-330097/36.
XX
XX XX Examining allergic diseases by differential display of genes showing
XX PT different expression particularly increase in remission stage in
XX PT eosinophils in patients.
XX XX
XX PS Example 1; Page 54; 74pp; Japanese.
XX
XX CC This invention relates to gene sequences that are differentially
XX CC expressed in eosinophils from patients with atopic dermatitis in the
XX CC increment stage as compared with those in the remission stage. These
XX CC sequences are used in a novel method for examining allergic diseases
XX CC comprising determining the expression levels of these genes and comparing
XX CC the expression level with that in the eosinophils of a healthy
XX CC individual. The method of the invention may have antiallergic or
XX CC dermatological activities. The method can be used to diagnose allergic
XX CC diseases particularly atopic dermatitis, and may also be used to screen
XX CC candidate compounds for remedies. The method of the invention can be
XX CC performed in high throughput, at low cost. The present sequence
XX CC represents the GT15a PCR primer used to amplify the differentially
XX CC amplified atopic dermatitis related cDNA sequences of the invention
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1128
ABX79793/c
ID ABX79793 standard; cDNA; 17 BP.
XX AC ABX79793;
XX XX
XX DT 17-APR-2003 (first entry)
XX DE
XX DE EST polymorphic DNA repeat polynucleotide #118.
XX KW EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX KW polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX OS Homo sapiens.
XX XX
XX PN US6472154-B1.
XX XX
XX PD 29-OCT-2002.
XX XX
XX PF 31-DEC-1999; 99US-00475947.
XX PR 31-DEC-1999; 99US-00475947.
XX XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
XX XX
```

DR WPI; 2003-208818/20.
XX Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX Example; Col 483; 588pp; English.
XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
SQ Sequence 17 BP; 0 A; 2 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1
RESULT 1129
ID ADB04274/c
XX ADB04274 standard; DNA; 17 BP.
AC ADB04274;
XX
DT 20-NOV-2003 (first entry)
XX Human MD27 scanning oligonucleotide SEQ ID 5260.
DE
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
PD 05-FEB-2003.
XX
PF 30-JUL-2002; 2002EP-00016874.
XX
PR 02-AUG-2001; 2001US-00922181.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MDZ12, e.g. cancer.
XX
PS Example 8; SEQ ID NO 5260; 103pp; English.

XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MDZ12. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder,
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAA 1749
Db 15 CAAAAAAAAAAAAA 1
RESULT 1130
ID ADC84469/c
XX ADC84469 standard; DNA; 17 BP.
AC ADC84469;
XX
DT 01-JAN-2004 (first entry)
XX
DE
XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 2.
KW Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
OS Synthetic.
XX
PN JP2003159071-A.
XX
PD 03-JUN-2003.
XX
XX 22-NOV-2001; 2001JP-00358366.
XX
XX 22-NOV-2001; 2001JP-00358366.
XX
PA (DOKU-) DOKURITSU GYOSEI HOJIN NOGYO SEIBUTSU SH.
XX
XX WPI; 2003-818678/77.
XX
PT New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX
PS Example 3; SEQ ID NO 2; 43pp; Japanese.
XX
XX The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
SQ Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 17;

```
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1131
ADC84468/c
ID ADC84468 standard; DNA; 17 BP.
AC ADC84468;
XX
XX 01-JAN-2004 (first entry)
XX
XX PCR primer for amplifying plant blastogenesis specific gene #SEQ ID 1.
XX
XX Plant blastogenesis; transformation; gene expression; tissue specific;
KW PCR; primer; ss.
XX
XX Synthetic.
XX
XX JP2003159071-A.
XX
XX 03-JUN-2003.
XX
XX 22-NOV-2001; 2001JP-00358366.
XX
XX 22-NOV-2001; 2001JP-00358366.
XX
XX (DOKU-) DOKURITSU GYOSHI HOJIN NOGYO SEIBUTSU SH.
XX
XX WPI; 2003-818678/77.
XX
XX New naturally derived DNA specifically expressed during blastogenesis of
PT a plant, useful for producing a transformed plant and for compulsive
PT expression of a protein.
XX
XX Example 3; SEQ ID NO 1; 43pp; Japanese.
XX
XX The invention relates to naturally derived DNA specifically expressed
CC during plant blastogenesis. The DNA of the invention is useful for
CC producing a transformed plant. Methods of the invention are also useful
CC for compulsive expression of this DNA. Methods of the invention are
CC useful for plant tissue specific expression of genes. Also, the growth
CC stage of a plant can be controlled specifically. The current sequence
CC represents a PCR primer for amplifying a plant blastogenesis specific
CC gene of the invention.
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1132
ADE77745/c
ID ADE77745 standard; DNA; 17 BP.
AC ADE77745;
XX
XX 29-JAN-2004 (first entry)
XX
XX DNA oligo (SeqID 5) related to the human B1799 gene.
XX
XX ss; allergic disease; B1799; antiallergic; antiinflammatory;
KW dermatological; gene therapy; atopic dermatitis.
```

```
XX Unidentified.
OS WO2003083139-A1.
XX
XX 09-OCT-2003.
XX
XX 25-FEB-2003; 2003WO-JP002047.
XX
XX 03-APR-2002; 2002JP-00100908.
XX
XX (GENO-) GENOX RES INC.
XX (NIGE-) JAPAN GEN AGENCY NATION.
XX
XX Matsumoto Y, Imai Y, Yoshida N, Oshida T, Sugita Y, Saito H;
XX WPI; 2003-804076/75.
XX
XX Examining allergic diseases, such as atopic dermatitis, comprises
PT comparing the expression levels of gene B1799 in T cells in a patient and
PT a healthy individual.
XX
XX Example 1; SEQ ID NO 5; 87pp; Japanese.
XX
XX This invention relates to a novel method for screening and examining
CC allergic diseases by the use of B1799 as the indicator gene.
CC Specifically, it comprises determining the expression level of this
CC indicator gene in a biological sample obtained from the patient, and
CC identifying differential expression (increased expression of B1799) in
CC comparison to that observed in a healthy individual. The present
CC invention describes the B1799 protein as antiallergic, antiinflammatory
CC and dermatological. As such, through the use of gene therapy, this method
CC can be used to treat allergic diseases particularly atopic dermatitis.
CC Furthermore, it is useful for determining a diagnosis that is convenient
CC and non-invasive, and is also applicable in high throughput screening to
CC identify candidate compounds for additional remedies. This
CC oligonucleotide sequence is the DNA oligo (SeqID 5) related to the human
CC B1799 gene of the invention.
XX
XX Sequence 17 BP; 0 A; 1 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1133
AAV54175/c
ID AAV54175 standard; cDNA; 18 BP.
XX
XX AAV54175;
AC
XX
XX 21-DEC-1998 (first entry)
XX
XX Nucleotide sequence PCR primer 12.
DE
XX
XX PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
XX Synthetic.
XX
XX WO9839437-A1.
XX
XX 11-SEP-1998.
XX
XX 05-MAR-1998; 98WO-JP000905.
XX
XX 05-MAR-1997; 97JP-00050302.
PR
XX
```

```

PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
PT Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 51; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1134
AAV54173/C
ID AAV54173 standard; cDNA; 18 BP.
XX
AC AAV54173;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 10.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
DE Nucleotide sequence DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 48; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1135
AAV54166/C
ID AAV54166 standard; cDNA; 18 BP.
XX
AC AAV54166;
XX
DT 21-DEC-1998 (first entry)
XX
DE Nucleotide sequence PCR primer 3.
XX
KW PCR; primer; amplification; apoptosis; antibody; inhibition; ss;
KW immunohistological staining.
XX
OS Synthetic.
XX
PN WO9839437-A1.
XX
PD 11-SEP-1998.
XX
PF 05-MAR-1998; 98WO-JP000905.
XX
PR 05-MAR-1997; 97JP-00050302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Sakaki Y;
XX
DR WPI; 1998-495844/42.
XX
DE Novel apoptosis-related DNAs and proteins - for diagnosis, preventing or
PT treating diseases associated with apoptosis.
XX
PS Example 1; Page 48; 70pp; Japanese.
XX
CC This is the nucleotide sequence of a PCR primer used in the method of the
CC invention, involving the use of novel apoptosis-related DNAs and
CC proteins. The inventions can be used as diagnostic reagents for apoptosis
CC e.g. (monoclonal) antibodies for the protein, as a reagent in
CC immunohistological staining, as apoptosis inhibitors. It can also be used
CC for treatment of apoptosis-related diseases
XX
SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 16 AAAAAAAAAAAAAA 2
RESULT 1136
AAV35391/C
ID AAV35391 standard; DNA; 18 BP.
XX
AC AAV35391;
XX
DT 13-OCT-1998 (first entry)
XX
DE HIV-1 gag protein DNA primer #4.
XX
KW Hypervariable region; ENV protein; vaccinia virus; gag gene; retrovirus;
KW vaccines; infection; protection; primer; ss.
XX

```


OS Synthetic.
 PN WO9822596-A1.
 XX
 XX
 PD 28-MAY-1998.
 XX
 XX 19-NOV-1997; 97WO-JP004216.
 PF
 XX 19-NOV-1996; 96JP-0023412.
 PR
 XX (NINA-) JAPAN NAT INST INFECTIOUS DISEASES.
 PA (JAPG) NIPPON ZEON KK.
 XX
 PI Kojima A, Kurata T, Yasuda A;
 XX
 XX WPI; 1998-312481/27.
 DR
 XX
 PT Recombinant vaccinia virus containing fusion H1B gag gene - for
 PT production in host cells of gag protein for use as vaccine.
 XX
 XX Example 1; Page 64; 84pp; Japanese.
 XX
 XX AAV35388-V35414 are primers used in a method which results in a
 CC recombinant vaccinia virus comprising of a gag gene from a retrovirus
 CC such as HIV-1 or HIV-2, fused to a DNA fragment containing an epitope
 CC region (30-300 bases in length) of a retroviral gene other than the gag
 CC gene. The gag gene may be altered so as to produce a gag protein modified
 CC from the natural sequence by the addition, deletion or substitution of at
 CC least 1 amino acid residue. The fusion gene is inserted into a region of
 CC a vaccinia virus not essential to its propagation, to give a recombinant
 CC vaccinia virus vector which is used to transform a host cell (such as
 CC HeLa, Vero, VEF, rabbit kidney RK13 or human myeloma TK-143 cells). Upon
 CC culturing the host cell produces particulate structures containing the
 CC fusion gag protein. The recombinant vaccinia virus or the fusion gag
 CC protein particles may be used in the production of vaccines for
 CC protecting against infection with retroviruses such as HIV
 XX
 XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 Db 18 AAAAAAAAAAAAAA 4
 RESULT 1137
 AAZ90649/c
 ID AAZ90649 standard; DNA; 18 BP.
 XX
 XX AAZ90649;
 AC
 XX 13-JUN-2000 (first entry)
 DT
 XX Human adipose tissue gene amplifying primer #10.
 DE
 XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX JP2000037190-A.
 PN
 XX 08-FEB-2000.
 PD
 XX 23-JUL-1998; 98JP-00225228.
 PF
 XX 23-JUL-1998; 98JP-00225228.
 PR
 XX (NISR) JAPAN TOBACCO INC.
 PA
 XX WPI; 2000-306578/27.
 DR
 XX A physiologically active protein specifically derived from mammal tissue.
 PT
 XX Example 2; Page 18; 50pp; Japanese.
 PS
 XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 Db 18 AAAAAAAAAAAAAA 4
 RESULT 1137
 AAZ90649/c
 ID AAZ90649 standard; DNA; 18 BP.
 XX
 XX AAZ90649;
 AC
 XX 13-JUN-2000 (first entry)
 DT
 XX Human adipose tissue gene amplifying primer #10.
 DE
 XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX JP2000037190-A.
 PN
 XX 08-FEB-2000.
 PD
 XX 23-JUL-1998; 98JP-00225228.
 PF
 XX 23-JUL-1998; 98JP-00225228.
 PR
 XX (NISR) JAPAN TOBACCO INC.
 PA
 XX WPI; 2000-306578/27.
 DR
 XX A physiologically active protein specifically derived from mammal tissue.
 PT
 XX Example 2; Page 18; 50pp; Japanese.
 PS
 XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 Db 18 AAAAAAAAAAAAAA 4

DR WPI; 2000-306578/27.
 XX
 XX A physiologically active protein specifically derived from mammal tissue.
 XX
 XX Example 2; Page 18; 50pp; Japanese.
 PS
 XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 Db 16 AAAAAAAAAAAAAA 2
 RESULT 1138
 AAZ90648/c
 ID AAZ90648 standard; DNA; 18 BP.
 XX
 XX AAZ90648;
 AC
 XX 13-JUN-2000 (first entry)
 DT
 XX Human adipose tissue gene amplifying primer #9.
 DE
 XX Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
 KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
 XX
 XX Homo sapiens.
 OS
 XX JP2000037190-A.
 PN
 XX 08-FEB-2000.
 PD
 XX 23-JUL-1998; 98JP-00225228.
 PF
 XX 23-JUL-1998; 98JP-00225228.
 PR
 XX (NISB) JAPAN TOBACCO INC.
 PA
 XX WPI; 2000-306578/27.
 DR
 XX A physiologically active protein specifically derived from mammal tissue.
 PT
 XX Example 2; Page 18; 50pp; Japanese.
 PS
 XX The invention relates to identification of genes and proteins of adipose
 CC tissue relating to obesity, particularly complications of visceral
 CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
 CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
 CC proteins (AAV67598-Y67600) are used in the genetic diagnosis, prevention
 CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
 CC represent PCR primers amplifying the human adipose tissue genes
 XX
 XX SQ Sequence 18 BP; 1 A; 1 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1736 AAAAAAAAAAAAAA 1750
 Db 16 AAAAAAAAAAAAAA 2

```

RESULT 1139
AAZ90651/c
ID AAZ90651 standard; DNA; 18 BP.
XX
AC AAZ90651;
XX
DT 13-JUN-2000 (first entry)
DE Human adipose tissue gene amplifying primer #12.
DE
XX
KW Adipose tissue; obesity; diabetes; hyperlipemia; hypertension; human;
KW arteriosclerosis; hyperuricemia; sleep apnea syndrome; PCR primer; ss.
OS Homo sapiens.
XX
PN JP2000037190-A.
PD 08-FEB-2000.
PF 23-JUL-1998; 98JP-00225228.
XX
PR 23-JUL-1998; 98JP-00225228.
XX
PA (NISR) JAPAN TOBACCO INC.
XX
DR WPI; 2000-306578/27.
XX
PT A physiologically active protein specifically derived from mammal tissue.
PS
PS Example 2; Page 18; 50pp; Japanese.
CC The invention relates to identification of genes and proteins of adipose
CC tissue relating to obesity, particularly complications of visceral
CC obesity including diabetes, hyperlipemia, hypertension, arteriosclerosis,
CC hyperuricemia and sleep apnea syndrome. The genes (AAZ90631-633) and the
CC proteins (AAZ90631-633) are used in the genetic diagnosis, prevention
CC and treatment of adipose tissue related diseases. Sequences AAZ90640-51
CC represent PCR primers amplifying the human adipose tissue genes
XX
SQ Sequence 18 BP; 0 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 16 AAAAAAAAAAAAAA 2

RESULT 1140
AAZ58385
ID AAZ58385 standard; DNA; 18 BP.
XX
AC AAZ58385;
XX
DT 01-NOV-2000 (first entry)
DE Polynucleotide # 1 used in a biomolecule detection system.
DE
XX
KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS Synthetic.
XX
PN WO200028088-A1.
XX
PD 18-MAY-2000.
PF 10-NOV-1999; 99WO-US026612.
XX
PR 10-NOV-1999; 99WO-US026612.
XX
PR 10-NOV-1998; 98US-0107828P.
XX

```

```

PR 09-NOV-1999; 99US-00437076.
XX (BIOC-) BIOCRYSTAL LTD.
XX
PI Barbera-Guillem E, Nelson MB, Castro S;
XX
XX WPI; 2000-376593/32.
XX
PT Functionalized nanocrystal carrying polynucleotide, used for detecting
PT target analyte, forms dendrimers with complementary nanocrystals to
PT amplify the fluorescent signal.
XX
PS Example 3; Page 68; 72pp; English.
XX
CC The present invention relates to functionalized nanocrystals for use in
CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
CC attached to their surfaces with one end of the polynucleotide extending
CC outwardly from the nanocrystal. The present sequence is one such
CC polynucleotide. These nanocrystals are used with a second series of
CC nanocrystals, which have polynucleotides complementary to the first
CC polynucleotides, so that the respective complementary strands hybridise
CC to each other and form a dendrimer. This dendrimer produces a signal
CC which can then be detected e.g. fluorescence. The present sequence is
CC composed mainly of Adenine bases. This sequence may therefore be used
CC with a polynucleotide composed mainly of Thymine bases (AAZ58386)
XX
SQ Sequence 18 BP; 15 A; 0 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 4 AAAAAAAAAAAAAA 18

RESULT 1141
AAZ58386/c
ID AAZ58386 standard; DNA; 18 BP.
XX
AC AAZ58386;
XX
DT 01-NOV-2000 (first entry)
DE Polynucleotide # 2 used in a biomolecule detection system.
DE
XX
KW Nanocrystal; biomolecule detection; nonisotopic detection system; ss.
XX
OS Synthetic.
XX
PN WO200028088-A1.
XX
PD 18-MAY-2000.
PF 10-NOV-1999; 99WO-US026612.
XX
PR 10-NOV-1998; 98US-0107828P.
PR 09-NOV-1999; 99US-00437076.
XX
XX (BIOC-) BIOCRYSTAL LTD.
XX
PI Barbera-Guillem E, Nelson MB, Castro S;
XX
XX WPI; 2000-376593/32.
XX
PT Functionalized nanocrystal carrying polynucleotide, used for detecting
PT target analyte, forms dendrimers with complementary nanocrystals to
PT amplify the fluorescent signal.
XX
XX Example 3; Page 69; 72pp; English.
XX

```

CC The present invention relates to functionalised nanocrystals for use in
 CC nonisotopic detection systems for biomolecules e.g. nucleic acids,
 CC proteins, lipids or drugs. The nanocrystals have polynucleotide strands
 CC attached to their surfaces with one end of the polynucleotide extending
 CC outwardly from the nanocrystal. The present sequence is one such
 CC polynucleotide. These nanocrystals are used with a second series of
 CC nanocrystals, which have polynucleotides complementary to the first
 CC polynucleotides, so that the respective complementary strands hybridise
 CC to each other and form a dendrimer. This dendrimer produces a signal
 CC which can then be detected e.g. fluorescence. The present sequence is
 CC composed mainly of Thymine bases. This sequence may therefore be used
 CC with a polynucleotide composed mainly of Adenine bases (AAAS58385)
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 3 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 Db 18 AAAAAAAAAAAAAA 4

RESULT 1142
 AAT06025/c
 ID AAT06025 standard; cDNA; 20 BP.

XX AAT06025;
 XX
 DT 13-APR-1996 (first entry)
 XX
 DE Oligonucleotide based on consensus from saponin glycosyl hydrolase.
 XX
 KW saponin glycosyl hydrolase; tomatinase; plant pathogenic fungi;
 KW avenacinase; deglycosylation; pore formation; cell death; primer; probe;
 KW consensus; ss.

XX Synthetic.

XX WO9530009-A2.

XX 09-NOV-1995.

XX 17-MAR-1995; 95WO-GB000592.

XX 29-APR-1994; 94GB-00008573.

XX (GATS-) GATSBY CHARITABLE FOUND.

XX Osbourn AE, Bowyer P, Daniels MJ;

XX WPI; 1995-393080/50.

XX New isolated saponin glycosyl hydrolase enzymes - used to develop prods.
 PT for the modification of microbial organisms and plants or plant prods.

XX Claim 35; Page 59; 113pp; English.

XX AAT06025-26 are oligonucleotides useful as probes or primers designed
 CC from sequences conserved between saponin glycosyl hydrolases, especially
 CC avenacinase, tomatinase and ALP's (TO6021-24). The enzymes are isolated
 CC from plant pathogenic fungi. The enzymes detoxify saponins by
 CC deglycosylation, which is sufficient to destroy the ability of the
 CC saponin to complex with membrane sterols. Saponin/sterol complexes in
 CC eukaryotic membranes results in pore formation and leakage of cell
 CC contents, with subsequent cell death. The DNA and proteins of the
 CC invention are useful in identification of related enzymes, structural
 CC studies of saponins and also for development of agents which can modulate
 CC SGH activity, e.g. for reducing pathogenicity of SGH-producing pathogens
 CC for specific hosts

XX Sequence 20 BP; 3 A; 6 C; 5 G; 0 T; 0 U; 6 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
 Best Local Similarity 63.2%; Pred. No. 6.9e+02;
 Matches 12; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 355 CCGCGGTGGGTGGGTCCC 373
 |||||
 Db 19 CCKGRTGGTGGCGKWC 1

RESULT 1143
 AAZ01703
 ID AAZ01703 standard; DNA; 20 BP.

XX AAZ01703;

XX 07-OCT-1999 (first entry)

XX PCR primer used to amplify an ORF of Chlamydia trachomatis.

XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
 KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
 KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis; PCR primer;
 KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.

XX Synthetic.

OS Chlamydia trachomatis.

XX WO9928475-A2.

XX 10-JUN-1999.

XX 27-NOV-1998; 98WO-IB001939.

XX 28-NOV-1997; 97FR-00015041.

PR 17-DEC-1997; 97FR-00016034.

PR 04-NOV-1998; 98US-0107077P.

XX (GEST) GENSET.

XX Griffais R;

XX WPI; 1999-371125/31.

XX Genome sequence of Chlamydia trachomatis.

XX Disclosure; Page 1464; 1755pp; English.

XX PCR primers AAZ01426-206209 were used to amplify open reading frames
 CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
 CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
 CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
 CC be used to control growth of the microorganism. Chlamydia trachomatis is
 CC responsible for a large number of diseases, e.g. eye diseases such as
 CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
 CC conjunctivitis; genital diseases such as nongonococcal urethritis;
 CC epididymitis, cervicitis, salpingitis, perihhepatitis, bartholinitis;
 CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
 CC The polypeptides of the invention may be of use in treating these
 CC diseases

XX Sequence 20 BP; 1 A; 3 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 TTTTCTTTTCTGGAG 71
 |||||
 Db 6 TTTTCTTTTCTGGAG 20

RESULT 1144

```
AAD36602/c
ID  AAD36602 standard; DNA; 20 BP.
XX
AC  AAD36602;
XX
DT  09-AUG-2002 (first entry)
XX
DE  Human Her-1 antisense oligonucleotide ISIS #128464.
XX
KW  Human; epidermal growth factor receptor; hyperproliferative disease;
KW  Her1; antisense; prophylaxis; psoriasis; phosphorothioate backbone;
KW  tumour; cancer; ss.
XX
OS  Homo sapiens.
XX
OS  Synthetic.
XX
FH  Key
FT  modified_base
FT  Location/Qualifiers
FT  1..20
FT  /tag= a
FT  /mod_base= OTHER
FT  /note= "Phosphorothioate backbone"
FT  modified_base
FT  1..5
FT  /tag= b
FT  /mod_base= OTHER
FT  modified_base
FT  3
FT  /note= "2'methoxyethyl nucleotides"
FT  /tag= d
FT  /mod_base= m5c
FT  modified_base
FT  4
FT  /tag= e
FT  /mod_base= m5c
FT  modified_base
FT  6
FT  /tag= f
FT  /mod_base= m5c
FT  modified_base
FT  13
FT  /tag= g
FT  /mod_base= m5c
FT  modified_base
FT  16..20
FT  /tag= c
FT  /mod_base= OTHER
FT  /note= "2'methoxyethyl nucleotides"
XX
PN  WO200226758-A1.
XX
XX
PD  04-APR-2002.
XX
PF  28-SEP-2001; 2001WO-US030551.
XX
PR  29-SEP-2000; 2000US-00676610.
XX
PA  (ISIS-) ISIS PHARM INC.
XX
PI  Bennett CF, Wyatt JR, Freier SM;
XX
XX  WPI; 2002-394234/42.
XX
PT  Novel antisense oligonucleotide that specifically hybridizes with and
PT  inhibits nucleic acid encoding epidermal growth factor receptor, useful
PT  for treating hyperproliferative disease such as cancer or psoriasis.
XX
PS  Claim 1; Page 46; 169pp; English.
XX
CC  The invention relates to an antisense oligonucleotide targetted to a
CC  nucleic acid molecule encoding human epidermal growth factor receptor
CC  (Her1) to inhibit its expression. The antisense compounds are useful for
CC  treating diseases or conditions associated with Her-1 such as
CC  hyperproliferative diseases especially cancer (lung, ovarian, colon or
CC  prostate cancer) and psoriasis. They are also useful as research
CC  reagents, diagnostics, therapeutics, kits and prophylactically e.g. to
CC  prevent or delay tumour formation. The present sequence is an antisense
CC  oligonucleotide targetted to human Her-1
XX
SQ  Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  907 CAGCCTCCAGAGGAT 921
DB  15 CAGCCTCCAGAGGAT 1
    |||||
RESULT 1145
ID  ABL57070 standard; DNA; 20 BP.
XX
AC  ABL57070;
XX
DT  22-JUL-2002 (first entry)
XX
DE  Molecular beacon target sequence.
XX
KW  Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
XX
OS  Synthetic.
XX
FH  Key
FT  misc_binding
FT  Location/Qualifiers
FT  1..20
FT  /tag= a
FT  /bound moiety= "Molecular beacon"
FT  /note= "forms double-stranded region with bases 1-20 of
FT  sequence in ABL57069"
XX
PN  WO200218951-A2.
XX
XX
PD  07-MAR-2002.
XX
PF  29-AUG-2001; 2001WO-US041941.
XX
PR  29-AUG-2000; 2000US-0228728P.
PR  30-MAR-2001; 2001US-0280350P.
XX
XX  (UTRQ ) UNIV ROCKEFELLER.
XX
PI  Dubertret B, Calame M, Libchaber A;
XX
XX  WPI; 2002-404569/43.
XX
PT  Sensitive detecting proximity changes in a system that utilizes an
PT  interacting fluorophore and quencher, for high sensitivity applications,
PT  involves utilizing a metal surface as quencher.
XX
PS  Example 2; Page 26; 62pp; English.
XX
CC  The present sequence is that of a perfectly matched target sequence for a
CC  molecular beacon comprising an oligonucleotide probe (see ABL57069)
CC  covalently attached at the 3' end to fluorescent dye and at the 5' end to
CC  a nanoparticle. In the native state, the probe forms a hairpin
CC  conformation with hybridised termini. The proximity of the fluorophore
CC  and quencher (gold nanoparticle) in the molecular beacon results in
CC  little or no detectable fluorescence. Upon hybridisation of the central
CC  complementary stretch of the probe to a target sequence, such as the
CC  present sequence, the hairpin undergoes a conformational change resulting
CC  in an increase in fluorescence, the extent of which is proportional to
CC  the amount of target sequence present. Single mismatches can be detected.
CC  The invention relates generally to the use of metal surface quenchers
CC  such as particles or films for high sensitivity applications in, for
CC  example, detection and diagnostic systems
XX
SQ  Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAA 1750
 Db 1 AAAAAAAAAAAAAA 15

RESULT 1146
 AAD35095/C
 ID AAD35095 standard; DNA; 20 BP.
 AC AAD35095;
 XX
 DT 25-JUL-2002 (first entry)
 XX
 DE HT15-C downstream PCR primer used for identification of genes.
 XX
 KW Mouse; X-chromosome; germ cell less gene; gcl gene; gene diagnosis;
 KW sex discrimination; infertility treatment; chromosomal manipulation;
 KW sperm separation; gene therapy; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN EP1195382-A2.
 XX
 PD 10-APR-2002.
 XX
 PF 02-OCT-2001; 2001EP-00123259.
 XX
 PR 03-OCT-2000; 2000JP-00303994.
 XX
 PA (LIVE-) LIVESTOCK IMPROVEMENT ASSOC JAPAN INC.
 PA (UYGU-) UNIV GUNMA.
 XX
 PI Aizawa A, Kawakami A, Kondo T;
 DR WPI; 2002-354153/39.
 XX
 PT New X-chromosome gene expressed in haploid cells of the testis, useful
 PT for gene diagnosis, discrimination of sex, separation of sperm,
 PT infertility treatment and chromosomal manipulation.
 XX
 PS Example 1; Page 4; 28pp; English.
 XX
 CC The present invention relates to genes located on the X-chromosome of
 CC mammals. These genes are specifically expressed in haploid cells of the
 CC testis and encode amino acid sequences having homology with the amino
 CC acid sequence encoded by drosophila germ cell less (gcl) gene. Sequences
 CC of the invention are used for gene diagnosis, discrimination of sex,
 CC separation of sperm, infertility treatment and chromosomal manipulation,
 CC especially in livestock. They are also used in gene therapy. The present
 CC DNA sequence is a PCR primer which is used for the identification of
 CC genes by differential display method
 XX
 SQ Sequence 20 BP; 2 A; 2 C; 1 G; 15 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
 Db 19 AAAAAAAAAAAAAA 5

RESULT 1147
 ABZ87313/C
 ID ABZ87313 standard; DNA; 20 BP.
 XX
 AC ABZ87313;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human oligonucleotide sequence.
 XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
 KW antiinflammatory steroid; ubiqunone; antiinflammatory; antiallergic;
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
 KW lung inflammation; respiratory disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200285308-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 23-APR-2002; 2002WO-US013135.
 XX
 PR 24-APR-2001; 2001US-0286137P.
 XX
 PA (EPIG-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Li Y, Sandrasegura A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX
 DR WPI; 2003-229219/22.
 XX
 PT Pharmaceutical composition for treating ailments associated with impaired
 PT respiration, has oligo(s) antisense to specific gene(s) or its
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
 PT ubiqunone.
 XX
 PS Disclosure; SEQ ID NO 2555; 872pp; English.
 XX
 CC The invention relates to a novel pharmaceutical composition, which has a
 CC first active agent comprising an oligonucleotide antisense to the
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
 CC junctions of genes encoding a polypeptide associated with lung and/or
 CC nasal airway dysfunction and a second active agent comprising an
 CC antiinflammatory steroid and ubiqunone. A composition of the invention
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
 CC immunosuppressive, and cytostatic activity. The composition may have a
 CC use in antisense gene therapy. The composition is useful for treating or
 CC preventing a respiratory, lung or malignant disease or condition, also
 CC for enhancing the prophylactic or therapeutic respiratory effect of an
 CC antiinflammatory steroid in a subject, for reducing or depleting levels
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine or
 CC receptor, producing bronchodilation, increasing levels of ubiqunone or
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
 CC lung inflammation, lung allergies, or a respiratory disease or condition.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 BP; 5 A; 7 C; 2 G; 6 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1398 GGAGACTGTGAGAAAT 1412
 Db 15 GGAGACTGTGAGAAAT 1

RESULT 1148
 ABZ98535
 ID ABZ98535 standard; DNA; 20 BP.
 XX
 AC ABZ98535;
 XX
 DT 17-OCT-2003 (first entry)
 XX
 DE Human ICAM oligonucleotide sequence.
 XX

Human; antinflammence; lung dysfunction; nasal airway dysfunction;
anti-inflammatory steroid; ubiquinone; anti-inflammatory; antiallergic;
antiasthmatic; hypotensive; immunosuppressive; cytosstatic; gene therapy;
antennse gene therapy; respiratory; lung; adenosine sensitivity;
adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
lung inflammation; respiratory disease; ds.

Hom sapiens.

W0200285308-A2.

31-OCT-2002.

23-APR-2002; 2002WO-US013135.

24-APR-2001; 2001US-0286137P.

(EPIG-) EPIGENESIS PHARM INC.

Nyce JW, Li Y, Sandraesagra A, Katz E, Pabalan J, Aguilar D;
Maller S, Tang L, Shahabuddin S;

WPI; 2003-229219/22.

Pharmaceutical composition for treating ailments associated with impaired
respiration, has oligo(s) antensen to specific gene(s) or its
corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
ubiquinone.

Disclosure; SEQ ID NO 13777; 872pp; English.

The invention relates to a novel pharmaceutical composition, which has a
first active agent comprising an oligonucleotide antensen to the
initiation codon, coding region, 5' or 3' end genomic flanking regions,
5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
junctions of genes encoding a polypeptide associated with lung and/or
nasal airway dysfunction and a second active agent comprising an
anti-inflammatory steroid and ubiquinone. A composition of the invention
has antinflammatory, antiallergic, antiasthmatic, hypotensive,
immunosuppressive, and cytosstatic activity. The composition may have a
use in antensen gene therapy. The composition is useful for treating or
preventing a respiratory, lung or malignant disease or condition, also
for enhancing the prophylactic or therapeutic respiratory effect of an
anti-inflammatory steroid in a subject, for reducing or depleting levels
of, or reducing sensitivity to adenosine, reducing levels of adenosine
receptor, producing bronchodilation, increasing levels of ubiquinone or
lung surfactant in a subject's tissue, or treating bronchoconstriction,
lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences

Sequence 20 BP; 4 A; 10 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred.No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 257 CCCACGGAGCAGCAC 271
DB 5 CCCACGGAGCAGCAC 19
|||||

RESULT 1149
ABZ89440
ID ABZ89440 standard; DNA; 20 BP.
XX AC
XX ABZ89440;
XX AC
XX
DT 17-OCT-2003 (first entry)
DE Human oligonucleotide sequence.
XX

KW	Human; antinense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiashtmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antinense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
OS	Homo sapiens.
XX	
FN	WO200285308-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013135.
XX	
PR	24-APR-2001; 2001US-0286137P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPI; 2003-229219/22.
XX	
PT	Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antinense to specific gene(s) or its
PT	corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT	ubiquinone.
XX	
PS	Disclosure; SEQ ID NO 4682; 872pp; English.
XX	
CC	The invention relates to a novel pharmaceutical composition, which has a
CC	first active agent comprising an oligonucleotide antinense to the
CC	initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC	5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC	junctions of genes encoding a polypeptide associated with lung and/or
CC	nasal airway dysfunction and a second active agent comprising an
CC	antiinflammatory steroid and ubiquinone. A composition of the invention
CC	has antiinflammatory, antiallergic, antiashtmatic, hypotensive, and
CC	immunosuppressive, and cytostatic activity. The composition may have a
CC	use in antinense gene therapy. The composition is useful for treating or
CC	preventing a respiratory, lung or malignant disease or condition, also
CC	for enhancing the prophylactic or therapeutic respiratory effect of an
CC	antiinflammatory steroid in a subject, for reducing or depleting levels
CC	of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC	receptor, producing bronchodilation, increasing levels of ubiquinone or
CC	lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC	lung inflammation, lung allergies, or a respiratory disease or condition.
CC	Note: The sequence data for this patent is not represented in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 20 BP; 14 A; 2 C; 2 G; 2 T; 0 U; 0 Other;
	Query Match 0.9%; Score 15; DB 1; Length 20;
	Best Local Similarity 100.0%; Pred. No. 6.9e+02;
	Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1735 CAAAAAARAAAAA 1749
Db	6 CAAAAAARAAAAA 20
RESULT 1150	
AB290649	
ID	AB290649 standard; DNA; 20 BP.
XX	
AC	AB290649;
XX	
DT	17-OCT-2003 (first entry)
XX	
DE	Human oligonucleotide sequence.

KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
FN WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 5891; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 14 A; 3 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1749
Dy 6 CAAAAAAAAAAAAA 20

RESULT 1151
ABZ25524/C
ID ABZ25524 standard; DNA; 20 BP.
XX
AC ABZ25524;
XX
XX 28-MAR-2003 (first entry)
XX
XX Human p53 exon 5 PCR primer 1.
XX

KW PCR; primer; ss; neoplastic; pre-neoplastic; heterozygosity; cytostatic;
KW urothelial neoplasia; p53; human.
XX
OS Homo sapiens.
XX
FN WO2002100246-A2.
XX
XX 19-DEC-2002.
XX
XX 11-JUN-2002; 2002WO-US018427.
XX
XX 12-JUN-2001; 2001US-0297813P.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX Czerniak B, Johnston D;
XX WPI; 2003-156900/15.
XX
XX Detecting a cell with a neoplastic or pre-neoplastic phenotype, useful
XX for diagnosing or treating neoplasia or pre-neoplastic conditions,
XX comprises testing the cell for the presence of loss of heterozygosity at
XX one or more loci.
XX
XX Example 6; Page 113; 248pp; English.
XX
XX The invention relates to a novel method for detecting a cell with a
XX neoplastic or pre-neoplastic phenotype, comprising testing a sample cell
XX for the presence of loss of heterozygosity at one or more loci on one or
XX more chromosomes. The chromosomes are selected from a group of chromosome
XX 1-22, where a loss of heterozygosity at one or more of the loci is
XX indicative of a neoplastic or pre-neoplastic phenotype. The method of the
XX invention has cytostatic activity. Detecting a cell with a neoplastic or
XX pre-neoplastic phenotype is useful for diagnosing, monitoring or treating
XX the progression of neoplasia or pre-neoplastic conditions, e.g.
XX urothelial neoplasia. The present sequence represents a PCR primer used
XX in the invention to amplify exon 5 of the p53 gene
XX
SQ Sequence 20 BP; 2 A; 8 C; 2 G; 8 T; 0 U; 0 Other;

Query Match 0.9%; Score 15; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 857 CTGCAGGAGAGGAA 871
Dy 15 CTGCAGGAGAGGAA 1

RESULT 1152
AAD57844
ID AAD57844 standard; DNA; 20 BP.
XX
AC AAD57844;
XX
XX 20-NOV-2003 (first entry)
XX
XX Target oligonucleotide #1 used in nonlinear optical technique.
XX
XX Nonlinear optical technique; screening; ss.
XX
XX Unidentified.
XX
XX WO2003064991-A2.
XX
XX 07-AUG-2003.
XX
XX 17-JUL-2002; 2002WO-US022681.
XX
XX 17-JUL-2001; 2001US-0306040P.
XX
XX 23-OCT-2001; 2001US-0347821P.
XX
XX 06-FEB-2002; 2002US-0354668P.
XX

PA (SALA/) SALAFSKY J S.
 PI Salafsky JS;
 XX
 DR WPI; 2003-646172/61.
 XX
 PT Screening candidate binding partner(s) for binding to test molecule by
 PT applying external force field to sample in homogeneous phase,
 PT illuminating sample with light beam(s) at fundamental frequencies, and
 PT measuring physical properties.
 XX
 PS Disclosure; Fig 20B; 146pp; English.
 XX
 CC The present invention relates to a method for detecting interactions
 CC between biological components using a nonlinear optical technique. The
 CC invention is used for screening candidate binding partner(s) for binding
 CC to test molecule. It can also be used to detect changes in orientation or
 CC conformation of the probe and/or target. The present sequence is a target
 CC oligonucleotide used in nonlinear optical technique
 XX
 SQ Sequence 20 BP; 15 A; 3 C; 1 G; 1 T; 0 U; 0 Other;
 Query Match 0.9%; Score 15; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 6.9e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 DB 1 AAAAAAAAAAAAAA 15
 RESULT 1153
 ID AAQ73381 standard; DNA; 18 BP.
 XX
 AC AAQ73381;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAY-1995 (first entry)
 DE Anti-HSV-1 G4 oligo #5653.
 XX
 KW Hybridise; herpes simplex virus; HSV; open reading frame;
 KW translation initiation site; coding region; 5' UTR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9419945-A1.
 XX
 PD 15-SEP-1994.
 XX
 PF 07-MAR-1994; 94WO-US002471.
 XX
 PR 12-MAR-1993; 93US-00031147.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Draper KG, Crooke ST, Mirabelli CK, Ecker DJ, Hanecak R;
 PI Anderson KP, Brown-Driver VL, Wyatt JR;
 XX
 DR WPI; 1994-302552/37.
 XX
 PT New oligonucleotide(s) hybridising with DNA or RNA of herpesvirus gene -
 PT are used in the treatment and diagnosis of herpes simplex virus;
 PT cytomegalovirus, Epstein Barr virus and varicella zoster infections.
 XX
 PS Claim 12; Page 36; 72pp; English.
 XX
 CC The sequences given in AAQ73325-81 represent oligonucleotides which
 CC hybridise specifically with DNA or RNA from a herpes virus gene
 CC corresponding to one of the open reading frames UL5, -8, -9, -20, -27-
 CC 29, -30, -42, -52 or IE175 of herpes simplex virus type 1 (HSV-1). These
 CC oligos pref. hybridise with a translation initiation site, a coding

CC region or a 5' untranslated region. These oligos may be used in
 CC compositions for the treatment and diagnosis of herpes viral infection,
 CC by contacting the virus or the animal, or its cells, tissues or body
 CC fluids with the oligo. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1019 TTGGGGATGGCGCTGGGG 1036
 DB 1 TTGGGGTTGGCGTTGGGG 18
 RESULT 1154
 ID AAQ61992 standard; DNA; 18 BP.
 XX
 AC AAQ61992;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX
 DE Guanine quartet containing oligomer, #3.
 XX
 KW Inhibition; replication; herpes simplex virus; HSV; HIV; retard;
 KW human cytomegalovirus; influenza virus; inflammation; telomere length;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy; aging; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18
 FT /*tag= a
 FT /note= "Phosphorothionate intersugar linkages"
 XX
 PN WO9408053-A1.
 XX
 PD 14-APR-1994.
 XX
 PF 29-SEP-1993; 93WO-US009297.
 XX
 PR 29-SEP-1992; 92US-00954185.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
 PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 XX
 DR WPI; 1994-135613/16.
 XX
 PT New modified oligo-nucleotide contg guanine quartet - inhibits activity
 PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 PT of chromosomes.
 XX
 PS Disclosure; Page 105; 144pp; English.
 XX
 CC The sequences given in AAQ61990-2001 are oligonucleotides which contain
 CC G4 or G3 stretches and which may be used for inhibiting replication of
 CC herpes simplex virus (HSV), activity of HIV, human cytomegalovirus or
 CC influenza virus, or for treating inflammatory and neurological disorders
 CC caused by phospholipase A2 activity in cases of hyper- proliferation,
 CC malignancy, cardiovascular disease and snake bite. Oligonucleotides such
 CC as these, may be used for inhibiting division of malignant cells by
 CC modulating telomere length, which may also retard aging. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 18;

Best Local Similarity 88.9%; Pred. No. 6.8e+02; Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGG 1036
 Db 1 TTGGGTTGGGTTGGGG 18

RESULT 1155
 AAQ61897
 ID AAQ61897 standard; DNA; 18 BP.
 XX
 AC AAQ61897;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX
 DE HSV replication inhibiting oligomer, ISIS no 5653.
 XX
 KW Inhibition; replication; herpes simplex virus; HSV; HIV;
 KW human cytomegalovirus; influenza virus; inflammation;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy;
 KW telomere length; retard; aging; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18
 FT /tag= a
 FT /note= "Phosphorothionate intersugar linkages"

WO9408053-A1.
 14-APR-1994.
 29-SEP-1993; 93WO-US009297.
 29-SEP-1992; 92US-00954185.
 (ISIS-) ISIS PHARM INC.
 Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL,
 Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 WPI; 1994-135613/16.
 New modified oligo-nucleotide contg guanine quartet - inhibits activity
 of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 of chromosomes.
 Claim 5; Page 19; 144pp; English.
 The sequences given in AAQ61895-50 and AAQ61896-906 are oligonucleotides
 which contain a G4 or two G3 stretches and which may be used for
 inhibiting replication of herpes simplex virus (HSV). Oligonucleotides
 such as these may also be used for inhibiting activity of HIV, human
 cytomegalovirus or influenza virus, or for treating inflammatory and
 neurological disorders caused by phospholipase A2 activity in cases of
 hyperproliferation, malignancy, cardiovascular disease and snake bite.
 They may also be used for inhibiting division of malignant cells by
 modulating telomere length, which may also retard aging. (Updated on 25-
 MAR-2003 to correct PN field.)

Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGG 1036
 Db 1 TTGGGTTGGGTTGGGG 18

RESULT 1157
 AAQ97983
 ID AAQ97983 standard; DNA; 18 BP.
 XX

RESULT 1156
 AAQ61913
 ID AAQ61913 standard; DNA; 18 BP.
 XX
 AC AAQ61913;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-NOV-1994 (first entry)
 XX
 DE HIV replication inhibiting oligomer, ISIS no 5666.
 XX
 KW Inhibition; replication; herpes simplex virus; HSV; HIV;
 KW human cytomegalovirus; influenza virus; inflammation;
 KW neurological disorders; phospholipase A2 activity; hyperproliferation;
 KW malignancy; cardiovascular disease; snake bite; malignancy;
 KW telomere length; retard; aging; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 1..18
 FT /tag= a
 FT /note= "Phosphorothionate intersugar linkages"

WO9408053-A1.
 14-APR-1994.
 29-SEP-1993; 93WO-US009297.
 29-SEP-1992; 92US-00954185.
 (ISIS-) ISIS PHARM INC.
 Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL,
 Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
 WPI; 1994-135613/16.
 New modified oligo-nucleotide contg guanine quartet - inhibits activity
 of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
 of chromosomes.
 Disclosure; Page 23; 144pp; English.
 The sequences given in AAQ61913-16 are oligonucleotides which contain a
 G4 stretch and which may be used for inhibiting replication of human
 immunodeficiency virus (HIV). Oligonucleotides such as these may also be
 used for inhibiting activity of HSV, human cytomegalovirus or influenza
 virus, or for treating inflammatory and neurological disorders caused by
 phospholipase A2 activity in cases of hyper- proliferation, malignancy,
 cardiovascular disease and snake bite. They may also be used for
 inhibiting division of malignant cells by modulating telomere length,
 which may also retard aging. (Updated on 25-MAR-2003 to correct PN
 field.)

Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1019 TTGGGATGGGCTGGGG 1036
 Db 1 TTGGGTTGGGTTGGGG 18

RESULT 1157
 AAQ97983
 ID AAQ97983 standard; DNA; 18 BP.
 XX

AAQ97983;
 25-MAR-2003 (revised)
 19-OCT-1995 (first entry)
 Peptide nucleic acid oligomer targetting HIV gene.
 Peptide nucleic acid; PNA; HIV; human immunodeficiency virus; AIDS;
 antiviral; antisense; triple helix; ss.
 Synthetic.
 Key Location/Qualifiers
 misc_feature 1..18
 /tag= a
 /note= "at least one (and preferably all) of the backbone
 subunits are composed of N-acetyl N-(2-aminoethyl)glycine
 peptide residues, the nucleobase being attached
 covalently to the acetyl group and the peptide linkage
 being formed by condensation of the glycine carboxy group
 of one residue with the amino group of the 2-aminoethyl
 moiety in the next residue"
 WO9504068-A1.
 09-FEB-1995.
 28-JUL-1994; 94WO-US008517.
 29-JUL-1993; 93US-00099718.
 (ISIS-) ISIS PHARM INC.
 Ecker DJ;
 WPI; 1995-082179/11.
 Oligomer hybridisable to HIV sequence and contg. peptide nucleic acid
 subunit - binds in complementary manner to DNA and RNA, and useful for
 modulating HIV viral activity, e.g. in treating AIDS.
 Claim 2; Page 176; 186pp; English.
 New peptide nucleic acid (PNA) oligomers are provided which (a) consist
 of naturally occurring nucleobases covalently bound to a polyamide
 backbone and (b) hybridise to the translation initiation AUG region, 5'
 untranslated region (5' UTR), 3' untranslated region (3' UTR), splice
 junctions or coding sequence of a human immunodeficiency virus gene
 chosen from env, gag, pol, rev and tat. The PNAs can be used to target
 RNA and single stranded DNA (ssDNA) to produce antisense-type gene
 regulation moieties. They have utility as gene-targeted drugs for
 modulating HIV processes. Hence they can be used to treat AIDS and other
 viral infections. They are also useful in diagnostic applications and as
 research tools. PNA oligomers have high affinity for complementary single
 stranded DNA. They are also able to form triple helices in which a first
 PNA strand binds with RNA or ssDNA and a second PNA strand binds with the
 resulting double helix or with the first PNA strand. The PNAs possess no
 significant charge and are water soluble, which facilitates cellular
 uptake. Further, since they contain amides of non-biological amino acids,
 they are biostable and resistant to enzymatic degradation by proteases.
 The present sequence is a specifically claimed PNA sequence (represented
 by the sequence of nucleobases) targetting HIV genes. (Updated on 25-MAR-
 2003 to correct PN field.)
 Sequence 18 BP; 0 A; 0 C; 12 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1019 TTGGGATGGGCTGGGG 1036
 |||||
 1 TTGGGTTGGGCTGGGG 18

RESULT 1158
 AAX70293/C
 ID AAX70293 standard; RNA; 18 BP.
 XX
 AC AAX70293;
 DT 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hairpin ribozyme substrate #61.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswigen J, Stinchcomb D, Escobedo J;
 XX
 DR WPI; 1997-259017/23.
 XX
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 94; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 18 BP; 5 A; 9 C; 2 G; 0 T; 2 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 773 GAGGTGAAGTCTGGGGC 790
 |||||
 18 GAGTTGTAGTCTGGGGC 1
 RESULT 1159
 AAZ25595
 ID AAZ25595 standard; DNA; 18 BP.
 XX
 AC AAZ25595;
 XX
 DT 21-DEC-1999 (first entry)
 XX
 DE Human RhoG antisense phosphorothioate oligonucleotide #36.

XX Human; RhoG; inhibition; antisense; phosphorothioate; expression; GTPase;
 KW mitosis; mitogen; DNA synthesis; cell cycle; cancer;
 KW dynamic organisation; actin cytoskeleton; ras-mediated transformation;
 KW diagnosis; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH modified_base 1..18
 FT /*tag= a
 FT /note= "phosphorothioate linkages"
 XX US5965370-A.
 XX 12-OCT-1999.
 XX 25-SEP-1998; 98US-00161015.
 XX 25-SEP-1998; 98US-00161015.
 XX (ISIS-) ISIS PHARM INC.
 XX Cowseert LM;
 XX WPI; 1999-579906/49.
 XX Antisense oligonucleotides useful for inhibiting the expression of the
 PT human RhoG gene.
 XX Example 15; Col 27; 24pp; English.
 XX AA225553 to AA225582 represent specifically claimed antisense
 CC oligonucleotides targeted to, and capable of inhibiting the expression of
 CC nucleic acids encoding human RhoG. RhoG is a member of the Rho subfamily
 CC of small GTPases the expression of which is associated with the induction
 CC of mitosis by mitogens. RhoG is thought to be required for entry into the
 CC DNA synthesis step of the cell cycle. It also effects the dynamic
 CC organisation of the actin cytoskeleton which regulates changes during
 CC cell cycle progression (e.g. cell rounding and pinching off during
 CC mitosis) and with determining the density to which cells will proliferate
 CC (RhoG affects an actin-dependent signal transduction pathway mediating
 CC the level of contact inhibition through surface signals). Additionally,
 CC RhoG is associated with the development of cancers (RhoG participates in
 CC a signalling pathway involving ras-mediated transformation). Antisense
 CC compounds from the present invention may be used for inhibiting the
 CC expression of human RhoG in cells and tissues in vitro and may be used
 CC diagnostically to determine the role of RhoG in various biochemical
 CC pathways (e.g. its role in mitosis, the organisation of the actin
 CC cytoskeleton and in cancer development). AA225590 to AA225599 represent
 CC more human RhoG antisense oligonucleotides, but they do not inhibit RhoG
 CC as strongly as the specifically claimed sequences
 XX Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1507 CCGCTGGATGGGCACATC 1524
 ||| |||||
 Db 1 CAGCAGGATGGGCACATC 18
 RESULT 1160
 AA252631/c
 ID AA252631 standard; DNA; 18 BP.
 XX
 AC AA252631;
 XX
 DT 29-FEB-2000 (first entry)
 XX

DE Human secreted protein clone yk261_1 probe SEQ ID NO:264.
 XX
 KW Human; secreted protein; immunostimulatory; haemostatic; cytokine;
 KW proliferative; differentiative; chemotactic; chemokinetic; vaccine;
 KW thrombolytic; antiinflammatory; cytostatic; immunosuppressive;
 KW gene therapy; hybridisation; probe; ss.
 XX Synthetic.
 OS Homo sapiens.
 XX WO9958642-A2.
 XX 18-NOV-1999.
 XX 14-MAY-1999; 99WO-US010843.
 XX 14-MAY-1998; 98US-0085472P.
 PR 17-AUG-1998; 98US-0096824P.
 PR 11-SEP-1998; 98US-0099843P.
 PR 11-SEP-1998; 98US-0099950P.
 PR 15-SEP-1998; 98US-0100424P.
 PR 29-SEP-1998; 98US-0102329P.
 PR 09-OCT-1998; 98US-0103615P.
 PR 11-DEC-1998; 98US-0111799P.
 PR 14-DEC-1998; 98US-0112159P.
 PR 31-DEC-1998; 98US-0114415P.
 PR 10-FEB-1999; 99US-00248059.
 PR 06-APR-1999; 99US-00287150.
 PR 13-MAY-1999; 99US-00311021.
 XX (GEMY) GENETICS INST INC.
 XX Wong GG, Clark HF, Fechtel K, Agostino MJ;
 XX WPI; 2000-053095/04.
 DR Novel polynucleotides and proteins having biological activities which
 XX make them suitable for treating, preventing or ameliorating medical
 PT conditions in humans or animals.
 PS Disclosure; Page 729; 730pp; English.
 XX The present invention describes human secreted proteins encoded by
 CC polynucleotides obtained from adult testes, foetal brain, adult brain,
 CC brain (foetal and adult), foetal kidney, adult spleen, and adult thymus
 CC cDNA libraries. The polynucleotides and proteins are predicted to have
 CC biological activities which would make them suitable for treating,
 CC preventing or ameliorating medical conditions in humans and animals.
 CC Suggested activities include nutritional activity, cytokine and cell
 CC proliferation/differentiation activity, immune stimulating (e.g. as
 CC vaccines) or suppressing activity, haematopoiesis regulating activity,
 CC tissue growth activity, activin/inhibin activity, chemotactic/
 CC chemokinetic activity, haemostatic and thrombolytic activity, receptor/
 CC ligand activity, anti-inflammatory activity, cadherin/tumour invasion
 CC suppressor activity, and tumour inhibition activity. The polynucleotides
 CC are also stated to be useful for gene therapy. Therapeutic compositions
 CC are also presently valuable for veterinary applications. AA252475 to
 CC AA252581 encode human secreted proteins, and AA252390 to AA252500
 CC represent human secreted proteins, given in the present invention.
 CC AA252582 to AA252631 represent probes for human secreted protein clones,
 CC used in the exemplification from the present invention
 XX Sequence 18 BP; 1 A; 11 C; 1 G; 5 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 14.8; DB 1; Length 18;
 Best Local Similarity 88.9%; Pred. No. 6.8e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 862 GGAAGAGGAGAGGAGGC 879
 ||| |||||
 Db 18 GGAGGTGGAGAGGAGGC 1

```
RESULT 1161
AAF94745
ID AAF94745 standard; DNA; 18 BP.
XX
AC AAF94745;
XX
DT 23-MAY-2001 (first entry)
XX
DE Rho G antisense phosphorothioate oligonucleotide SEQ ID 169.
XX
KW Rho; GTP binding protein; phosphorothioate antisense oligonucleotide;
KW RhoA; RhoC; RhoG; Rac 1; cdc42; hyperproliferative condition;
KW cancer; wound healing; clotting; ischaemia; reperfusion; reoxygenation;
KW ss.
XX
OS Homo sapiens.
XX
PN WO200115739-A1.
XX
PD 08-MAR-2001.
XX
PF 18-AUG-2000; 2000WO-US022808.
XX
PR 31-AUG-1999; 99US-00387341.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Roberts ML, Cowseert LM;
XX
DR WPI; 2001-191677/19.
XX
PT An antisense compound targeted to a nucleic acid molecule encoding a
PT member of the human Rho family of small GTP binding proteins useful for
PT treating e.g. cancer and ischemia.
XX
PS Example 18; Page 81; 156pp; English.
XX
CC This invention relates to an antisense compound targeted to a nucleic
CC acid molecule encoding a member of the human Rho family of small GTP
CC binding proteins, where the antisense compound inhibits the expression of
CC the member of the human Rho family. The invention includes antisense
CC oligonucleotides AAF94580 - AAF94637 which target a RhoA nucleotide
CC sequence, AAF94645 - AAF94684 which target a RhoB nucleotide sequence,
CC AAF94686 - AAF94725 which target a RhoC nucleotide sequence, AAF94727 -
CC AAF94766 which target RhoG nucleotide sequence, AAF94769 - AAF94790 which
CC target a Rac 1 nucleotide sequence and AAF94795 - AAF94809 which target
CC cdc42 nucleotide sequence. The antisense compound is useful for treating
CC hyperproliferative conditions, especially cancer, abnormal wound healing
CC or clotting conditions and ischaemia/reperfusion or reoxygenation injury.
CC The compound may also be used to diagnose the above conditions.
XX
SQ Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1507 CCGCTGGATGGGCACATC 1524
| | | | | | | | | | | | | | | |
Db 1 CAGCAGGATGGGCACATC 18
RESULT 1162
ABA91529/c
ID ABA91529 standard; DNA; 18 BP.
XX
AC ABA91529;
XX
DT 23-APR-2002 (first entry)
XX
DE DNA-RNA-DNA oligonucleotide AGT02013 used to test RNase H cleavage.
XX
KW DNA-RNA hybrid; RNase H; nucleic acid detection; ss.
```

```
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_RNA 8..9
FT /*tag= a
FT /label= RNA
XX
PN WO200206531-A2.
XX
PD 24-JAN-2002.
XX
PF 12-JUL-2001; 2001WO-US022166.
XX
PR 14-JUL-2000; 2000US-00616761.
PR 30-MAR-2001; 2001US-00823647.
XX
PA (GENE-) APPLIED GENE TECHNOLOGIES INC.
XX
PI Dattagupta N;
XX
DR WPI; 2002-171819/22.
XX
PT Probes for detecting target nucleotide sequence in sample, has sequence
PT that forms hairpin structure having a double-stranded segment and single-
PT stranded loop collectively forming region complementary to target
PT sequence.
XX
PS Example 4; Page 49; 72pp; English.
XX
CC The present sequence is that of DNA-RNA-DNA hybrid oligonucleotide
CC AGT02013. This is one of a set of oligonucleotides (see ABA91527-30) used
CC to assess the minimum number of ribonucleotides in DNA-RNA chimeric
CC oligonucleotides required for RNase H cleavage. Each oligonucleotide of
CC the set had a different number of ribonucleotides, 2 in the present case.
CC The oligonucleotides were mixed with target DNA oligonucleotide AGT02009
CC (see ABA91531) and incubated with RNase H (5 U/ml) at 37 degrees C for 30
CC minutes. The results showed that 4 ribonucleotides were the minimum
CC number for RNA cleavage. The invention provides probes for nucleic acid
CC hybridisation. The probes form a hairpin structure comprising a double-
CC stranded stem and a single-stranded loop, and are capable of both
CC intramolecular and intermolecular hybridisation. The double-stranded stem
CC may comprise a methylphosphonate DNA:RNA hybrid that is resistant to
CC RNase H cleavage. When the probe hybridises with a target DNA, the RNA
CC strand in the DNA:RNA duplex becomes sensitive to RNase H treatment and
CC can be removed. Arrays and methods for nucleic acid hybridisation using
CC the probes are provided
XX
SQ Sequence 18 BP; 2 A; 0 C; 0 G; 16 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAAAAAA 1753
| | | | | | | | | | | | | | | |
Db 18 AAAAAAAAAATTAAAAAAAAA 1
RESULT 1163
ABK27450/c
ID ABK27450 standard; DNA; 18 BP.
XX
AC ABK27450;
XX
DT 09-APR-2002 (first entry)
XX
DE Colon cancer associated cDNA CATX-8, 5' PCR primer.
XX
KW Human; colon cancer; tumour; abnormal cell growth; melanoma;
KW cervical cancer; colorectal adenocarcinoma; Wilms' tumour; leukaemia;
KW lymphoma; antisense therapy; CATX; probe; primer; ss.
XX
```

```

OS Homo sapiens.
XX WO200111047-A2.
XX
XX 15-FEB-2001.
XX
XX 08-AUG-2000; 2000WO-US021606.
XX
XX 09-AUG-1999; 99US-0147933P.
XX
XX (FARB ) BAYER CORP.
XX
XX Bowman BM, Wang K;
XX
XX WPI; 2002-121548/16.
XX
XX New isolated nucleic acid involved in growth regulation in human colonic
XX epithelial cells, termed CATX, for diagnosing and treating abnormal cell
XX growth, and for use as a probe/primer for detecting tumors.
XX
XX Example; Page 91; 130pp; English.
XX
XX The invention relates to an isolated nucleic acid (I) involved in growth
XX regulation in human colonic epithelial cells, termed CATX. (I) is useful
XX as a probe/primer for detecting tumours, preferably colon cancer. The
XX nucleic acid, encoded polypeptide and antibody are useful in diagnosis
XX and treatment of abnormal cell growth (such as cervical cancer,
XX melanomas, colorectal adenocarcinomas, Wilms' tumour, leukaemias and
XX lymphomas), in screening assays for the treatment of abnormal cell
XX growth, for raising antibodies, and to screen for peptide analogues and
XX antagonists. (I) is useful as a biomarker for human tumour cells, e.g.,
XX colon cancer cells, for generating probes and primers designed for
XX identifying and/or cloning homologues in other cell types, in antisense
XX therapy, and in tissue profiling. (I) identifies cancer cells at an early
XX stage of development, so that premalignant cells can be identified prior
XX to their spreading throughout the human body. (I) allows early detection
XX of potentially cancerous conditions, and treatment of the cancerous
XX conditions prior to spread of the cancer cells throughout the body, or
XX prior to development of an irreversible cancerous condition. ABK27426-
XX ABK27469 represent human colon cancer associated coding sequences and
XX primers of the invention
XX
XX Sequence 18 BP; 6 A; 1 C; 8 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 6.8e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 1617 CTCAGTTCCAGTTCCTCAT 1634
Db 18 CTCAGTTCCATTCCTCAT 1
XX
RESULT 1164
ABL43463
ID ABL43463 standard; DNA; 18 BP.
XX
XX ABL43463;
XX
XX 11-APR-2002 (first entry)
XX
XX Human chromosome 1p36-35 PCR primer SEQ ID NO:507.
XX
XX Human; chromosome 1p36-35; chromosome 21q22.1; genetic analysis; genome;
XX PCR primer; ss.
XX
XX Homo sapiens.
XX
XX JP2001321190-A.
XX
XX 20-NOV-2001.
XX
XX 12-MAR-2001; 2001JP-00068285.

```

```

XX 10-MAR-2000; 2000JP-00066716.
XX (RIKA ) RIKAGAKU KENKYUSHO.
XX (GENO-) GENOTEX YG.
XX
XX WPI; 2002-144136/19.
XX
XX Arraying genome clones.
XX
XX Claim 4; Page 14; 528pp; Japanese.
XX
XX The present invention describes a method of arraying genome clones. The
XX method comprises: (a) clones of the genomic libraries contained in
XX multiwell plates numbered for discrimination are mixed in each of the
XX multiwell plates; (b) a primer designed based on the chromosome marker
XX sequence is added to the mixture to carry out an amplification reaction;
XX (c) a signal corresponding to the marker is detected from the resultant
XX amplified product to specify the discrimination Nos. of the multiwell
XX plates containing the clones having said marker sequence; (d) the order
XX of the markers is changed so that the same discrimination Nos. succeed to
XX the maximum in the specified discrimination Nos. to array the multiwell
XX plates; (e) the clones in the multiwell plates of the specified
XX discrimination Nos. are mixed respectively in each wells of longitudinal
XX and lateral directions; (f) the mixed clones are cultured and the
XX resultant cultures are amplified by using the above primer; (g) signals
XX are detected from the amplified products; (h) the clones in the multiwell
XX plates are specified from the detected result; and (i) the clones are
XX reconstituted as the positions on the chromosome and arrayed. The
XX microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX PCR primers for human chromosome 1p36-35 DNA, and ABL45323 to ABL45634
XX represent PCR primers for human chromosome 21q22.1, which are
XX specifically claimed for use in the present invention
XX
XX Sequence 18 BP; 3 A; 4 C; 7 G; 4 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 14.8; DB 1; Length 18;
XX Best Local Similarity 88.9%; Pred. No. 6.8e+02;
XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 683 CACAGCCAGTGAGGGGCT 700
Db 1 CACAGCTTGAGGGGCT 18
XX
RESULT 1165
ABN89400/C
ID ABN89400 standard; DNA; 18 BP.
XX
XX AC ABN89400;
XX
XX 30-AUG-2002 (first entry)
XX
XX Rice acetolactic acid synthase PCR primer SEQ ID NO:3.
XX
XX Rice; Oryza sativa var. Kinmaze; acetolactic acid synthase; enzyme;
XX herbicide resistance; pyrimidinylcarboxy-based herbicide; plant;
XX PCR primer; ss.
XX
XX Oryza sativa.
XX
XX WO200244385-A1.
XX
XX 06-JUN-2002.
XX
XX 16-NOV-2001; 2001WO-JP010014.
XX
XX 29-NOV-2000; 2000JP-00362630.
XX
XX (TSUB ) KUMITAI CHEM IND CO LTD.
XX (NAG-) NAT INST AGROBIOLOGICAL SCI.
XX
XX Shimizu T, Nakayama I, Nagayama K, Fukuda A, Tanaka Y, Kaku K;

```

XX WPI; 2002-490301/52.
XX
PT Gene encoding acetolactate acid synthase, useful in providing new breeds
PT of plants with high resistance against pyrimidinylcarboxy-based
PT herbicides.
XX
PS Example 6; Page 32; 96pp; Japanese.
XX
CC The present invention describes acetolactate acid synthase (I) isolated
CC from *Oryza sativa* var. Kinmaze (rice). (I) has resistance against
CC pyrimidinylcarboxy (PC)-based herbicides as well as acetolactate acid
CC synthase activity. (I) can be used for providing plants with high
CC resistance against PC-based herbicides. The present sequence represents a
CC PCR primer for (I) which is used in an example from the present invention
XX
XX Sequence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
QY 1010 AAGATGTGTTGGGATG 1027
Db 18 AAGAGTGTGTTGGTATG 1
RESULT 1166
ADA27360
ID ADA27360 standard; DNA; 18 BP.
XX
AC ADA27360;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human microsatellite repeat M2_3_4.
XX
KW HLA-related research; HLA class II-associated disease;
KW transplantation matching; recombination hot spot identification;
KW linkage disequilibrium study; human; microsatellite.
XX
OS Homo sapiens.
XX
PN US2003108940-A1.
XX
PD 12-JUN-2003.
XX
PF 06-DEC-2002; 2002US-00314405.
XX
PR 15-NOV-2000; 2000US-00713616.
XX (INOK/) INOKO H.
XX
PI Inoko H, Tamiya G, Matsuzaka Y;
XX
DR WPI; 2003-616782/58.
XX
PT New oligonucleotide primer capable of specifically hybridizing to a DNA
PT having the sequence of the flanking regions of a microsatellite (e.g.
PT M249), useful for HLA-related research, e.g. transplantation matching.
XX
PS Example 2; Page 5; 20pp; English.
XX
CC The invention relates to an oligonucleotide primer capable of
CC specifically hybridizing to a DNA having the sequence of the flanking
CC regions of a microsatellite selected from M2-4-9, M2-2-9, M2-2-12, M2-3-
CC 11, M2-2-20, M2-2-21, M2-2-22, M2-2-23, M2-2-24, M2-4-26, M2-2-
CC 29, M2-2-32, M2-4-32, M2-4-33, M2-4-37, M2-2-36, M2-5-11, M2-2-
CC 46, and M2-2-48. The primer is useful for determining the number of
CC repeat units of the microsatellite cited above. The primer is useful in
CC HLA-related research, such as genetic mapping of HLA class II-associated
CC diseases, transplantation matching, population genetics, and
CC identification of recombination hot spots as well as linkage

CC disequilibrium studies. The present sequence represents the human
CC microsatellite repeat M2_3_4.
XX
SQ Sequence 18 BP; 7 A; 0 C; 11 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 863 GAAGAGGAGGAGGCG 880
Db 1 GAGGAGGAGGAGGAG 18
RESULT 1167
ADA27362/c
ID ADA27362 standard; DNA; 18 BP.
XX
AC ADA27362;
XX
DT 15-JAN-2004 (first entry)
XX
DE Rice acetolactate synthase related oligonucleotide ALS-Rsp6 SEQ ID NO:13.
XX ss; rice; acetolactate synthase; ALS; pyrimidinyl carboxy herbicide;
XX herbicide-resistance; herbicide.
XX
OS Synthetic.
XX
PN WO2003083118-A1.
XX
PD 09-OCT-2003.
XX
PF 21-FEB-2003; 2003WO-JP001917.
XX
PR 29-MAR-2002; 2002JP-00095721.
XX (TSUB) KUMIAI CHEM IND CO LTD.
XX PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.
XX
PI Kaku K, Shimizu T, Kawai K, Nagayama K, Fukuda A, Tanaka Y;
XX
DR WPI; 2003-902935/82.
XX
PT Genes of rice origin encoding pyrimidinyl carboxy herbicide resistant
PT acetolactate synthase for production of herbicide resistant strains or
PT rice and other plants.
XX
PS Example 4; SEQ ID NO 13; 96pp; Japanese.
XX
CC The invention relates to novel mutant forms of the rice acetolactate
CC synthase (ALS) gene encoding ALS resistant to pyrimidinyl carboxy
CC herbicides. Plants which may be transformed with the mutant gene include
CC rice, and also maize, barley, wheat, soya, cotton and tobacco. The mutant
CC gene may be useful in the production of herbicide-resistant plants which
CC can be cultivated in the presence of the herbicide. The present sequence
CC is used in the exemplification of the invention.
XX
XX Sequence 18 BP; 5 A; 9 C; 0 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.8; DB 1; Length 18;
Best Local Similarity 88.9%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1010 AAGATGTGTTGGGATG 1027
Db 18 AAGAGTGTGTTGGTATG 1
RESULT 1168
AAA82914
ID AAA82914 standard; DNA; 19 BP.
XX

AC AAA82914;
 XX
 DT 04-DEC-2000 (first entry)
 XX
 DE cdk4 ribozyme binding site #95.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO200032765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US028772.
 XX
 PR 04-DEC-1998; 98US-0110954P.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JW;
 XX
 XX WPI; 2000-412314/35.
 XX
 XX New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX
 PS Disclosure; Page 53; 109pp; English.
 XX
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
 XX
 Query Match 0.8%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 905 GCCAGCCTCCAGAGGATG 922
 Db 2 GGCTGCTCCAGAGGATG 19
 RESULT 1169
 AAZ57557
 ID AAZ57557 standard; DNA; 19 BP.
 AC AAZ57557;
 XX
 DT 13-APR-2000 (first entry)
 XX
 DE Mouse CD7 gene fragment detection probe construction PCR primer #2.
 XX
 KW Mouse; CD7; autoimmune disease; lipopolysaccharide induced shock; asthma;
 KW infection; tumour necrosis factor alpha; TNF-alpha; IFN-gamma;
 KW interferon gamma; septic shock; inflammation; immunosuppressant;
 KW antirheumatic; antiarthritis; antiinflammatory; vasotropic;
 KW antiasthmatic; rheumatoid arthritis; PCR primer ss.
 XX
 OS Mus sp.
 OS Synthetic.
 XX
 PN WO9964857-A1.
 XX
 PD 16-DEC-1999.
 XX

PF 10-JUN-1999; 99WO-US013210.
 XX
 PR 10-JUN-1998; 98US-0088800P.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Haynes BF, Patel DD, Lee D;
 XX
 XX WPI; 2000-116595/10.
 XX
 XX Diagnosing patients predisposed to autoimmune disease, lipopolysaccharide
 PT -induced shock or inflammatory conditions.
 XX
 XX Example 1; Page 16; 52pp; English.
 XX
 CC A method has been developed for identifying an individual predisposed to
 CC autoimmune disease, a condition mediate by tumour necrosis factor (TNF)
 CC alpha or interferon (IFN) gamma, or an inflammatory condition or
 CC infection. The method comprises detecting a mutated CD7 gene, which
 CC causes a predisposition, in a DNA-containing sample from the individual.
 CC The method is used to identify or treat a patient predisposed to or
 CC suffering from an autoimmune disease, especially rheumatoid arthritis, a
 CC condition mediated by TNF-alpha or IFN-gamma, particularly
 CC lipopolysaccharide-induced shock, an inflammatory condition or an
 CC infection, and asthma. The present sequence represents a PCR primer used
 CC in the construction of a probe for detecting a disrupted mouse CD7 gene
 CC fragment in an example from the present invention
 XX
 SQ Sequence 19 BP; 4 A; 6 C; 5 G; 4 T; 0 U; 0 Other;
 XX
 Query Match 0.8%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1576 ACCACTGACTGCTGAGTC 1593
 Db 1 AGCACTGCCCTGCTGAGTC 18
 RESULT 1170
 AAH58076
 ID AAH58076 standard; DNA; 19 BP.
 XX
 AC AAH58076;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Cell-cycle dependent kinase cdk4 ribozyme binding site SEQ ID NO:500.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulnery;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisking; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seboreic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 XX 26-OCT-2000; 2000WO-US029500.
 PF
 XX 26-OCT-1999; 99US-0161532P.
 PR
 XX (IMMU-) IMMUSOL INC.
 PA
 XX

PI Robbins JM, Tritz R;
 XX WPI; 2001-300427/31.
 XX Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.
 XX
 PS Example 1; Page 108; 408pp; English.
 CC The present invention describes a method for treating a proliferative
 CC skin or eye disease and scarring. The method involves administering a
 CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
 CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
 CC dependent kinase, growth factor or a reductase, or administering a
 CC nucleic acid molecule (II) comprising a promoter operably linked to a
 CC nucleic acid segment encoding (I). (I) can have antiproliferative,
 CC dermatological, cytostatic, antiseborrheic, antidiabetic, anticlacking,
 CC ophthalmological, vulvar, keratolytic and virucide activities, and
 CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
 CC in gene therapy. (I) and (II) are useful for treating proliferative skin
 CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
 CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
 CC also be used for treating proliferative eye diseases such as diabetic
 CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
 CC prematurity and retinal detachment, and for treating and preventing
 CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
 CC scar. AAH57577 to AAH62099 represent sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 19 BP; 3 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 905 GCCAGCTCCAGGATG 922
 Db 2 GGCTGCTCCAGGATG 19
 RESULT 1171
 ABK93655/C
 ID ABK93655 standard; DNA; 19 BP.
 AC ABK93655;
 XX 26-AUG-2002 (first entry)
 DE Human inhibitor of apoptosis, XIAP, antisense oligonucleotide #2.
 KW Human; ss; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA001379.
 XX
 PR 28-SEP-2000; 2000US-00672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX

DR WPI; 2002-479562/51.
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for enhancing
 PT apoptosis in a cell, for treating cancer and other proliferative
 PT diseases.
 XX
 PS Claim 8; Page 32; 135pp; English.
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse or
 CC human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is an IAP
 CC antisense molecule of the invention
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.8; DB 1; Length 19;
 Best Local Similarity 88.9%; Pred. No. 7e+02;
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 900 CCTGAGCCAGCCTCCAGA 917
 Db 18 CCTGAGCCAGCCTCTAGA 1
 RESULT 1172
 ADE36879
 ID ADE36879 standard; DNA; 19 BP.
 XX
 AC ADE36879;
 XX 29-JAN-2004 (first entry)
 DE Rhesus rotavirus (RRV) reverse transcription PCR primer SEQ ID NO:145.
 XX
 KW Rhesus rotavirus; RRV; rhesus:human reassortant virus; virucide;
 KW antidiarrhoeic; gene therapy; vaccine; immune response; human rotavirus;
 KW diarrhoeal gastroenteritis; reverse-transcription; PCR primer; ss.
 XX
 OS Synthetic.
 OS Rhesus rotavirus.
 XX
 PN WO2003072716-A2.
 XX
 PD 04-SEP-2003.
 XX
 PF 19-FEB-2003; 2003WO-US005172.
 XX
 PR 27-FEB-2002; 2002US-0359960P.
 XX
 PA (AMHP) WYETH.
 XX
 PI Buonagurio DA, Georgiu AF, Lerch RA, Mason BB, Murthy SC;
 PI Rappaport RS, Sidhu MS, Udem SA, Zamb TJ;
 XX
 DR WPI; 2003-712714/67.
 XX New nucleic acid molecule comprising a gene segment from a rhesus
 PT rotavirus or from one of 3 rhesus:human reassortant viruses, useful for
 PT eliciting protective immune responses to human rotaviruses.

XX Example 2; SEQ ID NO 145; 110pp; English.

XX The present invention describes an isolated nucleic acid molecule (I),

CC comprising a gene segment from a rhesus rotavirus (RRV) or from one of

CC the three rhesus human reassortant viruses. Also described: (1) a vector

CC comprising (1); (2) a recombinant host cell comprising the vector; and

CC (3) a method of producing a polypeptide encoded by (1), comprising

CC culturing the recombinant host cell under conditions suitable for

CC expression of the nucleic acid molecule. (I) has virucide and

CC antidiarrhoeic activities, and can be used in gene therapy and vaccines.

CC The nucleic acid (I), or its variant, can be used in eliciting protective

CC immune responses to human rotaviruses, which are major causes of

CC diarrhoeal gastroenteritis in infants and young children. The present

CC sequence represents a reverse transcription PCR primer which is used in

XX an example from the present invention.

XX Sequence 19 BP; 6 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

SQ

Query Match 0.8%; Score 14.8; DB 1; Length 19;

Best Local Similarity 88.9%; Pred. No. 7e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1678 GTCACCAATGCTGCTT 1695

Db 1 GTCACCAATGCTGCTAT 18

RESULT 1173

ABK32799

ID ABK32799 standard; DNA; 15 BP.

XX

AC ABK32799;

XX

DT 23-APR-2002 (first entry)

XX

DE Human APPBP1 gene, allele-specific oligonucleotide #29.

XX

KW Human; amyloid beta precursor protein binding protein 1; APPBP1; probe;

KW Alzheimer's disease; transgenic animal; platelet aggregation;

KW single nucleotide polymorphism; SNP; allele-specific oligonucleotide; ss.

XX

OS Homo sapiens.

XX

PN WO200202820-A1.

XX

PD 10-JAN-2002.

XX

PF 02-JUL-2001; 2001WO-US020951.

XX

PR 30-JUN-2000; 2000US-021551P.

XX

PA (GENA-) GENAISSANCE PHARM INC.

XX

PI Anastasio AE, Chew A, Choi JY, Kazemi A, Koshy B, Sausker EA;

PI Stephens CJ;

XX

DR WPI; 2002-164539/21.

XX

PT Amyloid beta precursor protein binding protein 159 kD (APPBP1) gene

PT polymorphic variants; useful e.g. in studying the expression and function

PT of APPBP1 and screening candidate drugs for treating Alzheimer's disease.

XX

PS Claim 17; Page 13; 104pp; English.

XX

CC The invention relates to an isolated polypeptide comprising a sequence

CC which is a polymorphic variant of a reference sequence for the amyloid

CC beta precursor protein binding protein 1, 59kD (APPBP1) protein or its

CC fragment. The polymorphic variants are useful in studying the expression

CC and function of APPBP1, in expressing APPBP1 protein for use in screening

CC for candidate drugs to treat diseases related to APPBP1 activity, in

CC studying the effect of the variation on the biological activity of

CC APPBP1, and the binding affinity of candidate drugs targeting APPBP1 for

CC the treatment of disorders such as Alzheimer's disease. The haplotyping

CC methods are useful in validating APPBP1 as a candidate target for

CC treating a specific condition or disease predicted to be associated with

CC APPBP1 activity, or in the design of clinical trials of candidate drugs

CC for treating a specific condition or disease associated with APPBP1

CC activity. The transgenic animals are useful for studying expression of

CC the APPBP1 isogenes in vivo, for in vivo screening and testing of drugs

CC targeted against APPBP1 protein, and for testing the efficacy of

CC therapeutic agents and compounds for disorders related to platelet

CC aggregation in a biological system. ABK32771-ABK32327 represent human

CC APPBP1 gene allele-specific oligonucleotides used in the method of the

XX invention

SQ Sequence 15 BP; 13 A; 1 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.8%; Score 14.6; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 6.3e+02;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAA AAAAAA 1749

Db 1 CAAAAA AAAAAA 15

RESULT 1174

AAV08586/c

ID AAV08586 standard; DNA; 16 BP.

XX

AC AAV08586;

XX

DT 15-FEB-1999 (first entry)

XX

DE Primer ACE/118PT for human ACE gene.

XX

KW PCR primer; human; ACE; angiotensin converting enzyme; angiotensinogen;

KW cardiovascular status; AGT; AT1; type 1 angiotensin II receptor; stroke;

KW polymorphic pattern; blood pressure; electrocardiographic profile;

KW cardiac condition diagnosis; myocardial infarction; atherosclerosis;

KW hypertension; cardiovascular disease; ss.

XX

OS Synthetic.

OS Homo sapiens.

XX

PN WO9845477-A2.

XX

PD 15-OCT-1998.

XX

PF 01-APR-1998; 98WO-IB000475.

XX

PR 04-APR-1997; 97US-0042930P.

XX

PA (EURO-) EURONA MEDICAL AB.

XX

PI Norberg LT, Andersson MK, Lindstroem PHR;

XX

DR WPI; 1998-568361/48.

XX

PT Assessing cardiovascular status in humans by polymorphic analysis - of

PT genes for angiotensin converting enzyme, angiotensinogen and angiotensin

PT II receptor, used to diagnose predisposition to disease and to predict

PT effect of therapy.

XX

PS Example 1; Page 27; 71pp; English.

XX

CC This sequence represents a PCR primer for the human ACE (angiotensin

CC converting enzyme) gene, and can be used in the method of the invention.

CC The method is for assessing cardiovascular status in humans by

CC determining the sequence of at least one polymorphic site in the ACE

CC (angiotensin converting enzyme), AGT (angiotensinogen) and/or AT1 (type 1

CC angiotensin II receptor) genes, and comparing the polymorphic pattern

CC with that in patients with predetermined markers of status. The method is

CC used to assess blood pressure or electrocardiographic profile, to

CC diagnose a cardiac condition such as (silent) myocardial infarction (MI),

CC hypertension, atherosclerosis or stroke. They can also be used to predict
CC response to treatments with ACE inhibitors, angiotensin II receptor
CC antagonists, diuretics, alpha- or beta-adrenergic receptor antagonists,
CC etc. It is also used to identify susceptibility to cardiovascular
CC disease. Libraries of nucleic acids containing polymorphic positions in
CC the 3 genes, and libraries of targets corresponding to the peptides from
CC the genes are used to screen for cardiovascular agents. The nucleic acids
CC contained in the library can be used as source of probes
XX
XX
SQ Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1385 AGCCAGGTCAGGAGGA 1400
Db 16 AGCCAGGTCAGGAGGA 1

RESULT 1175
AA18360/c
ID AAX18360 standard; DNA; 16 BP.
XX
AC AAX18360;
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 1.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over, indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 16 BP; 0 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1750
Db 16 CGAAAAA AAAAAAAAAA 1

RESULT 1177
AA18363/c
ID AAX18363 standard; DNA; 16 BP.
XX
AC AAX18363;
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 4.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX

RESULT 1176
AA18368/c
ID AAX18368 standard; DNA; 16 BP.
XX
AC AAX18368;
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 9.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX
PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
PR 18-JUL-1997; 97JP-00208312.
XX
PA (TAKI) TAKARA SHUZO CO LTD.
XX
DR WPI; 1999-183822/16.
XX
PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC natural number indicating the repetition of alpha; beta, delta = V or N;
CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC thymine; gamma = thymine; k = natural number of 3 or over, indicating the
CC repetition of gamma, in which thymine expressed by gamma is composed of
CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC useful as primers for RT-PCR and determination of base sequences. The new
CC sequences allow for reproductive and highly efficient analysis of gene
CC sequences
XX
SQ Sequence 16 BP; 1 A; 0 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1735 CAAAAA AAAAAAAAAA 1750
Db 16 CTA AAAAAAAAAA 1

RESULT 1177
AA18363/c
ID AAX18363 standard; DNA; 16 BP.
XX
AC AAX18363;
DT 11-MAY-1999 (first entry)
XX
DE RT-PCR primer of the invention SEQ ID 4.
XX
KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS Synthetic.
XX
PN JP11032765-A.
XX

PD 09-FEB-1999.
XX
PF 18-JUL-1997; 97JP-00208312.
XX
XX 18-JUL-1997; 97JP-00208312.
PR
XX (TAKI) TAKARA SHUZO CO LTD.
FA
XX WPI; 1999-183822/16.
DR
XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.
PT
XX
PS Disclosure; Page 10; 19pp; Japanese.
XX
XX This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproducible and highly efficient analysis of gene sequences
XX
SQ Sequence 16 BP; 0 A; 1 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1734 ACRAAAAAAAAAAAAAA 1749
Db 16 AGAAAAAAAAAAAAAAAAA 1
RESULT 1178
AA38212/c
ID AAA38212 standard; DNA; 16 BP.
XX
AC AA38212;
XX
DT 21-AUG-2000 (first entry)
XX
XX Human angiotensin-converting enzyme (ACE) PCR primer, SEQ ID NO:12.
DE
XX Angiotensin-converting enzyme gene; ACE; polymorphism;
KW polymorphic marker; cardiovascular disease; myocardial infarction;
KW unstable angina; hypertension; atherosclerosis; stroke; prognosis;
KW drug screening; treatment outcome; human; PCR primer; ss.
XX
OS Homo sapiens.
XX
XX WO200022166-A2.
PN
XX
PD 20-APR-2000.
XX
PF 13-OCT-1999; 99WO-IB001678.
XX
PR 14-OCT-1998; 98US-0104286P.
XX
PR 14-OCT-1998; 98US-0104302P.
XX
XX (EURO-) EURONA MEDICAL AB.
PA
XX Norberg LT, Andersson MK, Lindstrom PHR, Jonsson L;
PI
XX WPI; 2000-318010/27.
DR
XX
XX Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes

PT encoding specific proteins, with reference polymorphic pattern.
XX
PS Example 1; Page 48; 126pp; English.
XX
XX The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting enzyme (ACE), angiotensin II receptor type 1 (AT1) and type 2 (AT2), angiotensinogen (AGT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors 1 and 2. The method comprises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a treatment regimen comprising administration of cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) or calcium channel blockers). One or more polymorphic markers provides a basis for predicting the outcome of a treatment regimen. Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular library arrays for high throughput screening. The genes, and the proteins they encode are useful in the screening of potential cardiovascular drugs. Determination of an individual's polymorphic pattern reduces or eliminates trial and error in selecting a treatment for a particular individual cardiovascular patient. It also provides the ability to eliminate patients from clinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular treatment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be correlated with a sub-population of the test population, permitting exclusion of such sub-populations from the treatment group. Beneficial drugs can be approved for use in the appropriate population, thereby decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. Sequences AAA38201-A38239 represent PCR primers used in an exemplification of the invention to amplify short fragments of the human ACE gene (AAA38328-AAA38330) for sequence determination
XX
SQ Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1385 AGCCAGGTCAGGAGGA 1400
Db 16 AGCCAGGTCAGGAGGA 1
RESULT 1179
AAC61212/c
ID AAC61212 standard; DNA; 16 BP.
XX
XX AAC61212;
AC
XX
DT 30-JAN-2001 (first entry)
XX
XX Human ACE, AGT and AT1 genes polymorphisms PCR primer SEQ ID NO: 12.
DE
XX Human; genetic polymorphism; disease diagnosis; treatment; cancer;
KW cardiovascular system; nervous system; glaucoma; PCR primer; ss.
XX
XX Homo sapiens.
OS
XX WO200056922-A2.
PN
XX
XX 28-SEP-2000.
PD
XX
XX 23-MAR-2000; 2000WO-GB001102.
PF

```

XX 23-MAR-1999; 99US-0126046P.
PR 23-MAR-1999; 99WO-1B000497.
PR 24-MAR-1999; 99US-0126243P.
PR 23-DEC-1999; 99US-00471890.
XX (GEMI-) GEMINI GENOMICS AB.
XX Lindstrom PHR, Norberg LT, Jonsson L, Olaiisson E, Sanders R;
PI WPI; 2000-638268/61.
XX
XX Assessing disease status in individual by determining sequence(s) at one
PT or more polymorphic positions within the human genes encoding the
PT protein(s) involved in physiological pathway associated with treatment
PT regime.
XX
XX Example 1; Page 55; 14pp; English.
XX
XX The present invention is related to methods for determining the
CC polymorphic pattern of an individual and using the results to determine
CC their risk of a number of diseases, including cancer, cardiovascular
CC diseases, glaucoma and nervous system disorders such as depression and
CC neurodegenerative diseases. In addition, the methods can be used to
CC determine the effects of different types of treatment for individuals,
CC and thus enables appropriate therapies to be prescribed. The PCR primers
CC shown in sequences AAC61201-C61371 were all used to demonstrate the
CC methods of the invention
XX
XX Sequence 16 BP; 1 A; 8 C; 3 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. NO. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1385 AGCCAGGTCAGGAGGA 1400
DB 16 AGCCAGGTCAGGGGA 1
RESULT 1180
AAD44143/c
ID AAD44143 standard; DNA; 16 BP.
XX
XX AAD44143;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Oligo-dT PCR primer #3 used to illustrate the method of the invention.
DE
XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX
XX US6277571-B1.
PN
XX
XX 21-AUG-2001.
PD
XX
XX 30-SEP-1998; 98US-00163485.
PF
XX
XX 03-OCT-1997; 97US-00943162.
PR
XX 03-OCT-1997; 97US-0108152P.
PR
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
PA
XX Fillmore H, Broadus W, Gillies G;
PI
XX WPI; 2002-412824/44.
DR
XX
XX Sequential consensus region-directed amplification for sorting mixture of
PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
PT
2 samples, useful for disease diagnosis and gene analysis.
PT
XX Example; Fig 1C; 19pp; English.
PS
XX
XX The invention relates to a method of sequential consensus region-directed
CC amplification for sorting a mixture of DNAs into 2 or more subsets or
CC distinguishing gene expression patterns in 2 samples. The methods, kits
CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
CC for disease diagnosis and gene analysis. The present sequence is oligo dT
CC PCR primer used to illustrate the method of the invention
XX
XX Sequence 16 BP; 0 A; 0 C; 0 G; 15 T; 0 U; 1 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 16;
Best Local Similarity 93.8%; Pred. NO. 7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAAAAAA 1751
DB 16 AAAAAAAAAAAAAAAAAA 1
RESULT 1181
AAA25458/c
ID AAA25458 standard; DNA; 17 BP.
XX
XX AAA25458;
AC
XX
XX 19-JUL-2000 (first entry)
DT
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1956.
DE
XX
XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphorothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
OS
XX
XX WO9954459-A2.
PN
XX
XX 28-OCT-1999.
PD
XX
XX 19-APR-1999; 99WO-US008547.
PF
XX
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
PI
XX
XX WPI; 2000-013248/01.
DR
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 80; 148pp; English.
PS
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(dithio)ate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are

```


PF 09-FEB-2001; 2001WO-US004273.
XX 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
DR Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 131; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberyzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberyzyme molecule of the invention
XX
SQ Sequence 17 BP; 7 A; 0 C; 10 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 861 AGGAGAGGAGGAGGAGGA 876
Db 2 AGGAGAGGAGGAGGAGGA 17
RESULT 1184
ABN07886
ID ABN07886 standard; DNA; 17 BP.
XX
AC ABN07886;
XX
DT 29-MAY-2002 (first entry)
XX

DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7878.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
XX WO200192524-A2.
PN 06-DEC-2001.
PD 25-MAY-2001; 2001WO-US016981.
PF 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 7878; 214pp; English.
PS The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 2 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 834 CGAAGCTGCTGGGTC 849
|||||||

Db 1 GGGAGCTGCTGGGGTC 16

RESULT 1185

ABN07885

ID ABN07885 standard; DNA; 17 BP.

XX AC ABN07885;

XX DT 29-MAY-2002 (first entry)

XX DE Human GDMPL-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7877.

XX KW Human; genome-derived myosin-like protein 1; GDMPL-1; hGDMPL-1; heart;

XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;

XX KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PR 30-JAN-2001; 2001WO-US000861.

XX PR 30-JAN-2001; 2001WO-US000862.

XX PR 30-JAN-2001; 2001WO-US000863.

XX PR 30-JAN-2001; 2001WO-US000864.

XX PR 30-JAN-2001; 2001WO-US000865.

XX PR 30-JAN-2001; 2001WO-US000866.

XX PR 30-JAN-2001; 2001WO-US000867.

XX PR 30-JAN-2001; 2001WO-US000868.

XX PR 30-JAN-2001; 2001WO-US000869.

XX PR 05-FEB-2001; 2001US-0266860P.

XX PA (AEOM-) AEOMICA INC.

XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX DR WPI; 2002-179446/23.

XX PT New polypeptide, for raising antibodies that recognize hGDMPL-1 proteins,

XX PT or as specific biomolecule capture probes for surface-enhanced laser

XX PT desorption ionization, comprises human myosin-like protein hGDMPL-1.

XX PS Disclosure; SEQ ID NO 7877; 214pp; English.

XX CC The present invention describes a human genome-derived myosin-like

XX CC protein 1 (hGDMPL-1). The protein and polynucleotide sequences of hGDMPL-

XX CC 1 can be used in gene therapy and vaccine production. The hGDMPL-1

XX CC nucleic acids can be used as probes to detect, characterize and quantify

XX CC hGDMPL-1 nucleic acids in samples, as amplification substrates, to

XX CC provide initial substrates for the recombinant engineering of hGDMPL-1

XX CC protein variants having desired phenotypic improvements, and for

XX CC expressing the proteins. The hGDMPL-1 proteins or polypeptides may be

XX CC used as immunogens to raise antibodies that specifically recognise hGDMPL

XX CC -1 proteins, as standards in assays used to determine the concentration

XX CC and/or amount specifically of hGDMPL proteins, as specific biomolecule

XX CC capture probes for surface-enhanced laser desorption/ionisation, as

XX CC therapeutic supplement in patients having specific deficiency in hGDMPL-1

XX CC production, and in vaccines or for replacement therapy. The

XX CC polynucleotide sequences encoding hGDMPL-1 may be used for diagnosing a

XX CC disorder associated with the expression of hGDMPL-1, in particular heart

XX CC and skeletal muscle disorders. hGDMPL-1 is localised to chromosome 22.

XX CC The present sequence represents an oligomer used in the screening of the

XX CC hGDMPL-1 sequence in the exemplification of the present invention. N.B.

XX CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pot_sequence

XX

SQ Sequence 17 BP; 1 A; 4 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 7.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 834 GGAAGCTGCTGGGGTC 849

DB 2 GGGAGCTGCTGGGGTC 17

RESULT 1186

ABK18188

ID ABK18188 standard; RNA; 17 BP.

XX AC ABK18188;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 835.

XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

XX KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

XX KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

XX KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

XX KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

XX KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;

XX KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

XX KW Ogler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;

XX KW anberzyme.

XX OS Homo sapiens.

XX PN WO200188124-A2.

XX PD 22-NOV-2001.

XX PF 16-MAY-2001; 2001WO-US015866.

XX PR 16-MAY-2000; 2000US-00572021.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX DR WPI; 2002-082995/11.

XX PT Novel polynucleotide which down regulates expression of Ets-related gene,

XX PT useful for treating cancer, diabetic retinopathy, macular degeneration,

XX PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX PS Claim 4; Page 74; 149pp; English.

XX CC The invention relates to a nucleic acid molecule (I) which down regulates

XX CC expression of an Ets-related gene (ERG). (I) is useful for treating

XX CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

XX CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

XX CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

XX CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge

XX CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Ogler-Weber-rendu

XX CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

XX CC treating a patient having a condition associated with the level of ERG,

XX CC by contacting cells of the patient with (I) under conditions suitable for

XX CC the treatment. The method comprises the use of one or more therapies

XX CC under conditions suitable for the treatment. Leukaemia or tumour

XX CC angiogenesis is treated by administering (I) to the patient in

XX CC conjunction with one or more of other therapies such as radiation or

XX CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

XX CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 2 A; 11 C; 3 G; 0 T; 1 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;

Best Local Similarity 87.5%; Pred. No. 7.3e+02;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 268 GCATCTCAGCCGCCACC 283

DB 2 GCCCUCCAGCCGCCACC 17

RESULT 1187

ACA06469/c

ID ACA06469 standard; RNA; 17 BP.

AC ACA06469;

DT 03-JUN-2003 (first entry)

DE NFkB sub-unit modulating inozyme substrate #288.

KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

OS Homo sapiens.

XX US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

PA (MCSW/) MCSWIGGEN J.

PA (DRAP/) DRAPER K G.

PI Stinchcomb DT, Mcswiggen J, Draper KG;

DR WPI; 2003-340953/32.

XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.

PS Claim 3; Page 31; 72pp; English.

XX The invention describes an enzymatic nucleic acid molecule (I) which down

CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyne
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX

SQ Sequence 17 BP; 3 A; 10 C; 1 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 17;

Best Local Similarity 93.8%; Pred. No. 7.3e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1022 GGGATGGGGTGGGGT 1037

DB 16 GGGATGGGGTGGGGT 1

RESULT 1188

ACA06579

ID ACA06579 standard; RNA; 17 BP.

AC ACA06579;

DT 03-JUN-2003 (first entry)

DE NFkB sub-unit modulating inozyme substrate #398.

KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberyne; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

XX Homo sapiens.

OS US2002177568-A1.

XX 28-NOV-2002.

XX 23-MAY-2001; 2001US-00864785.

XX 07-DEC-1992; 92US-00987132.

XX 18-MAY-1994; 94US-00245466.

XX 15-AUG-1994; 94US-00291932.

XX 23-DEC-1996; 96US-00777916.

XX (STIN/) STINCHOMB D T.

PA (MCSW/) MCSWIGGEN J.
 XX (DRAP/) DRAPER K G.
 PI Stinchcomb DT, Mcswiggen J, Draper KG;
 XX WPI; 2003-340953/32.
 DR
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 XX Claim 3; Page 33; 72pp; English.
 XX
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or ambenzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate.
 CC acid molecules are also useful for treating inflammatory disease such as
 CC gancitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 XX Sequence 17 BP; 2 A; 7 C; 7 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 7.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 704 GCCCACCAGCGGGG 719
 Db 1 GCCCACCAGCGGCGG 16
 RESULT 1189
 ACA06578
 ID ACA06578 standard; RNA; 17 BP.
 XX
 AC ACA06578;
 XX
 XX 03-JUN-2003 (first entry)
 DT
 XX
 DE NFkB sub-unit modulating inozyme substrate #397.
 XX
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; ambenzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gancitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.

OS Homo sapiens.
 XX US2002177568-A1.
 XX
 XX 28-NOV-2002.
 PD
 XX
 XX 23-MAY-2001; 2001US-00864785.
 PF
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-0077916.
 XX
 XX (STIN/) STINCHOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI
 XX WPI; 2003-340953/32.
 DR
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 XX Claim 3; Page 33; 72pp; English.
 XX
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or ambenzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gancitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 XX Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;
 SQ
 Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 7.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 704 GCCCACCAGCGGGG 719
 Db 2 GCCCACCAGCGGCGG 17
 RESULT 1190
 ADB04268/C
 ID ADB04268 standard; DNA; 17 BP.
 XX
 AC ADB04268;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX Human MD27 scanning oligonucleotide SEQ ID 5254.
 DE
 XX

KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX Homo sapiens.
PN EP1281758-A2.
XX 05-FEB-2003.
XX 30-JUL-2002; 2002EP-00016874.
XX 02-AUG-2001; 2001US-00922181.
XX (AEOM-) AEOMICA INC.
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX New zinc finger-containing proteins and nucleic acids, useful in
XX manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27 or MD212, e.g. cancer.
XX Example 8; SEQ ID NO 5254; 103pp; English.
XX The present invention relates to novel human zinc finger-containing
XX proteins and their coding sequences; MD23, MD24, MD27, MD212. MD23 is
XX encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX or in manufacturing a medicament for treating or preventing a disorder
XX associated with decreased or increased expression or activity of MD23,
XX MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX acids and proteins are also useful for diagnosing or monitoring a disease
XX caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX acids can also be used as probes to detect and characterize gross
XX alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX useful in constructing microarrays for measuring gene expression. The
XX proteins are useful as therapeutic agents for gene therapy or as
XX vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 1 A; 1 C; 0 G; 15 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 93.8%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAA 1751
DB 17 AAAAAAAAAAAAAA 2
RESULT 1191
ABZ65136
ID ABZ65136 standard; RNA; 17 BP.
XX ABZ65136;
AC ABZ65136;
XX 21-MAR-2003 (first entry)
XX Human HER2 DNzyme substrate #593.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX

PD 05-DEC-2002.
XX 29-MAY-2002; 2002WO-US016840.
XX 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX (RIBO-) RIBOZYME PHARM INC.
XX Mcswiggen J;
XX WPI; 2003-140484/13.
XX Novel short interfering RNA and enzymatic nucleic acid useful for
XX treating cancer, modulates the expression of a nucleic acid encoding
XX HER2, K-Ras, H-Ras, and human deficiency virus sequences.
XX Claim 4; Page 144; 185pp; English.
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
XX acid molecule or an enzymatic nucleic acid molecule, that modulates
XX expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX rheumatic activity. The nucleic acid molecules are useful for reducing
XX HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX also useful for treating breast, ovarian, colorectal, lung, prostate,
XX bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
SQ Sequence 17 BP; 3 A; 7 C; 3 G; 0 T; 4 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 17;
Best Local Similarity 68.8%; Pred. No. 7.3e+02;
Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
OY 1650 TCTCCCTGACATCCAC 1665
DB 1 UCUGCCUGACAUCAC 16
RESULT 1192
ABZ62051
ID ABZ62051 standard; RNA; 17 BP.
XX ABZ62051;
AC ABZ62051;
XX 21-MAR-2003 (first entry)
XX Human H-Ras DNzyme target #842.
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX Homo sapiens.
XX WO200297114-A2.
XX 05-DEC-2002.
XX 29-MAY-2002; 2002WO-US016840.
XX 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX (RIBO-) RIBOZYME PHARM INC.
XX Mcswiggen J;
XX

XX WPI; 2003-140484/13.
 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX Claim 58; Page 129; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ6530 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 1 A; 10 C; 2 G; 0 T; 4 U; 0 Other;
 Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 68.8%; Pred. No. 7.3e+02;
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 1233 CCACCTGGCTGCTTC 1248
 Db |||||:||||:||||
 1 CCACCCUGGCCUUC 16
 RESULT 1193
 ABZ60919/c
 ID ABZ60919 standard; RNA; 17 BP.
 AC ABZ60919;
 XX 21-MAR-2003 (first entry)
 DT Human K-Ras DNzyme substrate #1031.
 DE Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
 KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
 KW anti-rheumatic; cancer; AIDS; ss.
 XX Homo sapiens.
 OS WO200297114-A2.
 PN 05-DEC-2002.
 PD 29-MAY-2002; 2002WO-US016840.
 PF 29-MAY-2001; 2001US-0294140P.
 PR 06-JUN-2001; 2001US-0296249P.
 PR 10-SEP-2001; 2001US-0318471P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA Mcswiggen J;
 XX WPI; 2003-140484/13.
 DR Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX Claim 58; Page 104; 185pp; English.
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
 XX
 SQ Sequence 17 BP; 6 A; 6 C; 3 G; 0 T; 2 U; 0 Other;
 Query Match 0.8%; Score 14.4; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 7.3e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1603 GTACCTGCTGGTCTTCT 1618
 Db |||||:||||:||||
 16 GTAACTGCTGGGTCTTCT 1
 RESULT 1194
 AAT94794
 ID AAT94794 standard; DNA; 18 BP.
 AC AAT94794;
 XX 19-FEB-1998 (first entry)
 DT Human leukocyte antigen class I gene URS10 probe 350-367.
 DE Human leukocyte antigen; HLA; probe; tissue transplantation; MHC gene;
 KW major histocompatibility complex; paternity test; forensic medicine;
 KW haematological malignancy; inherited disorder; adoptive immunotherapy;
 KW identification; ss.
 XX Synthetic.
 OS Homo sapiens.
 OS WO9720197-A2.
 PN 05-JUN-1997.
 PD 29-NOV-1996; 96WO-GB002959.
 XX 29-NOV-1995; 95GB-00024381.
 PR (NOLA-) NOLAN BONE MARROW TRUST ANTHONY.
 PA Arguello R, Avakian H, Madrigal A;
 XX WPI; 1997-310717/28.
 DR Identifying unknown allele(s) of a polyallelic gene using panel of
 XX probes each recognising a sequence motif present in some allele(s) -
 PT useful for donor matching in tissue transplantation.
 PS Claim 5; Page 19; 64pp; English.
 XX A novel method has been developed for identifying an unknown allele of a
 CC polyallelic gene. The method involves: (a) contacting the unknown allele
 CC with a panel of probes, each of which recognises a sequence motif that is
 CC present in some alleles of the polyallelic gene but not in others; (b)
 CC observing which probes recognise the unknown allele so as to obtain a
 CC fingerprint of the unknown allele; and (c) comparing the fingerprint with
 CC fingerprints of known alleles. The present sequence represents a
 CC specifically claimed probe for use in the method where the polyallelic
 CC gene is a human leukocyte antigen class I gene. The method can be used
 CC for genes such as mammalian MHC genes, specifically the HLA class I and
 CC II genes, the T cell receptor genes in mammals, TAP, LMP, ras,
 CC nonclassical HLA class I genes, human complement factor genes C4 and C2,
 CC Bf in the HLA complex, and genes located in mitochondrial DNA, bacterial

CC chromosomes and viral DNA. The method is particularly useful for matching
CC the alleles of the HLA genes in a prospective donor and a prospective
CC recipient in tissue or organ transplantations. The method can also be
CC used in paternity testing, in forensic medicine, as a follow up technique
CC in treatment of haematological malignancies or inherited disorders, in
CC adoptive immunotherapy, and in identification of bacteria and viruses.
CC The method can provide for the identification of alleles of the
CC polyallelic genes using a limited number of selected recurring motif
CC probes

XX Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 CAGCCTCCAGAGGATG 922
DB |||||||
2 CACCCTCCAGAGGATG 17

RESULT 1195
AAZ65420
ID AAZ65420 standard; DNA; 18 BP.

XX AAZ65420;
AC
DT 10-APR-2000 (first entry)

XX Human CD71 phosphorothioate antisense oligonucleotide SEQ ID NO:71.

XX Human; CD71; transferrin receptor; antisense; phosphorothioate;
KW antiproliferative; anticancer; anti-inflammatory; gene therapy; ss.
XX Homo sapiens.

OS US06004814-A.

PN 21-DEC-1999.

PD 25-SEP-1998; 98US-00161244.

XX 25-SEP-1998; 98US-00161244.

XX (ISIS-) ISIS PHARM INC.

PI Bennett CF, Cowse LM;

XX WPI; 2000-105082/09.

PT Antisense oligonucleotides targeted to genes encoding CD71, useful for
PT preventing, diagnosing and treating inflammatory disorders and tumors.

PS Claim 1; Col 28; 34pp; English.

XX Sequences AAZ65357-265440 represent novel phosphorothioate antisense
CC oligonucleotides targeted against the human CD71 gene, which encodes the
CC CD71 transferrin receptor. Upon uptake in the small intestine, iron
CC immediately combines with the ubiquitous serum protein transferrin, the
CC primary vehicle by which iron is transported around the body. The uptake
CC of circulating iron-transferrin complexes is mediated by the transferrin
CC receptor, CD71. The requirement of both iron-transferrin complexes and
CC CD71 for cell proliferation suggests that inhibition of iron utilisation
CC could represent a strategy for the treatment of cancer. The
CC oligonucleotides may be used in the treatment of an animal suspected of
CC having a disease or disorder which can be treated by inhibition of CD71
CC expression. Use of the antisense compounds and methods of the invention
CC may also be useful prophylactically to prevent or delay infection,
CC inflammation or tumour formation. The antisense compounds may
CC additionally be useful for research and as diagnostic tools. The
CC antisense oligonucleotides provide a tool for effectively downregulating
CC CD71 expression. Prior art methods utilised antibodies specific for CD71
CC proteins; however, this resulted in the development of resistant tumour

CC cells, due to the development of mutations in CD71 which altered the
CC epitope recognised by the antibodies
XX Sequence 18 BP; 0 A; 7 C; 4 G; 7 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 729 GGCTTCTGGGCCCTC 744
DB |||||||
3 GGCTTCTGGGCCCTC 18

RESULT 1196
AAC72279/C
ID AAC72279 standard; DNA; 18 BP.

XX AAC72279;

AC
DT 09-FEB-2001 (first entry)

XX Single nucleotide polymorphism PCR primer #1406.

XX Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.

XX Homo sapiens.

XX WO200058519-A2.

XX 05-OCT-2000.

XX 30-MAR-2000; 2000WO-US008440.

XX 31-MAR-1999; 99US-0127248P.

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX (AFFY-) AFFYMETRIX INC.

PI Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;

XX WPI; 2000-611722/58.

XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.

PS Claim 8; Fig 5; 214pp; English.

XX The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases

XX Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 391 ACCGAGGGGCTCCCTG 406
DB |||||||
17 ACCGAGGGGATCCCTG 2

RESULT 1197
AACT72267/c
ID AAC72267 standard; DNA; 18 BP.
XX AC AAC72267;
XX AC AAC72267;
DT 09-FEB-2001 (first entry)
XX XX
XX Single nucleotide polymorphism PCR primer #1398.
XX XX
XX Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX OS Homo sapiens.
XX WO200058519-A2.
PN 05-OCT-2000.
PD 30-MAR-2000; 2000WO-US008440.
PF 31-MAR-1999; 99US-0127248P.
PR (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX (AFFY-) AFFYMETRIX INC.
PA Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipschutz RJ, Patil N, Sklar P;
XX WPI; 2000-611722/58.
XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX Claim 8; Fig 5; 214pp; English.
XX The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX Sequence 18 BP; 3 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 391 ACGCAGGGGCTCCCTG 406
| | | | | | | | | | | | | | | | | | | | | |
DB 17 ACGCAGGGGATCCCTG 2
RESULT 1198
AAH37550/c
ID AAH37550 standard; DNA; 18 BP.
XX AC AAH37550;
XX 14-AUG-2001 (first entry)
DT SNP specific lower PCR primer SEQ ID 346.
DE Single nucleotide polymorphism; SNP; single nucleotide primer extension;
KW SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer;

KW Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia;
KW polycystic kidney disease; osteogenesis imperfecta; autoimmune disease;
KW acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis;
KW inflammation; forensic investigation; paternity analysis; PCR primer; ss.
XX OS Homo sapiens.
XX WO200129262-A2.
PN 26-APR-2001.
PD 13-OCT-2000; 2000WO-US028436.
PF 15-OCT-1999; 99US-0160096P.
XX (ORCH-) ORCHID BIOSCIENCES INC.
XX Picoult-Newburg L, Pohl M;
XX WPI; 2001-290930/30.
DR New genotyping oligonucleotide, useful for detecting the presence,
PT absence or identity of single polynucleotide polymorphism in a nucleic
PT acid sample.
XX Claim 1; Page 51; 83pp; English.
XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide
CC primer extension (SNPE) primers, and the sequences of regions flanking
CC sites of single nucleotide polymorphisms SNPs. The present invention
CC includes kits for determining the presence or absence of a SNP, using the
CC oligonucleotides of the invention. The PCR primers are used to amplify a
CC SNP flanking sequence, the SNPE primer is used as a genotyping primer.
CC The oligonucleotides are useful for genotyping a nucleic acid sample by
CC performing a single-nucleotide primer extension reaction. The
CC oligonucleotides are useful for determining the presence, absence or
CC identity of a SNP and for genotyping nucleic acid samples, for e.g. to
CC assess by association analysis the genotype of an individual or group of
CC individuals, having a pathological phenotypic trait suspected of being
CC caused by one or more SNPs. Phenotypic traits include diseases e.g.
CC agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, familial hypercholesterolaemia, polycystic kidney disease,
CC osteogenesis imperfecta and acute intermittent porphyria. Phenotypic
CC traits also include symptoms of or susceptibility to multifactorial
CC disease of which a component is or may be genetic such as autoimmune
CC diseases, including, rheumatoid arthritis, multiple sclerosis,
CC inflammation, cancer, nervous system diseases and infection by pathogenic
CC microorganism. The method is also useful in forensic investigations and
CC paternity analysis. The present sequence represents a PCR primer specific
CC for a human SNP containing DNA sequence
XX Sequence 18 BP; 3 A; 3 C; 8 G; 4 T; 0 U; 0 Other;
Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 64 TTCTGGAGTCCCAAC 79
| | | | | | | | | | | | | | | | | | | | | |
DB 18 TCTTGGAGTCCCAAC 3
RESULT 1199
AAD38936/c
ID AAD38936 standard; DNA; 18 BP.
XX AC AAD38936;
XX 23-SEP-2002 (first entry)
DT Human Her-2 antisense oligonucleotide, ISIS #27963.
DE Human; Her-2; epidermal growth factor receptor 2; infection; cancer;
KW Human; Her-2; epidermal growth factor receptor 2; infection; cancer;

KW hyperproliferative disorder; prophylaxis; inflammation; antisense;
KW tumour; gene therapy; phosphorothioate backbone; ss.
OS Homo sapiens.
OS Synthetic.

XX Key Location/Qualifiers
FH modified_base 1..18
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT modified_base 1..4
FT /tag= b
FT /mod_base= OTHER
FT modified_base 9
FT /note= "2'methoxyethyl nucleotides"
FT /tag= d
FT /mod_base= m5c
FT modified_base 13
FT /tag= e
FT /mod_base= m5c
FT modified_base 15..18
FT /tag= c
FT /mod_base= OTHER
FT /note= "2'methoxyethyl nucleotides"

XX WO200222636-A1.
XX 21-MAR-2002.
XX 12-SEP-2001; 2001WO-US028572.
XX 15-SEP-2000; 2000US-00663834.
XX (ISIS-) ISIS PHARM INC.
XX Bennett CF, Cowse LM;
XX WPI; 2002-471192/50.
XX Novel antisense oligonucleotide which modulates the expression of Human
XX Epidermal Growth Factor receptor, Her2, is useful for treating tumors
XX inflammation or to prevent infection in humans.
XX Claim 1; Page 89; 116pp; English.
XX The invention relates to antisense compounds targetted to a nucleic acid
XX molecule encoding Her2 (human Epidermal Growth Factor receptor 2) that
XX specifically hybridises with and inhibits the expression of Her2.
XX Antisense compounds of the invention are used for treating diseases or
XX conditions associated with Her2 such as hyperproliferative disorders e.g.
XX lung, breast, gastric, oesophageal, colon, bladder, salivary, neural or
XX cardiac cancer. They are also useful prophylactically e.g. to prevent or
XX delay infection, inflammation and tumour formation. The invention is also
XX used in gene therapy. The present sequence is an antisense
XX oligonucleotide targetted to human Her-2
XX Sequence 18 BP; 4 A; 2 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1650 TCTCCCTGACATCCAC 1665
DB 16 TCTCCCTGACATCCAC 1
RESULT 1200
ACA60611/c
ID ACA60611 standard; DNA; 18 BP.
XX ACA60611;
AC ACA60611;

XX 11-JUN-2003 (first entry)
DT Antisense inhibition of human cyclin D2 related oligonucleotide #48.
DE Human; cyclin D2; diagnostic; therapeutic; prophylaxis;
KW cyclin 2 inhibition; ss.
XX Homo sapiens.
XX US6492173-B1.
XX 10-DEC-2002.
XX 01-AUG-2001; 2001US-00920760.
XX 01-AUG-2001; 2001US-00920760.
XX (ISIS-) ISIS PHARM INC.
XX Cowse LM;
XX WPI; 2003-361492/34.
XX Novel antisense compound useful for treating diseases associated with
XX Cyclin D2 expression, comprises an oligonucleotide comprising up to 50
XX nucleobases in length, which inhibits expression of Cyclin D2 in cells or
XX tissues in vitro.
XX Example 15; Col 45-46; 40pp; English.
XX The invention describes a compound (I) of up to 50 nucleobases in length,
XX which inhibits the expression of Cyclin D2 (I) is useful for inhibiting
XX the expression of Cyclin D2 in cells or tissues in vitro. (I) is thus
XX useful for treating disease associated with Cyclin D2 expression. (I) is
XX useful for diagnostics, therapeutics, prophylaxis and as research
XX reagents and kits. This sequence represents human cyclin D2 inhibition
XX associated oligonucleotide
XX Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 18;
Best Local Similarity 93.8%; Pred. No. 7.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1518 GCACATCTTGCGAAG 1533
DB 17 GCACATCTTGCGAAG 2
RESULT 1201
AAV65956
ID AAV65956 standard; DNA; 19 BP.
XX AAV65956;
XX 15-DEC-1998 (first entry)
DT Downstream PCR primer recognising the 5' region of beta1-AR DNA.
DE alpha-myosin heavy chain promoter; alpha-MHC;
KW human beta1-adrenergic receptor; beta1-AR; transgene;
KW heart tissue-specific promoter; transgenic animal model;
KW heart muscle disease; heart failure; PCR primer; ss.
XX Synthetic.
XX WO9844092-A1.
XX 08-OCT-1998.
XX 02-APR-1998; 98WO-US006791.
XX

```

PR 03-APR-1997; 97US-0041966P.
XX
PA (UYTE-) UNIV TECHNOLOGY CORP.
XX
PI Port JD, Bristow MR;
XX
XX WPI; 1998-557104/47.
DR
XX Transgenic mice as models for heart disease - having incorporated in
PT their genome a heart tissue-specific promoter operatively linked to DNA
PT coding for a beta-1-adrenergic receptor.
XX
XX Example 1; Page 18; 40pp; English.
XX
XX PCR primers AAV65954-57 were used to screen for the transgene of the
CC invention. The upstream primers recognise the alpha-myosin heavy chain
CC promoter (alpha-MHC) and the downstream primers recognise 5' region of
CC the human beta1-adrenergic receptor (beta1-AR) coding region. The
CC specification describes a transgenic animal, especially a mouse, which
CC has incorporated into its genome a transgene comprising a heart tissue-
CC specific promoter operatively linked to a coding sequence comprising
CC beta1-1AR, the transgene being expressed in at least the myocardium of
CC the heart of the transgenic animal. The transgenic animal can be used as
CC a model for heart muscle disease and heart failure in a mammal. The
CC transgene can also be used for treating heart failure
XX
XX Sequence 19 BP; 2 A; 6 C; 7 G; 4 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 110 CAGAGGCTCGGGGCTT 125
Db 2 CAGCGGCTCGGGGCTT 17

RESULT 1202
AAC69249
ID AAC69249 standard; DNA; 19 BP.
XX
AC AAC69249;
XX
XX 29-JAN-2001 (first entry)
XX
XX Human ABC1 gene exon 40 5' PCR primer, SEQ ID NO:148.
XX
XX Human ABC1 cholesterol transporter; chromosome 9q31;
XX ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
XX Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
XX cardiovascular disease; coronary artery disease; coronary restenosis;
XX cerebrovascular disease; peripheral vascular disease;
XX Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
XX X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
XX prognosis; prophylaxis; drug screening; transgenic animal; PCR primer;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200055318-A2.
XX
XX 21-SEP-2000.
XX
XX 15-MAR-2000; 2000WO-IB000532.
XX
XX 15-MAR-1999; 99US-0124702P.
XX 08-JUN-1999; 99US-0138048P.
XX 17-JUN-1999; 99US-0139600P.
XX 01-SEP-1999; 99US-0151977P.
XX
XX (UYBR-) UNIV BRITISH COLUMBIA.
XX (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN;
XX
XX WPI; 2000-587528/55.
XX
XX New ABC1 polypeptide is useful for treating diseases associated with ABC1
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and
PT cancer.
XX
XX Disclosure; Fig 10; 229pp; English.
XX
XX The invention relates to the human ABC1 cholesterol transporter protein
CC (B3082) and to nucleic acid sequences (C69120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds. It
CC further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents a human ABC1 gene PCR primer which may be
CC used to amplify an exon of the human ABC1 gene
XX
XX Sequence 19 BP; 5 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14.4; DB 1; Length 19;
Best Local Similarity 93.8%; Pred. No. 7.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1184 GCTCCAGCCCATCCT 1199
Db 4 GCTACCAGCCCATCCT 19

RESULT 1203
AAZ94997/C
ID AAZ94997 standard; DNA; 19 BP.
XX
XX AAZ94997;
XX
XX 15-AUG-2000 (first entry)
XX
XX Oligonucleotide KC295/KC296 used in scTCR-scFv fusion construction.
XX T cell receptor; single chain; scTCR; TCR; single chain antibody; scFv;
XX polypeptide binding molecule; cancer; infection; tumour;
XX graft rejection; immunosuppressive; antitumour; therapy; mouse; ds.
XX
XX Mus musculus.
XX

```

FH Key Location/Qualifiers
 FT misc_feature 19
 FT /*tag= a
 FT /note= "single-stranded overhang on complementary strand
 FT of sequence 5'-CCGG-3"
 XX
 PN WO200023087-A1.
 XX
 PD 27-APR-2000.
 XX
 PF 21-OCT-1999; 99WO-US024645.
 XX
 PR 21-OCT-1998; 98US-0105164P.
 XX
 PA (SUNO-) SUNOL MOLECULAR CORP.
 XX
 PI Weidanz JA, Card K, Sherman LA, Klinman NR, Wong HC;
 XX
 DR WPI; 2000-339516/29.
 XX
 XX Single-chain polypeptide binding protein used for preventing or treating
 PT a cancer comprising human-leukocyte-associated antigen-expressing tumor
 PT cells comprises a single-chain T-cell receptor linked to a single-chain
 PT antibody.
 XX
 PS Example 5; Fig 21B-3; 130pp; English.
 XX
 CC Double-stranded oligonucleotide KC295/KC296 codes for a G4S peptide
 CC linker that was used to connect a single chain T cell receptor (scTCR)
 CC and a single chain antibody (scFv) in the construction of a single chain
 CC polypeptide binding molecule (sc-PBM) of the invention. Such sc-PBMs can
 CC be used for killing a target cell comprising a MHC or human leukocyte
 CC associated antigen (HLA) and for preventing or treating cancer in a
 CC patient in which the cancer features HLA-expressing tumour cells
 CC (claimed). Targets include tumour cells or virally infected cells. The sc
 CC -PBM can be used to selectively control T-cell mediated immune responses
 CC such as T-cell proliferation, differentiation, activation or B lymphocyte
 CC stimulation. This can be used to reduce or eliminate an immune response
 CC e.g. in patients undergoing transplant surgery
 XX
 SQ Sequence 19 BP; 4 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 527 ATGAGCCCCCGCCACC 542
 DB 19 ATGAGCCCCCGCCACC 4
 RESULT 1204
 AAA84353
 ID AAA84353 standard; DNA; 19 BP.
 AC
 AA84353;
 DT 04-DEC-2000 (first entry)
 XX
 DE Cyclin D2 ribozyme binding site #50.
 XX
 KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
 XX
 OS Mammalia.
 XX
 PN WO20002765-A2.
 XX
 PD 08-JUN-2000.
 XX
 PF 06-DEC-1999; 99WO-US028772.
 XX
 PR 04-DEC-1998; 98US-0110954P.
 XX

PA (IMMU-) IMMUSOL INC.
 XX
 PI Tritz R, Welch PJ, Barber JR, Robbins JM;
 XX
 DR WPI; 2000-412314/35.
 XX
 PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
 PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
 PT PCNA and Cyclin B1.
 XX
 PS Disclosure; Page 75; 109pp; English.
 XX
 CC The present invention relates to a hairpin or hammerhead ribozyme,
 CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
 CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
 CC Representative examples of ribozyme recognition sites are given in
 CC AA82415 to AA86787. The ribozyme of the invention is useful for
 CC inhibiting restenosis by introduction of the ribozyme into cells. The
 CC ribozyme is resistant to endonuclease activity and hence is efficient in
 CC restenosis treatment
 XX
 SQ Sequence 19 BP; 5 A; 6 C; 4 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14.4; DB 1; Length 19;
 Best Local Similarity 93.8%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1518 GCACATCTTGTCGAAG 1533
 DB 2 GCACATCTTGTCGAAG 17
 RESULT 1205
 AAH59515
 ID AAH59515 standard; DNA; 19 BP.
 AC
 AAH59515;
 DT 10-SEP-2001 (first entry)
 XX
 DE Cyclin D2 ribozyme binding site SEQ ID NO:1939.
 XX
 KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
 KW recognition site; target; ribozyme binding site; eye disease; vulneryary;
 KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
 KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
 KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
 KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
 KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
 KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
 KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
 KW sickle cell retinopathy; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200130362-A2.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-US029500.
 XX
 PR 26-OCT-1999; 99US-0161532P.
 XX
 PA (IMMU-) IMMUSOL INC.
 XX
 PI Robbins JM, Tritz R;
 XX
 DR WPI; 2001-300427/31.
 XX
 PT Treating proliferative skin or eye diseases and scarring, using ribozymes
 PT that cleave RNA encoding cytokines involved in inflammation, matrix
 PT metalloproteinases, growth factors and cell-cycle dependent kinases.

XX PS Example 1; Page 213; 408pp; English.

XX CC The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a

CC ribozyme (I) which cleaves RNA encoding a cytokine involved in

CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle

CC dependent kinase, growth factor or a reductase, or administering a

CC nucleic acid molecule (II) comprising a promoter operably linked to a

CC nucleic acid segment encoding (I). (I) can have antiproliferative,

CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,

CC ophthalmological, vulvar, keratolytic and virucide activities, and

CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used

CC in gene therapy. (I) and (II) are useful for treating proliferative skin

CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,

CC squamous or basal cell carcinoma and viral or seborrheic wart. They can

CC also be used for treating proliferative eye diseases such as diabetic

CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of

CC prematurity and retinal detachment, and for treating and preventing

CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn

CC scar. AAH57577 to AAH62099 represent sequences used in the

CC exemplification of the present invention

XX SQ Sequence 19 BP; 5 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 7.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1518 GCACATCTTGGCAAG 1533

Db 2 GCACATCTTGGCAAG 17

RESULT 1206

ABX94535

ID ABX94535 standard; DNA; 19 BP.

XX AC ABX94535;

XX DT 13-JUN-2003 (first entry)

XX DE 235/16S rRNA detecting probe SEQ ID 4.

XX KW Detection; probe; contaminant; drinking water; Legionella; coliform;

XX KW faecal streptococci; soil; sputum; biopsy; urine; food; pharmaceutical;

XX KW cosmetic; fluorescent in situ hybridisation; FISH; ss.

XX OS Legionella sp.

XX OS Legionella pneumophila.

XX FN WO2002102824-A2.

XX PD 27-DEC-2002.

XX PF 19-JUN-2002; 2002WO-EP006809.

XX PR 19-JUN-2001; 2001DE-01029411.

XX PR 11-DEC-2001; 2001DE-01060666.

XX PA (VERM-) VERMICON AG.

XX PI Beinfuhr C, Snaldr J;

XX DR WPI; 2003-167479/16.

XX CC New oligonucleotides, useful for detecting bacteria that may contaminate

PT drinking water, provide quick results for many species in parallel.

XX PS Claim 7; Page 12; 53pp; German.

XX CC This invention describes novel oligonucleotide probes used to detect

CC contaminant bacteria that may be present in drinking water. The probes

CC can detect bacteria (especially Legionella, faecal streptococci and

CC coliforms) that may contaminate drinking water in environmental samples

CC (water or soil), clinical samples (sputum, biopsies, urine etc.), in

CC bathing and drinking water and in foods, pharmaceuticals and cosmetics,

CC by in situ hybridisation. The probes combine the advantages of

CC fluorescent in situ hybridisation with those of culture methods. Only a

CC relatively short culture step is required; analysis takes 24-48 hours

CC (contrast many days for conventional methods) and all relevant bacteria

CC can be tested simultaneously. The oligonucleotides can differentiate

CC between species of the same genus and are easy to use, allowing simple

CC analysis of a large number of samples. ABX94532-ABX94578 represent the

CC oligonucleotide probes described in the invention

XX SQ Sequence 19 BP; 3 A; 11 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 19;

Best Local Similarity 93.8%; Pred. No. 7.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 753 CCACCTTTCCTCTCCCA 768

Db 1 CCACCTTTCCTCTCCCA 16

RESULT 1207

ACC82908

ID ACC82908 standard; DNA; 20 BP.

XX AC ACC82908;

XX DT 27-AUG-2003 (first entry)

XX DE Human TRIP6 antisense oligonucleotide ISIS #198780.

XX KW Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;

XX KW OPA-interacting protein-1; OIP-1; tyxin-related protein-1; prophylaxis;

XX KW inflammation; therapy; hyperproliferative disorder; infection; cancer;

XX KW chromosome 7q22; ZRP-1; phosphorothioate; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified_base 1..20

FT FT /*tag= a

FT FT /mod_base= OTHER

FT FT /note= "Phosphorothioate backbone; All cytidine residues

FT FT are 5-methylcytidines"

FT modified_base 1..5

FT FT /*tag= b

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

FT modified_base 16..20

FT FT /*tag= c

FT FT /mod_base= OTHER

FT FT /note= "2'-methoxyethyl (2'-MOE) nucleotides"

XX PN WO2003040328-A2.

XX PD 15-MAY-2003.

XX PF 05-NOV-2002; 2002WO-US035479.

XX PR 08-NOV-2001; 2001US-00008789.

XX PA (ISIS-) ISIS PHARM INC.

XX PI Bennett CF, Dobie K;

XX DR WPI; 2003-430662/40.

XX CC New antisense oligonucleotides targeted to nucleic acids encoding thyroid

PT hormone receptor interactor 6, useful for diagnosing or treating

PT hyperproliferative disorders, such as cancer.

PS Claim 3; Page 76; 111pp; English.

XX The invention relates to antisense compounds targetted to a nucleic acid
 CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
 CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
 CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
 CC Antisense compounds of the invention are useful for modulating the
 CC expression of TRIP6 and for treating diseases or conditions associated
 CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
 CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
 CC to prevent or delay infection, inflammation or tumour formation, as
 CC research reagents and kits and in distinguishing between functions of
 CC various members of a biological pathway. They are also useful in antisense
 CC therapy. The present sequence is an antisense oligo targetted to human
 CC TRIP6 DNA. This oligo is used in the exemplification of the invention
 XX

SQ Sequence 20 BP; 7 A; 9 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 14.4; DB 1; Length 20;

Best Local Similarity 93.8%; Pred. No. 8.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 462 CACCACGCTGGCCAAA 477

Db 5 CACCACACTGGCCAAA 20

RESULT 1208

AAA47676/c

ID AAA47676 standard; cDNA; 15 BP.

AC AAA47676;

DT 08-NOV-2000 (first entry)

DE Oligo d(T) primer for human DDAH1.

XX Dimethylarginine dimethylaminohydrolase; DDAH; DDAH1; DDAH2;
 KW arginine deaminase; hyperlipidemia; renal failure; hypertension;
 KW restenosis; atherosclerosis; schizophrenia; multiple sclerosis; cancer;
 KW ischemia reperfusion injury; septic shock; multi organ failure;
 KW arthritis; skin disorders; inflammatory cardiac disease; migraine;
 KW infection; ss.

OS Homo sapiens.

XX WO200044888-A2.

XX 03-AUG-2000.

PF 26-JAN-2000; 2000WO-GB000226.

XX 26-JAN-1999; 99GB-00001705.

PR 04-JUN-1999; 99GB-00013066.

XX (UNLO) UNIV COLLEGE LONDON.

XX Vallance PUT, Leiper JM, Whitley GSJ, Charles IG;

XX WPI; 2000-543392/49.

XX Novel methylarginase polypeptides and polynucleotides, used to identify
 PT modulators of them, which are used in the treatment of e.g. cancer,
 PT hypertension, and bacterial infections.

XX Example 1; Page 33; 68pp; English.

XX Nucleotides encoding methylarginase polypeptides, vectors comprising
 CC these nucleotides and the polypeptides themselves can be used in
 CC medicaments for the treatment of hyperlipidemia, renal failure,
 CC hypertension, restenosis after angioplasty, atherosclerosis,

CC complications of heart failure, schizophrenia, multiple sclerosis or
 CC cancer. Modulators of the enzyme can be used in medicaments for the
 CC treatment of ischemia-reperfusion injury of the brain or heart, cancer,
 CC lethal hypertension in severe inflammatory conditions such as septic
 CC shock or multi-organ failure, or local and systemic inflammatory
 CC disorders including arthritis, skin disorders, inflammatory cardiac
 CC disease, migraine, or microbial or bacterial infection. The sequence of
 CC human DDAH1 was obtained by data base searching. The EST's used in the
 CC process are given in GENESBQ records AAA47661-A47677

SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14.2; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 7.1e+02;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAIAAAAAAAAA 1749

Db 15 BAAAAAIAAAAAAAAA 1

RESULT 1209

AA44150

ID AA44150 standard; DNA; 15 BP.

AC AA44150;

DT 13-DEC-2002 (first entry)

DE Oligo-AT PCR primer #1 used to illustrate the method of the invention.

XX Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
 KW primer; ss.

OS Unidentified.

XX US6277571-B1.

XX 21-AUG-2001.

PF 30-SEP-1998; 98US-00163485.

PR 03-OCT-1997; 97US-00943162.

PR 03-OCT-1997; 97US-0108152P.

XX (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.

XX Fillmore H, Broadus W, Gillies G;

XX WPI; 2002-412824/44.

XX Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.

PS Example; Fig 1D; 19pp; English.

XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is oligo AT
 CC PCR primer used to illustrate the method of the invention

SQ Sequence 15 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 1 Other;

Query Match 0.8%; Score 14.2; DB 1; Length 15;

Best Local Similarity 93.3%; Pred. No. 7.1e+02;

Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAIAIAAAAAAAAA 1748

```

Db      1  AAAAAAAAAAAAAAA 15
      |:|||||
RESULT 1210
AA18387/C
ID  AA18387 standard; DNA; 16 BP.
XX
AC
XX
AC
XX
DT  11-MAY-1999 (first entry)
XX
DE  RT-PCR primer of the invention SEQ ID 28.
XX
KW  RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
OS  Synthetic.
XX
PN  JP11032765-A.
XX
PD  09-FEB-1999.
XX
PF  18-JUL-1997; 97JP-00208312.
XX
PR  18-JUL-1997; 97JP-00208312.
XX
PA  (TAKI ) TAKARA SHUZO CO LTD.
XX
WPI; 1999-183822/16.
XX
PT  Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
PS  Example 1; Page 12; 19pp; Japanese.
XX
CC  This sequence represents a primer of the invention. The invention relates
CC  to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
CC  -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
CC  a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
CC  natural number indicating the repetition of alpha; beta, delta = V or N;
CC  V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
CC  thymine; gamma = thymine; k = natural number of 3 or over indicating the
CC  repetition of gamma, in which thymine expressed by gamma is composed of
CC  1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
CC  useful as primers for RT-PCR and determination of base sequences. The new
CC  sequences allow for reproductive and highly efficient analysis of gene
CC  sequences
XX
SQ  Sequence 16 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 2 Other;

      Query Match      0.8%; Score 14.2; DB 1; Length 16;
      Best Local Similarity 93.3%; Pred. No. 7.4e+02;
      Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA
Db      15 BAAAAA
      :|||||
RESULT 1211
AA18387/C
ID  AA18387 standard; DNA; 16 BP.
XX
AC
XX
AC
XX
DT  27-JUN-2001 (first entry)
XX
DE  Human TSA7005 gene isolation related PCR primer SEQ ID NO:4.
XX
KW  Human; TSA7005; Reg; pancreatic beta cell growth; hypoglycaemic;
XX  diagnosis; PCR primer; ss.
XX
OS  Homo sapiens.

      Query Match      0.8%; Score 14.2; DB 1; Length 16;
      Best Local Similarity 93.3%; Pred. No. 7.4e+02;
      Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1735 CAAAAA
Db      15 BAAAAA
      :|||||
      1736 CAAAAA
      :|||||
      15 DAAAAA
RESULT 1212
AA18387/C
ID  AA18387 standard; DNA; 16 BP.
XX
AC  AA18387;
XX
DT  15-AUG-2001 (first entry)
XX
DE  Primer used in human LUNX cDNA isolation.
XX
KW  LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
OS  Homo sapiens.
XX
PN  JP2001078772-A.
XX
PD  27-MAR-2001.
XX
PF  07-SEP-1999; 99JP-00253186.
XX
PR  07-SEP-1999; 99JP-00253186.
XX
PA  (SAKA ) OTSUKA PHARM CO LTD.
XX
WPI; 2001-313367/33.
XX
PT  Polynucleotide encoding LUNX gene product useful for the detection of
XX  cancer especially micrometastatic cancer.
XX
PS  Example 1; Page 27; 30pp; Japanese.
XX
CC  This invention relates to the human LUNX protein and the polynucleotide
CC  sequence encoding it. The invention includes a vector containing a LUNX
CC  polynucleotide, a host cell transformed with the vector, and an antibody
CC  that binds to LUNX. The gene can be used for cancer diagnosis and
CC  diagnosis of micrometastatic cancer and for the production of the LUNX

```

```

XX      JP2001025389-A.
XX      30-JAN-2001.
XX      15-JUL-1999; 99JP-00201279.
XX      15-JUL-1999; 99JP-00201279.
XX      (SAKA ) OTSUKA PHARM CO LTD.
XX      WPI; 2001-303742/32.
XX      TSA7005 gene, encoding a polypeptide useful for the diagnosis and
XX      treatment of diseases associated with its expression.
XX      Example 1; Page 24; 25pp; Japanese.
XX      The present sequence represents a PCR primer which is used in an example
XX      from the present invention for the isolation of human TSA7005 gene. The
XX      human TSA7005 protein shares 32% homology with human and mouse Reg
XX      proteins, and 34% homology with the rat Reg protein. TSA7005 has
XX      pancreatic beta cell growth activity and hypoglycaemic activity. The
XX      TSA7005 protein can be used for the diagnosis and treatment of diseases
XX      associated with the gene and its expression product
XX
SQ  Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

      Query Match      0.8%; Score 14.2; DB 1; Length 16;
      Best Local Similarity 93.3%; Pred. No. 7.4e+02;
      Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1736 AAAAAA
Db      15 DAAAAA
      :|||||
      1736 AAAAAA
      :|||||
      15 DAAAAA
RESULT 1212
AA18387/C
ID  AA18387 standard; DNA; 16 BP.
XX
AC  AA18387;
XX
DT  15-AUG-2001 (first entry)
XX
DE  Primer used in human LUNX cDNA isolation.
XX
KW  LUNX; human; cancer; micrometastatic cancer; primer; ss.
XX
OS  Homo sapiens.
XX
PN  JP2001078772-A.
XX
PD  27-MAR-2001.
XX
PF  07-SEP-1999; 99JP-00253186.
XX
PR  07-SEP-1999; 99JP-00253186.
XX
PA  (SAKA ) OTSUKA PHARM CO LTD.
XX
WPI; 2001-313367/33.
XX
PT  Polynucleotide encoding LUNX gene product useful for the detection of
XX  cancer especially micrometastatic cancer.
XX
PS  Example 1; Page 27; 30pp; Japanese.
XX
CC  This invention relates to the human LUNX protein and the polynucleotide
CC  sequence encoding it. The invention includes a vector containing a LUNX
CC  polynucleotide, a host cell transformed with the vector, and an antibody
CC  that binds to LUNX. The gene can be used for cancer diagnosis and
CC  diagnosis of micrometastatic cancer and for the production of the LUNX

```



```

ID  AAV09227 standard; DNA; 14 BP.
XX  AC
XX  AAV09227;
XX  DT
XX  07-JUL-1998 (first entry)
XX  DE
XX  3' poly(T) primer 3.
XX  3' poly(T) primer; PCR; amplification; cytochrome P450 gene;
KW  oxidative metabolism; P450RAI; retinoic acid; RA; promoter; ss.
XX  OS
XX  Synthetic.
XX  FN
XX  WO9749832-A2.
XX  PD
XX  31-DEC-1997.
XX  PF
XX  23-JUN-1997; 97WO-CA000488.
XX  PR
XX  21-JUN-1996; 96US-00667546.
XX  PR
XX  01-OCT-1996; 96US-00724466.
XX  PA
XX  (TOOH ) UNIV QUEENS KINGSTON.
XX  FI
XX  Petkovich PM;
XX  DR
XX  WPI; 1998-077193/07.
XX  PT
XX  23-JUN-1997; 97WO-CA000488.
XX  PR
XX  21-JUN-1996; 96US-00667546.
XX  PR
XX  01-OCT-1996; 96US-00724466.
XX  PA
XX  (TOOH ) UNIV QUEENS KINGSTON.
XX  FI
XX  Petkovich PM;
XX  DR
XX  WPI; 1998-077193/07.
XX  PT
XX  Identifying DNA encoding inducible or suppressible cytochrome P450 - by
XX  screening for drugs which reduce the catabolism of retinoic acid, useful
XX  in cancer chemotherapy and the treatment of acne and psoriasis.
XX  Example 1; Page 50; 113pp; English.
XX  CC
XX  This is a 3' poly(T) PCR primer used in the amplification of the
XX  inducible cytochrome P450RAI gene which specifically metabolises a
XX  derivative of the retinoic acid (RA). The cytochrome P450 gene in general
XX  produces enzymes involved in the oxidative metabolism of endogenous and
XX  exogenous compounds. The cytochrome P450 nucleotide sequence can be used
XX  to induce or suppress the expression of its protein. P450RAI is highly
XX  induced by RA in cell lines and tissues. This allows for the development
XX  of a drug screen using promoters and nucleotide sequences to identify
XX  drugs which are useful for reducing the catabolism of RA
XX  SQ
XX  Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
XX  Query Match 0.8%; Score 14; DB 1; Length 14;
XX  Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1734 ACAAAAAAAAAA PCA 1747
XX  Db 14 ACAAAAAAAAAA 1
XX  RESULT 1216
XX  AAV12219/c
XX  ID AAV12219 standard; DNA; 14 BP.
XX  AC
XX  AAV12219;
XX  DT
XX  22-JUN-1998 (first entry)
XX  DE
XX  Poly(T) oligonucleotide used in differential display PCR.
XX  Retinoid metabolising protein; P450RAI; retinoid oxidase; retinoic acid;
KW  zebrafish; inhibitor; antisense; cancer; actinic keratosis;
KW  oral leukoplakia; head tumour; neck tumour;
KW  non-small cell lung carcinoma; basal cell carcinoma;
KW  acute promyelocytic leukaemia; skin cancer; acne; psoriasis; ichthyosis;
KW  therapy; diagnosis; screening; differential display; PCR; primer; ss.
XX  OS
XX  Synthetic.
XX  FN
XX  WO9749815-A1.
XX  PD
XX  31-DEC-1997.
XX  PF
XX  23-JUN-1997; 97WO-CA000440.
XX  PR
XX  21-JUN-1996; 96US-00667546.
XX  PR
XX  01-OCT-1996; 96US-00724466.
XX  PA
XX  (TOOH ) UNIV QUEENS KINGSTON.
XX  FI
XX  Petkovich PM, White JA, Beckett BR, Jones G;
XX  DR
XX  WPI; 1998-077178/07.
XX  PT
XX  Retinoid metabolising protein - useful to develop products to treat, e.g.
XX  cancer, actinic keratosis, oral leukoplakia, acne, psoriasis or
XX  ichthyosis.
XX  Disclosure; Page 14; 110pp; English.
XX  CC
XX  PolyT oligonucleotides (see AAV12217-28) were used in reverse
XX  transcription reactions on polyA+ RNA isolated from the fins of control
XX  or retinoic acid-treated zebrafish (Danio rerio). Several combinations of
XX  the polyT primers were used with degenerate upstream primers (see
XX  AAV12229-33) for differential display PCR. Bands demonstrating
XX  reproducible differential amplifications were found using the primers
XX  given in AAV12221 and AAV12231. This PCR product was reamplified (see
XX  AAV12234-35). A differential display product (see AAV12213) which
XX  exhibited a dependence on the presence of retinoic acid for its
XX  expression was isolated, and was used to isolate a full-length clone (see
XX  AAV12203) coding for a novel retinoid metabolising protein (see
XX  AAW44159), designated zp450RAI
XX  SQ
XX  Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
XX  Query Match 0.8%; Score 14; DB 1; Length 14;
XX  Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX  Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  Qy 1734 ACAAAAAAAAAA 1747
XX  Db 14 ACAAAAAAAAAA 1
XX  RESULT 1217
XX  AAX02698/c
XX  ID AAX02698 standard; DNA; 14 BP.
XX  AC
XX  AAX02698;
XX  DT
XX  10-MAY-1999 (first entry)
XX  DE
XX  Barley HPPD primer #4.
XX  HPPD; barley; hydroxyphenylpyruvate dioxygenase; plant; transformation;
KW  transgenic; plant cell; callus tissue, protoplast; electroporation;
KW  particle bombardment; soya; barley; wheat; oilseed rape; maize; primer;
KW  sunflower; tobacco; ss.
XX  OS
XX  Hordeum vulgare.
XX  FN
XX  DE19730066-A1.
XX  PD
XX  21-JAN-1999.
XX  PF
XX  14-JUL-1997; 97DE-01030066.
XX  PR
XX  14-JUL-1997; 97DE-01030066.
XX  PA
XX  (BADI ) BASF AG.
XX  OS

```

```

PI  Seulberger H, Lerchl J, Schmidt R, Kurpinska K, Falk J;
XX  WPI; 1999-096742/09.
XX  DNA encoding barley hydroxyphenylpyruvate dioxygenase - for producing
XX  plants with increased vitamin E content, etc.
XX  Example 1; Page 9; 26pp; German.
XX  AAX02695-X02708 are primers used in the isolation of a novel barley
XX  (Hordeum vulgare) hydroxyphenylpyruvate dioxygenase (HPPD) protein. This
XX  protein is useful for plant transformation to produce transgenic plants
XX  especially where an expression cassette is introduced into a plant cell,
XX  callus tissue, a whole plant or protoplasts by Agrobacterium tumefaciens
XX  transformation, electroporation or particle bombardment and where the
XX  plants are selected from soya, barley, wheat, oilseed rape, maize and
XX  sunflower, or where the DNA is expressed in tobacco plants, especially in
XX  leaves or seeds
XX  Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
SQ  Query Match 0.8%; Score 14; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 7.1e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1734 ACACAAAAA 1747
DB  14 ACACAAAAA 1

RESULT 1218
AAX14689/c
ID  AAX14689 standard; DNA; 14 BP.
XX
XX  AAX14689;
XX  24-MAR-1999 (first entry)
XX  Triple helix third strand of Esterase D gene nucleotides 962-975.
XX  Triplex formation; DNA detection; triple helix; identification; bacteria;
XX  oncogene; virus; ss.
XX  Synthetic.
XX  Homo sapiens.
XX  US5861244-A.
XX  19-JAN-1999.
XX  22-DEC-1993; 93US-00173489.
XX  29-OCT-1992; 92US-00968436.
XX  (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX  Hepburn AG, Wang C;
XX  WPI; 1999-130384/11.
XX  Assay of genetic sequences based on triplex formation from double
XX  stranded analyte - and hybrid of anchor and reporter sequences, with
XX  reporter released if triplex formation occurs, used e.g. to identify
XX  bacteria.
XX  Disclosure; Col 15-16; 168pp; English.
XX  The present sequence represents a polynucleotide that is able to form a
XX  triple helix with a double stranded sequence. Cytosine bases in the
XX  present can be replaced with 5-methylcytosine for increased triplex
XX  stability. The present sequence is used in the assay of the invention,
XX  where it can be part of the anchor DNA or reporter DNA sequence. The
XX  assay comprises adding a sample containing double-stranded DNA test
CC  sequences to an aqueous medium containing at least one complex of anchor
CC  DNA, attached to a solid support, and reporter DNA, where either a part
CC  of the anchor DNA or reporter DNA is designed to form a triple-strand
CC  structure with part of the test sequence. Triplex formation results in
CC  displacement of the reporter DNA which is detected as an indication of
CC  the presence of the DNA test sequence. The method is used to detect DNA
CC  sequences, particularly for identification of bacteria (by detecting
CC  genes for ribosomal RNA) in clinical samples, but also detection of
CC  oncogenes and Hepatitis B virus
XX  Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
SQ  Query Match 0.8%; Score 14; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 7.1e+02;
    Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1736 AAAAAA 1749
DB  14 AAAAAA 1

RESULT 1219
AAX14688
ID  AAX14688 standard; DNA; 14 BP.
XX
XX  AAX14688;
XX  24-MAR-1999 (first entry)
XX  Triple helix forming nucleotides 962-975 of Esterase D gene.
XX  Triple-helix forming region; Triplex formation; DNA detection;
XX  identification; bacteria; oncogene; virus; ds.
XX  Homo sapiens.
XX  US5861244-A.
XX  19-JAN-1999.
XX  22-DEC-1993; 93US-00173489.
XX  29-OCT-1992; 92US-00968436.
XX  (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX  Hepburn AG, Wang C;
XX  WPI; 1999-130384/11.
XX  Assay of genetic sequences based on triplex formation from double
XX  stranded analyte - and hybrid of anchor and reporter sequences, with
XX  reporter released if triplex formation occurs, used e.g. to identify
XX  bacteria.
XX  Disclosure; Col 15-16; 168pp; English.
XX  The present sequence represents a potential triple-helix forming region.
XX  It can be used to demonstrate the assay of the invention. The assay
XX  comprises adding a sample containing double-stranded DNA test sequences,
XX  e.g. containing the present sequence, to an aqueous medium containing at
XX  least one complex of anchor DNA, attached to a solid support, and
XX  reporter DNA, where either a part of the anchor DNA or reporter DNA is
XX  designed to form a triple-strand structure with part of the test
XX  sequence. Triplex formation results in displacement of the reporter DNA
XX  which is detected as an indication of the presence of the DNA test
XX  sequence. The method is used to detect DNA sequences, particularly for
XX  identification of bacteria (by detecting genes for ribosomal RNA) in
XX  clinical samples, but also detection of oncogenes and Hepatitis B virus
XX  Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
SQ  Query Match 0.8%; Score 14; DB 1; Length 14;

```

```
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 1220
AAX57019/C
ID AAX57019 standard; DNA; 14 BP.
XX
AC AAX57019;
XX
DT 19-JUL-1999 (first entry)
XX
DE WO9923258 oligonucleotide primer 1.
XX
KW Visual; nucleic acid detection; target; hybridisation; probe; primer;
KW agglutination; bridging molecule; ss.
XX
OS Synthetic.
XX
PN WO9923258-A1.
XX
PD 14-MAY-1999.
XX
XX 30-OCT-1998; 98WO-US023267.
XX
XX 31-OCT-1997; 97US-0063969P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Weisburg WG, Stull PD, Reshatoff MR;
XX
DR WPI; 1999-326994/27.
XX
PT Optical detection of hybridization complexes for specific target nucleic
PT acid sequences.
XX
PS Example 1; Page 40; 46pp; English.
XX
CC This invention describes a novel method for the visual detection of
CC target nucleic acid presence in a sample. A preferred target is a
CC Mycobacterium complex nucleic acid sequence. The detection method uses
CC visual detection of a change in the hybridization without aid of
CC instrumentation. Multiple copies of a target nucleic acid sequence are
CC mixed with first and second detectable probes under hybridizing
CC conditions favouring particle agglutination via a bridging molecule
CC allowing for visual detection of the target nucleic acid sequence. The
CC bridging molecule enhances or inhibits formation of a hybridization
CC complex
XX
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14

RESULT 1221
AAX19475/C
ID AAX19475 standard; DNA; 14 BP.
XX
AC AAX19475;
XX
DT 21-MAY-1999 (first entry)
XX
DE Human senescence factor p23 T12 anchor primer SEQ ID NO:17.
```

```
XX Human; senescence factor; p23; cancer; persistent inflammation;
KW proliferative disorder; degenerative disorder; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9907893-A1.
XX
PD 18-FEB-1999.
XX
XX 05-AUG-1998; 98WO-US016343.
XX
XX 08-AUG-1997; 97US-00908873.
XX
PA (UNIWI ) UNIV WASHINGTON.
XX
PI Swisselhelm K, Hostler S, Kubbies M;
XX
DR WPI; 1999-167454/14.
XX
PT Newly isolated nucleic acid molecule (designated p23) encoding a p23
PT polypeptide - useful for inducing a senescence phenotype in a cell.
XX
PS Example 1; Page 18; 44pp; English.
XX
CC The present invention describes human senescence factor p23. An
CC expression vector for p23 is useful for inducing a senescent phenotype in
CC a cell (preferably eukaryotic). This may help in regulating diseases,
CC including cancer, persistent inflammation, and various proliferative and
CC degenerative disorders. These transgenic cells are useful in gene therapy
CC for treating cancer, particularly where antisense oligonucleotides are
CC useful for blocking normal or mutant p23 expression in cancer cells or
CC other proliferating cells. Transgenic cells are also useful for producing
CC the p23 polypeptide in large quantities. The antibodies are useful for
CC raising antiserum against p23, and for identifying senescent cells in
CC culture and tissue biopsies. The p23 polynucleotides are useful for
CC modulating or altering p23 activity in a cell, and for identifying and
CC isolating the whole gene encoding p23, and variants of p23. Assays based
CC on p23 elements, which detect p23 levels and activity are useful as
CC diagnostic markers for staging tumours, determining prognosis, and/or
CC predicting therapeutic success. These elements also provide an assay for
CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The
CC isolation of the p23 polynucleotide permits the manipulation of malignant
CC growth in cancer. The present sequence represents a primer used in an
CC example from the present invention
XX
SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1734 AAAAAAAAAAAAAA 1747
Db 14 AAAAAAAAAAAAAA 1

RESULT 1222
AAG62349/C
ID AAG62349 standard; DNA; 14 BP.
XX
AC AAG62349;
XX
XX 06-NOV-2000 (first entry)
XX
DE Oligonucleotide #1 containing 3'-C-amino-5'(S)-C,3'-N-ethanothymidine.
KW Conformationally-locked oligonucleotide; antisense inhibitor;
KW bicyclic sugar nucleoside analogue; gene probe; ds.
XX
XX Synthetic.
XX
```

PH	Key	Location/Qualifiers
FT	modified_base	1
FT		/*tag= a
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"
FT	modified_base	3
FT		/*tag= b
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"
FT	modified_base	5
FT		/*tag= c
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"
FT	modified_base	7
FT		/*tag= d
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"
FT	modified_base	9
FT		/*tag= e
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"
FT	modified_base	10
FT		/*tag= f
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"
FT	modified_base	12
FT		/*tag= g
FT		/mod_base= OTHER
FT		/note= "3'-C-amino-5' (S)-C,3'-N-ethanothymidine"

US6083482-A.

04-JUL-2000.

11-MAY-1999: 99US-00309742.

11-MAY-1999; 99US-00309742.

(ICNC) ICN PHARM INC.

Wang G;

WPI; 2000-451496/39.

New conformationally restricted 3',5'-bridged nucleosides and

oligonucleotides useful as antisense therapeutics or as gene-specific diagnostics.

Example 20; Col 16; 10pp; English.

The present sequence is an oligonucleotide containing 3'-C-amino-5'-(S)-C, 3'-N-ethanothymidine, a bicyclic-sugar nucleoside. All nucleotides in the sequence were incorporated by phosphoramidite chemistry using a DNA synthesiser. Bicyclic sugar nucleosides are conformationally restricted for 3',5'-bridged nucleosides which can be used as building blocks for oligonucleotides. Oligonucleotides can be produced that have certain, desired, geometrical shapes and entropy advantages. They may have superior hybridisation to DNA and RNA, and excellent biological stability. The conformationally-modified oligonucleotides may be useful as antisense inhibitors of gene expression or as gene probes, and may therefore be used in antisense therapeutics or gene-specific diagnostics.

```
Query Match          0.84; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAA 1749
Db 14 AAAAAAAAAAAAAA 1

14 AAAAAAAAAAAAAA 1

RESULT 1223	
AAF84160/c	
ID	AAF84160 standard; DNA; 14 BP.
XX	
XX	
AC	AAF84160;
XX	
DT	08-JUN-2001 (first entry)
XX	
DE	Oligonucleotide #2.
XX	
KW	Light responsive oligonucleotide; light irradiation; gene therapy; ss.
XX	
OS	Unidentified.

PN	WO200121637-A1.
XX	
XX	
PD	29-MAR-2001.
XX	
XX	
DF	20-SEP-2000; 2000WO-JP006415.
XX	
XX	20-SEP-1999; 99JP-00304479.
PR	
XX	(KOMI/) KOMIYAMA M.
XX	
XX	Komiyama M, Asanuma H, Yoshida T;
PI	
XX	WPI; 2001-266061/27.
DR	
XX	
XX	Light-responsive oligonucleotides, useful in controlling DNA synthesis
PT	and gene expression, have structural isomerization on irradiation, and
PT	reversible change in melting temperature of the formed double or triple
PT	strands.
PT	
XX	
XX	Example 3; Page 20; 43pp; Japanese.
PS	

```
Query Match          0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1736 AAAAAAAAAAAAAA 1749
 |||||
 Db 14 AAAAAAAAAAAAAA 1

14 AAAAAAAAAAAAAA 1

RESULT 1224
AAC83821
ID AAC83821 standard; RNA; 14 BP.
XX
AC AAC83821;

XX	28-FEB-2001 (first entry)
DT	
XX	RNA oligonucleotide #1 used in a binding assay.
DE	

XX	L-ribo-configurated Locked Nucleoside Analogue; L-ribo-INA analogue; ss.
KW	
XX	Unidentified.
OS	
XX	
PN	WO200066604-A2.

PD 09-NOV-2000.
PF 04-MAY-2000; 2000WO-DK0000225.
PR 04-MAY-1999; 99DK-00000603.
PR 01-SEP-1999; 99DK-00001225.
PR 11-JAN-2000; 2000DK-00000032.
PA (EXIQ-) EXIQON AS.
PI Wengel J;
PI WPI; 2001-060972/07.
DR Oligomers comprising L-ribo-Locked Nucleic Acid (LNA) nucleosides, useful
XX for therapeutic purposes e.g. in the construction of oligonucleotides, as
XX substrates for nucleic acids polymerases and in RNA mediated catalytic
XX processes.
XX Example 11; Page 56; 79pp; English.
XX The present invention relates to an oligomer comprising L-ribo-
XX configured Locked Nucleoside Analogues (L-ribo-LNA analogues). The
XX present sequence is an RNA oligonucleotide. Binding studies of the L-ribo
XX -LNA analogues towards the present sequence were carried out, to
XX determine the thermostability of the L-ribo-LNA analogues. The analogs of
XX the present invention have a variety of uses e.g. in the preparation of
XX conjugates of the L-ribo-LNA modified oligonucleotides (oligomers)
SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
RESULT 1225
ABQ83278/C
ID ABQ83278 standard; DNA; 14 BP.
XX
AC ABQ83278;
XX
DT 18-JAN-2003 (first entry)
XX
DE EGI cdna tag related oligonucleotide SEQ ID NO:51.
XX
KW cdna tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
FN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
XX
PA (KURE) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX
DR WPI; 2002-759896/82.
XX
PT Construction of cdna tags for identifying expressed genes with specific
XX linkers and recognition sequences, applicable in gene expression

PT analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX The present invention describes a method for constructing a cdna tag for
XX identifying an expressed gene. The method comprises: (a) preparation of
XX complementary deoxyribonucleic acid; (b) producing cdna fragment by
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX linker Y ligated material; and (e) cleaving the amplification product.
XX The method can be used for the construction of cdna tags for identifying
XX expressed genes, which is applicable in gene expression analysis, disease
XX diagnosis and identifying target for gene therapy, including the
XX clarification of difference in function or morphology of cells under
XX physiological or pathological conditions. The cdna or cells for assay can
XX be specifically expressed, with reproducibility and accuracy in the
XX detection of genes. The present sequence represents an expressed gene
XX identification (EGI) cdna tag related oligonucleotide which is used in an
XX example from the present invention
SQ Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1749
Db 1 AAAAAAAAAAAAAA 14
RESULT 1226
ABQ83274/C
ID ABQ83274 standard; DNA; 14 BP.
XX
AC ABQ83274;
XX
DT 18-JAN-2003 (first entry)
XX
DE EGI cdna tag related oligonucleotide SEQ ID NO:47.
XX
KW cdna tag; identification; gene expression analysis; linker;
KW expressed gene identification; EGI; ss.
XX
OS Synthetic.
XX
FN WO200274951-A1.
XX
PD 26-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-JP002338.
XX
PR 15-MAR-2001; 2001JP-00073959.
XX
PA (KURE) KUREHA CHEM IND CO LTD.
PA (YAMA/) YAMAMOTO M.
PA (YAMA/) YAMAMOTO N.
XX
PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX
DR WPI; 2002-759896/82.
XX
PT Construction of cdna tags for identifying expressed genes with specific
XX linkers and recognition sequences, applicable in gene expression
XX analysis, disease diagnosis and identifying target for gene therapy.
XX
XX Example 1; Page 24; 59pp; Japanese.
XX The present invention describes a method for constructing a cdna tag for
XX identifying an expressed gene. The method comprises: (a) preparation of
XX complementary deoxyribonucleic acid; (b) producing cdna fragment by
XX cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX fragment ligated material; (d) amplification of the linker X-cDNA tag-

CC linker Y ligated material; and (e) cleaving the amplification product.
CC The method can be used for the construction of cDNA tags for identifying
CC expressed genes, which is applicable in gene expression analysis, disease
CC diagnosis and identifying target for gene therapy, including the
CC clarification of difference in function or morphology of cells under
CC physiological or pathological conditions. The cDNA or cells for assay can
CC be specifically expressed, with reproducibility and accuracy in the
CC detection of genes. The present sequence represents an expressed gene
CC identification (EGI) cDNA tag related oligonucleotide which is used in an
CC example from the present invention
XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAA 1747
DB 14 ACAAAAAAAAAAAAAA 1
RESULT 1227
ABQ83277/c
ID ABQ83277 standard; DNA; 14 BP.
XX AC ABQ83277;
XX DT 18-JAN-2003 (first entry)
XX DE EGI cDNA tag related oligonucleotide SEQ ID NO:50.
XX KW cDNA tag; identification; gene expression analysis; linker;
XX KX expressed gene identification; EGI; ss.
XX OS Synthetic.
XX PN WO200274951-A1.
XX PD 26-SEP-2002.
XX PF 13-MAR-2002; 2002WO-JP002338.
XX PR 15-MAR-2001; 2001JP-00073959.
XX PA (KURE) KUREHA CHEM IND CO LTD.
XX PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX DR
XX CC Construction of cDNA tags for identifying expressed genes with specific
XX PT linkers and recognition sequences, applicable in gene expression
XX PT analysis, disease diagnosis and identifying target for gene therapy.
XX PS Example 1; Page 24; 59pp; Japanese.
XX CC The present invention describes a method for constructing a cDNA tag for
XX CC identifying an expressed gene. The method comprises: (a) preparation of
XX CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX CC linker Y ligated material; and (e) cleaving the amplification product.
XX CC The method can be used for the construction of cDNA tags for identifying
XX CC expressed genes, which is applicable in gene expression analysis, disease
XX CC diagnosis and identifying target for gene therapy, including the
XX CC clarification of difference in function or morphology of cells under
XX CC physiological or pathological conditions. The cDNA or cells for assay can
XX CC be specifically expressed, with reproducibility and accuracy in the
XX CC detection of genes. The present sequence represents an expressed gene
XX CC identification (EGI) cDNA tag related oligonucleotide which is used in an

CC example from the present invention
XX SQ Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1735 CAAAAAAAAAAAAA 1748
DB 14 CAAAAAAAAAAAAA 1
RESULT 1228
ABQ83269
ID ABQ83269 standard; DNA; 14 BP.
XX AC ABQ83269;
XX DT 18-JAN-2003 (first entry)
XX DE EGI cDNA tag related oligonucleotide SEQ ID NO:42.
XX KW cDNA tag; identification; gene expression analysis; linker;
XX KX expressed gene identification; EGI; ss.
XX OS Synthetic.
XX PN WO200274951-A1.
XX PD 26-SEP-2002.
XX PF 13-MAR-2002; 2002WO-JP002338.
XX PR 15-MAR-2001; 2001JP-00073959.
XX PA (KURE) KUREHA CHEM IND CO LTD.
XX PA (YAMA/) YAMAMOTO M.
XX PA (YAMA/) YAMAMOTO N.
XX PI Yamamoto M, Yamamoto N, Hirose K, Kasai J;
XX WPI; 2002-759896/82.
XX DR
XX CC Construction of cDNA tags for identifying expressed genes with specific
XX PT linkers and recognition sequences, applicable in gene expression
XX PT analysis, disease diagnosis and identifying target for gene therapy.
XX PS Example 1; Page 24; 59pp; Japanese.
XX CC The present invention describes a method for constructing a cDNA tag for
XX CC identifying an expressed gene. The method comprises: (a) preparation of
XX CC complementary deoxyribonucleic acid; (b) producing cDNA fragment by
XX CC cleavage with II type restriction enzyme; (c) obtaining a linker X-cDNA
XX CC fragment ligated material; (d) amplification of the linker X-cDNA tag-
XX CC linker Y ligated material; and (e) cleaving the amplification product.
XX CC The method can be used for the construction of cDNA tags for identifying
XX CC expressed genes, which is applicable in gene expression analysis, disease
XX CC diagnosis and identifying target for gene therapy, including the
XX CC clarification of difference in function or morphology of cells under
XX CC physiological or pathological conditions. The cDNA or cells for assay can
XX CC be specifically expressed, with reproducibility and accuracy in the
XX CC detection of genes. The present sequence represents an expressed gene
XX CC identification (EGI) cDNA tag related oligonucleotide which is used in an
XX CC example from the present invention
XX SQ Sequence 14 BP; 14 A; 0 C; 0 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1749

```
Db      1 AAAAAAAAAAAAAA 14
RESULT 1229
AAD24489/c
ID      AAD24489 standard; DNA; 14 BP.
XX
AC
XX
DT      07-MAR-2002 (first entry)
XX
DE      Retinoid-regulated gene isolating poly(T) PCR primer #3.
XX
KW      Retinoid metabolism; retinoic acid; RA; haeme-binding motif; vitamin A;
KW      cytochrome P450; prostate cancer; drug screening; PCR primer;
KW      retinoid-regulated gene; ss.
XX
OS      Unidentified.
XX
XX      US6306624-B1.
XX
PN      23-OCT-2001.
XX
XX
PF      25-JUN-1997; 97US-00892164.
XX
PR      21-JUN-1996; 96US-00667546.
PR      01-OCT-1996; 96US-00724466.
PR      23-JUN-1997; 97WO-CA000440.
XX
XX      (TOOH ) UNIV QUEENS KINGSTON.
XX
XX      Petkovich PM, White JA, Beckett BR, Jones G;
XX
XX      WPI; 2002-033254/04.
XX
XX
XX      New DNA fragments having promoter activity, useful in retinoid
XX      metabolism, as well as in producing retinoic acid metabolizing cytochrome
XX      P450s that are useful as targets for the treatment of certain cancers.
XX
XX      Disclosure; Col 13; 75pp; English.
XX
XX      The present invention relates to retinoid (e.g., retinoic acid (RA),
XX      vitamin A) metabolising proteins and nucleic acid sequences encoding
XX      them. RA metabolising proteins contain a haeme-binding motif which is
XX      characteristic of the group of proteins known as cytochrome P450s. The
XX      sequences of the invention are useful in retinoid metabolism and in
XX      producing retinoic acid metabolising cytochrome P450s. They are
XX      particularly useful as targets for the treatment of certain cancers such
XX      as prostate cancer. The invention also relates to a method of screening
XX      drugs for their effect on activity of RA inducible proteins. The present
XX      DNA sequence is poly(T) PCR primer which is used for isolating retinoid
XX      regulating genes by differential display of mRNAs
XX
XX      Sequence 14 BP; 0 A; 0 C; 1 G; 13 T; 0 U; 0 Other;
XX
XX      Query Match      0.8%; Score 14; DB 1; Length 14;
XX      Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1734 AAAAAAAAAAAAAA 1747
XX      |||||||
XX      14 AAAAAAAAAAAAAA 1
XX
XX      RESULT 1230
XX      ABA93701/c
XX      ID      ABA93701 standard; DNA; 14 BP.
XX
XX      AC      ABA93701;
XX
XX      DT      30-APR-2002 (first entry)
XX
XX
```

```
DE      Light responsive oligonucleotide (X1)T14.
XX
XX      Light responsive; detection; single nucleotide polymorphism; SNP;
XX      irradiation; ss.
XX
XX      Synthetic.
XX
XX      JP2001346579-A.
XX
XX      18-DEC-2001.
XX
XX      02-JUN-2000; 2000JP-00165441.
XX
XX      02-JUN-2000; 2000JP-00165441.
XX
XX      (KOMI/) KOMIYAMA S.
XX      (ASAN/) ASANUMA H.
XX
XX      WPI; 2002-145181/19.
XX
XX      Detecting single nucleotide polymorphism for expressing sensitivity
XX      information of diseases and drugs, comprises using a new oligonucleotide.
XX
XX      Example 3; Page 11; 14pp; Japanese.
XX
XX      The present invention describes a method for detecting single nucleotide
XX      polymorphisms (SNPs). Also described is an oligonucleotide used in the
XX      detection of an SNP, prepared by binding an oligonucleotide having a
XX      complementary sequence or those devoid of up to several bases with 1 or
XX      more organic group(s) to be tested by light irradiation of a specific
XX      wave length to vary a double strand formation property of the
XX      oligonucleotide to be tested. The method is used for detecting SNPs. The
XX      present sequence represents a light responsive oligonucleotide which is
XX      used in an example from the present invention
XX
XX      Sequence 14 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
XX
XX      Query Match      0.8%; Score 14; DB 1; Length 14;
XX      Best Local Similarity 100.0%; Pred. No. 7.1e+02;
XX      Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1736 AAAAAAAAAAAAAA 1749
XX      |||||||
XX      14 AAAAAAAAAAAAAA 1
XX
XX      RESULT 1231
XX      AAT52238/c
XX      ID      AAT52238 standard; RNA; 15 BP.
XX
XX      AC      AAT52238;
XX
XX      DT      25-MAR-2003 (revised)
XX      DT      01-APR-1997 (first entry)
XX
XX      DE      Mouse ICAM hammerhead ribozyme target sequence (nt. position 510).
XX
XX      Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX      gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX      intercellular adhesion molecule; rel A; tumour necrosis factor;
XX      TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX      translocation; chronic myelogenous leukaemia; CML; cancer;
XX      Philadelphia chromosome; inflammation; autoimmune disease;
XX      atherosclerosis; myocardial infarction; stroke; restenosis;
XX      transplant rejection; rheumatoid arthritis; psoriasis;
XX      myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX      human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX      ss.
XX
XX      Mus musculus.
XX
XX      WO9523225-A2.
XX
```

```

PD 31-AUG-1995.
XX
PF 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 18-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozyms having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 177; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
XX nucleotide base position indicated in the DE line. Regions of the mRNA
XX that do not form secondary folding structures and that contain potential
XX hammerhead and hairpin ribozyme cleavage sites were identified by
XX computer analysis. Ribozymes directed against these mRNA sequences were
XX designed and synthesised with modifications that improve their nuclease
XX resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
XX inhibit ICAM-1 expression, making them useful for reducing transplant
XX rejection and alleviating symptoms in patients with rheumatoid arthritis,
XX asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
XX correct PI field.)
XX
XX Sequence 15 BP; 0 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
SQ
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 CCCACGGAGCAGCA 270
DB 14 CCCACGGAGCAGCA 1
RESULT 1232
AAT54816
ID AAT54816 standard; RNA; 15 BP.
XX

```

```

AC AAT54816;
XX
XX 25-MAR-2003 (revised)
DT 07-APR-1997 (first entry)
XX
DE Mouse relA hammerhead ribozyme target sequence (nt. position 129).
XX
XX Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
XX gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
XX intercellular adhesion molecule; rel A; tumour necrosis factor;
XX TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
XX translocation; chronic myelogenous leukaemia; CML; cancer;
XX Philadelphia chromosome; inflammation; autoimmune disease;
XX atherosclerosis; myocardial infarction; stroke; restenosis;
XX transplant rejection; rheumatoid arthritis; psoriasis;
XX myocardial ischaemia; Kawasaki disease; septic shock; HIV;
XX human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
XX ss.
XX
XX Mus musculus.
OS
XX
XX WO9523225-A2.
PN
XX
XX 31-AUG-1995.
PD
XX
XX 23-FEB-1995; 95WO-IB000156.
PF
XX
XX 23-FEB-1994; 94US-00201109.
PR
XX 29-MAR-1994; 94US-00218934.
PR
XX 04-APR-1994; 94US-00222795.
PR
XX 07-APR-1994; 94US-00224483.
PR
XX 15-APR-1994; 94US-00227958.
PR
XX 18-APR-1994; 94US-00228041.
PR
XX 18-MAY-1994; 94US-00245736.
PR
XX 06-JUL-1994; 94US-00271280.
PR
XX 15-AUG-1994; 94US-00291433.
PR
XX 16-AUG-1994; 94US-00291433.
PR
XX 17-AUG-1994; 94US-00292620.
PR
XX 19-AUG-1994; 94US-00293520.
PR
XX 02-SEP-1994; 94US-00300000.
PR
XX 08-SEP-1994; 94US-00303039.
PR
XX 23-SEP-1994; 94US-00311486.
PR
XX 23-SEP-1994; 94US-00311749.
PR
XX 28-SEP-1994; 94US-00314397.
PR
XX 03-OCT-1994; 94US-00316771.
PR
XX 07-OCT-1994; 94US-00319492.
PR
XX 11-OCT-1994; 94US-00321993.
PR
XX 04-NOV-1994; 94US-00334847.
PR
XX 10-NOV-1994; 94US-00337608.
PR
XX 28-NOV-1994; 94US-00345516.
PR
XX 16-DEC-1994; 94US-00357577.
PR
XX 23-DEC-1994; 94US-00363233.
PR
XX 30-JAN-1995; 95US-00380734.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
XX Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, McSwiggen JA;
XX Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
XX Tracz D, Usman N, Wincott FE, Woolf T;
XX
XX WPI; 1995-351090/45.
XX
XX Ribozyms having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
XX Claim 2; Page 225; 407pp; English.
XX
XX The present sequence represents a preferred target sequence for an
XX enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
XX nucleotide base position indicated in the DE line. The relA gene product
XX is a subunit of the transcriptional regulator NF-kappaB and is implicated
XX specifically in the induction of inflammatory responses. Regions of the

```

CC mRNA that do not form secondary folding structures and that contain
 CC potential hammerhead and hairpin ribozyme cleavage sites were identified
 CC by computer analysis. Ribozymes directed against these mRNA sequences
 CC were designed and synthesised with modifications that improve their
 CC nuclease resistance. The ribozymes are designed to cleave the target
 CC sequences and thereby inhibit relA expression, making them potentially
 CC useful for treating rheumatoid arthritis, restenosis and asthma as well
 CC as for increasing tolerance to transplanted tissues. The potential
 CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
 CC that uses are limited to local delivery, acute indications or ex vivo
 CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 15 BP; 1 A; 5 C; 5 G; 0 T; 4 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 15;
 Best Local Similarity 78.6%; Pred. No. 7.5e+02;
 Matches 11; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 727 CAGGCTTCGGCC 740
 Db 1 CAGGCUUCUGGCC 14
 RESULT 1233
 AAT52140/c
 ID AAT52140 standard; RNA; 15 BP.
 XX
 AC AAT52140;
 XX
 DT 25-MAR-2003 (revised)
 DT 25-MAR-1997 (first entry)
 XX
 DE Human ICAM hammerhead ribozyme target sequence (nt. position 2912)..
 XX
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis; HIV;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 ss.
 XX Homo sapiens.
 OS
 XX
 FN WO9523225-A2.
 XX
 PD 31-AUG-1995.
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 XX
 PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314357.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.

PR 11-OCT-1994; 94US-00321993.
 PR 04-NOV-1994; 94US-00334847.
 PR 10-NOV-1994; 94US-00337608.
 PR 28-NOV-1994; 94US-00345516.
 PR 16-DEC-1994; 94US-00357577.
 PR 23-DEC-1994; 94US-00363233.
 PR 30-JAN-1995; 95US-00380734.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Stinchcomb DT, Chowrira B, Drenzo A, Draper KG, Dudycz LW;
 PI Grimm S, Karpelesky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
 PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
 PI Tracz D, Ueman N, Wincott FE, Woolf T;
 DR WPI; 1995-351090/45.
 XX
 XX Ribozymes having modified bases and methods for producing them - for use
 PT in inhibiting disease related genes.
 XX
 XX Claim 2; Page 175; 407pp; English.
 XX
 CC The present sequence represents a preferred target sequence for an
 CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
 CC nucleotide base position indicated in the DE line. Regions of the mRNA
 CC that do not form secondary folding structures and that contain potential
 CC hammerhead and hairpin ribozyme cleavage sites were identified by
 CC computer analysis. Ribozymes directed against these mRNA sequences were
 CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)
 XX
 SQ Sequence 15 BP; 0 A; 1 C; 0 G; 0 T; 14 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1749
 Db 14 AAAAAAAAAAAAAA 1
 RESULT 1234
 AAT51820/c
 ID AAT51820 standard; RNA; 15 BP.
 XX
 AC AAT51820;
 XX
 XX 25-MAR-2003 (revised)
 DT 09-MAR-1997 (first entry)
 XX
 XX Human ICAM hammerhead ribozyme target sequence (nt. position 510)..
 DE
 KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
 KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
 KW intercellular adhesion molecule; rel A; tumour necrosis factor;
 KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
 KW translocation; chronic myelogenous leukaemia; CML; cancer;
 KW Philadelphia chromosome; inflammation; autoimmune disease;
 KW atherosclerosis; myocardial infarction; stroke; restenosis;
 KW transplant rejection; rheumatoid arthritis; psoriasis;
 KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
 KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
 ss.
 XX Homo sapiens.
 OS
 XX
 FN WO9523225-A2.
 XX
 PD 25-MAR-1995.
 XX
 XX 23-FEB-1995; 95WO-IB000156.
 XX
 PR 23-FEB-1994; 94US-00201109.
 PR 29-MAR-1994; 94US-00218934.
 PR 04-APR-1994; 94US-00222795.
 PR 07-APR-1994; 94US-00224483.
 PR 15-APR-1994; 94US-00227958.
 PR 15-APR-1994; 94US-00228041.
 PR 18-MAY-1994; 94US-00245736.
 PR 06-JUL-1994; 94US-00271280.
 PR 15-AUG-1994; 94US-00291932.
 PR 16-AUG-1994; 94US-00291433.
 PR 17-AUG-1994; 94US-00292620.
 PR 19-AUG-1994; 94US-00293520.
 PR 02-SEP-1994; 94US-00300000.
 PR 08-SEP-1994; 94US-00303039.
 PR 23-SEP-1994; 94US-00311486.
 PR 23-SEP-1994; 94US-00311749.
 PR 28-SEP-1994; 94US-00314357.
 PR 03-OCT-1994; 94US-00316771.
 PR 07-OCT-1994; 94US-00319492.

```

PD 31-AUG-1995.
XX 23-FEB-1995; 95WO-IB000156.
XX 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 07-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 10-NOV-1994; 94US-00337608.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX (RIBO-) RIBOZYME PHARM INC.
XX Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kiseich K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX Claim 2; Page 172; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA.
CC Regions of the mRNA that do not form secondary folding structures and
CC that contain potential hammerhead and hairpin ribozyme cleavage sites
CC were identified by computer analysis. Ribozymes directed against these
CC mRNA sequences were designed and synthesised with modifications that
CC improve their nuclease resistance. The ribozymes cleave the ICAM-1 target
CC sequences and thereby inhibit ICAM-1 expression, making them useful for
CC reducing transplant rejection and alleviating symptoms in patients with
CC rheumatoid arthritis, asthma and other inflammatory disorders. (Updated
CC on 25-MAR-2003 to correct PI field.)
XX Sequence 15 BP; 0 A; 4 C; 7 G; 0 T; 4 U; 0 Other;
SQ Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 257 CCCACGGAGCAGCA 270
Db 14 CCCACGGAGCAGCA 1
RESULT 1235
AAT52134/c
ID AAT52134 standard; RNA; 15 BP.
XX
AC AAT52134;

```

```

XX 25-MAR-2003 (revised)
DT 25-MAR-1997 (first entry)
XX Human ICAM hammerhead ribozyme target sequence (nt. position 2909).
DE Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX Homo sapiens.
OS WO9523225-A2.
PN 31-AUG-1995.
PD 23-FEB-1995; 95WO-IB000156.
XX 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 07-APR-1994; 94US-00222795.
PR 15-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 10-NOV-1994; 94US-00337608.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX (RIBO-) RIBOZYME PHARM INC.
PA Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kiseich K, Matulic-Adamic J, McSwiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX WPI; 1995-351090/45.
XX Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX Claim 2; Page 175; 407pp; English.
XX The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves ICAM-1 mRNA at the
CC nucleotide base position indicated in the DE line. Regions of the mRNA
CC that do not form secondary folding structures and that contain potential
CC hammerhead and hairpin ribozyme cleavage sites were identified by
CC computer analysis. Ribozymes directed against these mRNA sequences were

```

CC designed and synthesised with modifications that improve their nuclease
 CC resistance. The ribozymes cleave the ICAM-1 target sequences and thereby
 CC inhibit ICAM-1 expression, making them useful for reducing transplant
 CC rejection and alleviating symptoms in patients with rheumatoid arthritis,
 CC asthma and other inflammatory disorders. (Updated on 25-MAR-2003 to
 CC correct PI field.)

SQ Sequence 15 BP; 1 A; 0 C; 0 G; 0 T; 14 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
 Db 15 AAAAAAAAAAAAAA 2

RESULT 1236
 AAX18364/c
 ID AAX18364 standard; DNA; 15 BP.

AC AAX18364;

DT 11-MAY-1999 (first entry)

DE RT-PCR primer of the invention SEQ ID 5.

KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.

OS Synthetic.

PN JP11032765-A.

PD 09-FEB-1999.

PF 18-JUL-1997; 97JP-00208312.

PR 18-JUL-1997; 97JP-00208312.

PA (TAKI) TAKARA SHUZO CO LTD.

XX WPI; 1999-183822/16.

XX Peptides having at least two new nucleotides - useful as primers in RT-PCR.

PS Disclosure; Page 10; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with a voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences

SQ Sequence 15 BP; 0 A; 0 C; 2 G; 13 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAAAAAAAAA 1748
 Db 14 CAAAAAAAAAAAAA 1

RESULT 1237
 AAF16603

ID AAF16603 standard; DNA; 15 BP.

AC AAF16603;

DT 13-MAR-2001 (first entry)

DE Gastric acid production inhibiting oligonucleotide SEQ ID NO: 90.

KW Gastric acid disturbance; gastric reflux; gastritis; dyspepsia;

KW stomach ulcer; duodenal ulcer; Helicobacter pylori; antisense;

KW DNA-RNA hybrid; ss.

OS Homo sapiens.

PN WO200071164-A1.

PD 30-NOV-2000.

PF 24-MAY-2000; 2000WO-AU000498.

PR 24-MAY-1999; 99AU-00000510.

PA (TACH/) TACHAS G.

XX Tachas G;

XX WPI; 2001-025093/03.

XX Treating gastric acid disturbance by administering an oligonucleotide
 PT which modulates the activity of a polypeptide involved in gastric acid
 PT production or secretion.

PS Example 3; Page 148; 164pp; English.

CC The present invention provides oligonucleotides, and methods for their
 CC use, which are useful in modulating the action of proteins involved in
 CC gastric acid production. The target protein is preferably the histamine
 CC H2 receptor or one of the proteins which form part of the gastric proton
 CC pump. The sequences and methods of the invention are useful in the
 CC treatment of gastric reflux, gastritis, dyspepsia, stomach ulcers,
 CC duodenal ulcers and other gastric acid disturbances, most of which are
 CC caused by Helicobacter pylori

SQ Sequence 15 BP; 14 A; 0 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
 Db 2 AAAAAAAAAAAAAA 15

RESULT 1238
 AAF49042/c

ID AAF49042 standard; DNA; 15 BP.

AC AAF49042;

DT 30-MAR-2001 (first entry)

DE IGF-I oligonucleotide #2.

XX Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; viricide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; ptyriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhoea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;


```

XX PF 16-DEC-1993; 93US-00168920.
XX PF
XX PR 17-SEP-1992; 92US-00946976.
XX PR
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PA
XX PI Dervan PB, Beal PA;
XX PI
XX DR WPI; 2002-536030/57.
XX DR
XX XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX PT oligonucleotide which binds in parallel and antiparallel orientation,
XX PT respectively, for targeting sequences on alternate strands of DHNA to
XX PT control gene expression.
XX XX
XX PS Example 7; Fig 24A; 108pp; English.
XX PS
XX CC The present invention relates to methods and oligonucleotides for forming
XX CC a triple-helix comprising a double helical nucleic acid comprising first
XX CC and second substantially complementary strands, and an oligonucleotide
XX CC bound to a purine-rich target sequence within the double helical nucleic
XX CC acid, where the oligonucleotide binds in a parallel and antiparallel
XX CC orientation, respectively, to target sequences on alternate strands of
XX CC the double helical nucleic acid. The method has therapeutic applications,
XX CC where gene expression is controlled by selective triple-helix formation
XX CC within expression regulatory sequences of a target gene. The
XX CC oligonucleotides can be used to form triple-helices, and are useful to
XX CC detect the presence or absence of specific sequences within genomic DNA
XX CC for diagnostic and therapeutic purposes. The oligonucleotides can be
XX CC selected to specifically bind to pathogenic double-stranded DNA including
XX CC specific sequences required by pathogenic bacteria or viruses for
XX CC replication or virulence, reducing their pathogenicity. Alternatively,
XX CC the oligonucleotide can be chosen to target a unique sequence of the
XX CC pathogen which is not found in the genome of pathogen's host. The
XX CC oligonucleotides can be used in cancer treatment by way of triple-helix
XX CC suppression of specific oncogenes including those of endogenous or viral
XX CC origin. Such therapeutic oligonucleotides are capable of forming triple-
XX CC helices with such sequences in cancerous cells containing the activated
XX CC oncogene, so preferentially killing or repressing the cancer causing
XX CC cell. The present sequence represents an oligonucleotide used in the
XX CC methods of the present invention.
XX CC
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
XX
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1241
ABK98168/c
ID ABK98168 standard; DNA; 15 BP.
XX
XX AC ABK98168;
XX
XX XX 07-OCT-2002 (first entry)
XX
XX DE Triple helix forming associated oligonucleotide #38.
XX
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX KW pathogenic bacteria; virus; replication; virulence; cancer;
XX KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
XX OS Synthetic.
XX
XX FN US6403302-B1.
XX

```

```

PD 11-JUN-2002.
XX
XX PF 16-DEC-1993; 93US-00168920.
XX PF
XX PR 17-SEP-1992; 92US-00946976.
XX PR
XX PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX PA
XX PI Dervan PB, Beal PA;
XX PI
XX DR WPI; 2002-536030/57.
XX DR
XX XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX PT oligonucleotide which binds in parallel and antiparallel orientation,
XX PT respectively, for targeting sequences on alternate strands of DHNA to
XX PT control gene expression.
XX XX
XX PS Example 6; Fig 20A; 108pp; English.
XX PS
XX CC The present invention relates to methods and oligonucleotides for forming
XX CC a triple-helix comprising a double helical nucleic acid comprising first
XX CC and second substantially complementary strands, and an oligonucleotide
XX CC bound to a purine-rich target sequence within the double helical nucleic
XX CC acid, where the oligonucleotide binds in a parallel and antiparallel
XX CC orientation, respectively, to target sequences on alternate strands of
XX CC the double helical nucleic acid. The method has therapeutic applications,
XX CC where gene expression is controlled by selective triple-helix formation
XX CC within expression regulatory sequences of a target gene. The
XX CC oligonucleotides can be used to form triple-helices, and are useful to
XX CC detect the presence or absence of specific sequences within genomic DNA
XX CC for diagnostic and therapeutic purposes. The oligonucleotides can be
XX CC selected to specifically bind to pathogenic double-stranded DNA including
XX CC specific sequences required by pathogenic bacteria or viruses for
XX CC replication or virulence, reducing their pathogenicity. Alternatively,
XX CC the oligonucleotide can be chosen to target a unique sequence of the
XX CC pathogen which is not found in the genome of pathogen's host. The
XX CC oligonucleotides can be used in cancer treatment by way of triple-helix
XX CC suppression of specific oncogenes including those of endogenous or viral
XX CC origin. Such therapeutic oligonucleotides are capable of forming triple-
XX CC helices with such sequences in cancerous cells containing the activated
XX CC oncogene, so preferentially killing or repressing the cancer causing
XX CC cell. The present sequence represents an oligonucleotide used in the
XX CC methods of the present invention.
XX CC
XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
XX
Query Match 0.8%; Score 14; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 7.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1242
ABK98167/c
ID ABK98167 standard; DNA; 15 BP.
XX
XX AC ABK98167;
XX
XX XX 07-OCT-2002 (first entry)
XX
XX DE Triple helix forming associated oligonucleotide #37.
XX
XX KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX KW pathogenic bacteria; virus; replication; virulence; cancer;
XX KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
XX OS Synthetic.
XX
XX FN US6403302-B1.
XX

```

```

XX 11-JUN-2002.
XX
XX
XX 16-DEC-1993; 93US-00168920.
XX
XX 17-SEP-1992; 92US-00946976.
XX
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression.
XX
XX Example 6; Fig 20A; 108pp; English.
XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences required by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or suppressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
XX
XX Query Match 0.8%; Score 14; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 7.5e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAA 1750
XX ||||| |||||
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1243
XX ABK98186/c
XX ID ABK98186 standard; DNA; 15 BP.
XX
XX AC ABK98186;
XX
XX 07-OCT-2002 (first entry)
XX
XX Triple helix forming associated oligonucleotide #50.
XX
XX Triple-helix formation; purine-rich target sequence; double-helix DNA;
XX gene expression; regulatory sequence; pathogenic double-stranded DNA;
XX pathogenic bacteria; virus; replication; virulence; cancer;
XX oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
XX Synthetic.
XX

```

```

PN US6403302-B1.
XX
XX 11-JUN-2002.
XX
XX 16-DEC-1993; 93US-00168920.
XX
XX 17-SEP-1992; 92US-00946976.
XX
XX (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
XX Dervan PB, Beal PA;
XX
XX WPI; 2002-536030/57.
XX
XX A triple-helix comprising a double helical nucleic acid (DHNA) and an
XX oligonucleotide which binds in parallel and antiparallel orientation,
XX respectively, for targeting sequences on alternate strands of DHNA to
XX control gene expression.
XX
XX Example 7; Fig 24A; 108pp; English.
XX
XX The present invention relates to methods and oligonucleotides for forming
XX a triple-helix comprising a double helical nucleic acid comprising first
XX and second substantially complementary strands, and an oligonucleotide
XX bound to a purine-rich target sequence within the double helical nucleic
XX acid, where the oligonucleotide binds in a parallel and antiparallel
XX orientation, respectively, to target sequences on alternate strands of
XX the double helical nucleic acid. The method has therapeutic applications,
XX where gene expression is controlled by selective triple-helix formation
XX within expression regulatory sequences of a target gene. The
XX oligonucleotides can be used to form triple-helices, and are useful to
XX detect the presence or absence of specific sequences within genomic DNA
XX for diagnostic and therapeutic purposes. The oligonucleotides can be
XX selected to specifically bind to pathogenic double-stranded DNA including
XX specific sequences required by pathogenic bacteria or viruses for
XX replication or virulence, reducing their pathogenicity. Alternatively,
XX the oligonucleotide can be chosen to target a unique sequence of the
XX pathogen which is not found in the genome of pathogen's host. The
XX oligonucleotides can be used in cancer treatment by way of triple-helix
XX suppression of specific oncogenes including those of endogenous or viral
XX origin. Such therapeutic oligonucleotides are capable of forming triple-
XX helices with such sequences in cancerous cells containing the activated
XX oncogene, so preferentially killing or suppressing the cancer causing
XX cell. The present sequence represents an oligonucleotide used in the
XX methods of the present invention
XX
XX Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
XX
XX Query Match 0.8%; Score 14; DB 1; Length 15;
XX Best Local Similarity 93.3%; Pred. No. 7.5e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1736 AAAAAAAAAAAAAA 1750
XX ||||| |||||
XX Db 15 AAAAAAAAAAAAAA 1
XX
XX RESULT 1244
XX ABX79833/c
XX ID ABX79833 standard; cDNA; 15 BP.
XX
XX AC ABX79833;
XX
XX 17-APR-2003 (first entry)
XX
XX EST polymorphic DNA repeat polynucleotide #158.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
XX Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
XX Haw River syndrome; Huntington's disease; fragile-X syndrome;
XX Friedreich's ataxia; myotonic dystrophy; hyperandrogenaemia;
XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX

```

XX OS Homo sapiens.
 XX FN US6472154-B1.
 XX PD 29-OCT-2002.
 XX PF 31-DEC-1999; 99US-00475947.
 XX PR 31-DEC-1999; 99US-00475947.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Garner HR, Wren JD, Minna JD, Fondon JW;
 XX DR WPI; 2003-208818/20.
 XX PT Identifying a candidate polymorphic repeat within a coding sequence, for
 PT understanding or treating genetic disease, comprises detecting tandem
 PT repeats in a target coding sequence and scoring the repeats for
 PT polymorphic probability.
 XX XX
 XX PS Example; Col 747; 588pp; English.
 XX CC The invention discloses a method for identifying a candidate polymorphic
 CC repeat within a coding sequence (expressed sequence tag, EST), which
 CC comprises detecting tandem repeats in a target coding sequence, scoring
 CC the repeats for polymorphic probability and generating a dataset
 CC correlating the repeats with polymorphic probability to identify a
 CC candidate polymorphic repeat. The computational methods (polymorphic
 CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
 CC useful for identifying and detecting candidate polymorphic repeats in
 CC human genes, which can be used to understand, treat or eliminate genetic
 CC diseases, predispositions or adverse drug-treatment reactions. Examples
 CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
 CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
 CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
 CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
 CC the polymorphic repeats identified for a search of human ESTs
 XX XX
 XX SQ Sequence 15 BP; 0 A; 0 C; 0 G; 14 T; 0 U; 1 Other;
 Query Match 0.8%; Score 14; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1750
 Db |||||
 15 AAAAAAAAAAAAAA 1
 RESULT 1245
 AAX18362/C
 ID AAX18362 standard; DNA; 16 BP.
 XX AC AAX18362;
 XX XX
 XX DT 11-MAY-1999 (first entry)
 XX DE RT-PCR primer of the invention SEQ ID 3.
 XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX OS Synthetic.
 XX XX
 XX FN JPI1032765-A.
 XX XX
 XX PD 09-FEB-1999.
 XX PF 18-JUL-1997; 97JP-00208312.
 XX XX
 XX PR 18-JUL-1997; 97JP-00208312.

PA (TAKI) TAKARA SHUZO CO LTD.
 XX DR WPI; 1999-183822/16.
 XX PT Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX PS Disclosure; Page 10; 19pp; Japanese.
 XX CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are
 CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences
 XX XX
 XX SQ Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1749
 Db |||||
 14 AAAAAAAAAAAAAA 1
 RESULT 1246
 AAX18365/C
 ID AAX18365 standard; DNA; 16 BP.
 XX AC AAX18365;
 XX XX
 XX DT 11-MAY-1999 (first entry)
 XX DE RT-PCR primer of the invention SEQ ID 10.
 XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
 XX OS Synthetic.
 XX XX
 XX FN JPI1032765-A.
 XX XX
 XX PD 09-FEB-1999.
 XX PF 18-JUL-1997; 97JP-00208312.
 XX XX
 XX PR 18-JUL-1997; 97JP-00208312.
 XX PA (TAKI) TAKARA SHUZO CO LTD.
 XX DR WPI; 1999-183822/16.
 XX PT Peptides having at least two new nucleotides - useful as primers in RT-
 PT PCR.
 XX PS Disclosure; Page 10; 19pp; Japanese.
 XX CC This sequence represents a primer of the invention. The invention relates
 CC to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta
 CC -N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or
 CC a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n =
 CC natural number indicating the repetition of alpha; beta, delta = V or N;
 CC V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or
 CC thymine; gamma = thymine; k = natural number of 3 or over indicating the
 CC repetition of gamma, in which thymine expressed by gamma is composed of
 CC 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are

CC useful as primers for RT-PCR and determination of base sequences. The new
 CC sequences allow for reproductive and highly efficient analysis of gene
 CC sequences

XX Sequence 16 BP; 1 A; 1 C; 0 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
 Db 14 AAAAAAAAAAAAAA 1

RESULT 1247

AAZ40730
 ID AAZ40730 standard; DNA; 16 BP.

XX AAZ40730;

XX 21-FEB-2000 (first entry)

XX Primer for sequencing the heavy chain of antibody CC83.

XX VhalphatAG; anti-tumour associated sialylated glycoprotein antigen;
 KW TAG-72; variable region; heavy chain; carcinoma; detect; tumour; ss;
 KW mouse-human chimeric antibody; therapeutic agent; intraoperative therapy;
 KW primer.

XX Synthetic.

OS Mus sp.

XX US5993813-A.

XX 30-NOV-1999.

XX 24-MAR-1997; 97US-00822028.

XX 19-OCT-1988; 88US-00259943.

XX 24-OCT-1988; 88US-00261942.

XX 19-OCT-1989; 89US-00424362.

XX 31-MAR-1993; 93US-00040687.

XX (DOWC) DOW CHEM CO.

XX Mezes PS, Gourlie BB, Schlom J, Kaplan DA, Anderson WHK;

PI Rixon MW;

XX WPI; 2000-038240/03.

XX New mouse-human chimeric antibody, useful for in vivo diagnosis of
 PT cancer.

XX Example; Col 37; 120pp; English.

XX AAZ40722-240734 are primers used in the sequencing of the light chain
 CC variable region exons and heavy chain variable region exons of antibodies
 CC CC49 and CC83. The CC antibodies are directed against TAG-72, and are
 CC produced from the rearrangement of VhalphatAG (AAZ40701). The antibodies
 CC are used in the invention which relates to a new anti-tumour associated
 CC sialylated glycoprotein antigen (TAG)-72 mouse-human chimeric antibody.
 CC The variable region of the antibody has a heavy chain (VH) where VH is
 CC encoded by a DNA sequence homologous to the VhalphatAG germline gene. The
 CC invention includes a method for in vivo carcinoma targeting through the
 CC administration to an animal of an anti-TAG-72 mouse-human chimeric
 CC antibody produced by specific cell lines. The antibody or a fragment are
 CC conjugated to an imaging marker or therapeutic agent, in a
 CC pharmaceutically acceptable, nontoxic, sterile carrier. The chimeric
 CC antibody binds to TAG-72 which is found on certain human tumour cells.
 CC The tissue regions containing the tumours can be detected via the markers
 CC and/or can be treated via the therapeutic agents. The method is useful
 CC for in vivo diagnosis and treatment of cancer by administering to an

CC animal an effective amount of a composition for the in situ detection of
 CC carcinoma lesions. The method is useful for intraoperative therapy,
 CC consisting of locating the position of a tumour through the
 CC administration of the antibody, followed by excising the tumour

XX Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1396 GAGGAGACTGTGAG 1409
 Db 3 GAGGAGACTGTGAG 16

RESULT 1248

AAZ40717

ID AAZ40717 standard; DNA; 16 BP.

XX AAZ40717;

XX 21-FEB-2000 (first entry)

XX Primer for sequencing antibody CC83 heavy chain.

XX VhalphatAG; anti-tumour associated sialylated glycoprotein antigen;
 KW TAG-72; variable region; heavy chain; carcinoma; detect; tumour; ss;
 KW mouse-human chimeric antibody; therapeutic agent; intraoperative therapy;
 KW primer.

XX Synthetic.

OS Mus sp.

XX US5993813-A.

XX 30-NOV-1999.

XX 24-MAR-1997; 97US-00822028.

XX 19-OCT-1988; 88US-00259943.

XX 24-OCT-1988; 88US-00261942.

XX 19-OCT-1989; 89US-00424362.

XX 31-MAR-1993; 93US-00040687.

XX (DOWC) DOW CHEM CO.

XX Mezes PS, Gourlie BB, Schlom J, Kaplan DA, Anderson WHK;

PI Rixon MW;

XX WPI; 2000-038240/03.

XX New mouse-human chimeric antibody, useful for in vivo diagnosis of
 PT cancer.

XX Example; Col 34; 120pp; English.

XX AAZ40715-240718 are primers used to sequence the heavy chains of
 CC monoclonal antibodies directed against TAG-72, designated colon cancer
 CC (CC) antibodies. The CC antibodies are produced from the rearrangement of
 CC VhalphatAG (AAZ40701). The antibodies are used in the invention which
 CC relates to a new anti-tumour associated sialylated glycoprotein antigen
 CC (TAG)-72 mouse-human chimeric antibody. The variable region of the
 CC antibody has a heavy chain (VH) where VH is encoded by a DNA sequence
 CC homologous to the VhalphatAG germline gene. The invention includes a
 CC method for in vivo carcinoma targeting through the administration to an
 CC animal of an anti-TAG-72 mouse-human chimeric antibody produced by
 CC specific cell lines. The antibody or a fragment are conjugated to an
 CC imaging marker or therapeutic agent, in a pharmaceutically acceptable,
 CC nontoxic, sterile carrier. The chimeric antibody binds to TAG-72 which is
 CC found on certain human tumour cells. The tissue regions containing the
 CC tumours can be detected via the markers and/or can be treated via the
 CC therapeutic agents. The method is useful for in vivo diagnosis and

CC treatment of cancer by administering to an animal an effective amount of
 CC a composition for the in situ detection of carcinoma lesions. The method
 CC is useful for intraoperative therapy, consisting of locating the position
 CC of a tumour through the administration of the antibody, followed by
 CC excising the tumour

XX Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1396 GAGGAGACTGTGAG 1409
 Db 3 GAGGAGACTGTGAG 16
 |||||

RESULT 1249

AAA29709
 ID AAA29709 standard; DNA; 16 BP.

XX AAA29709;

AC AAA29709;

DT 14-AUG-2000 (first entry)

XX CC83 heavy chain oligonucleotide primer SEQ ID NO:39.

XX Chimeric antibody; VHA1phaTAG; TAG-72; human; mouse; diagnosis;

KW tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma;

KW cancer; detection; therapy; primer; ds.

XX Homo sapiens.

OS Mus sp.

XX US6051225-A.

PN 18-APR-2000.

PD 31-MAR-1993; 93US-00040687.

XX 19-OCT-1988; 88US-00259943.

PR 24-OCT-1988; 88US-00261942.

PR 19-OCT-1989; 89US-00424362.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Kaplan DA, Schlom J, Gourlie BB, Mezes PS;

PI Rixon MW;

XX WPI; 2000-349294/30.

XX Novel family of chimeric antibodies for treating cancer with high

PT affinities to a high molecular weight tumor-associated sialylated

PT glycoprotein antigen of human origin.

XX Example; Col 37; 122pp; English.

XX The present invention describes an antibody (I) produced by one of the

CC following cell lines: CH44-1 (ATCC HB9884); CH44-2 (ATCC HB9880); CH44-4

CC (ATCC HB9877); CH88-1 (ATCC HB9882); CH88-2 (ATCC HB9881); CH88-3 (ATCC

CC HB9876); CH88-4 (ATCC HB9874); and CH84-1 (ATCC HB9883); CH84-2 (ATCC

CC HB9875); and CH84-3 (ATCC HB9878); and CH84-4 (ATCC HB9875), capable of binding to

CC tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at

CC least 25% greater than B72.3. (I) can be used for treating and diagnosing

CC cancer, and for the in situ detection of carcinoma lesions and for in

CC vivo therapy. AAA29682 to AAA29744, and AAA90714 to AAA90723, represent

CC sequences used in the exemplification of the present invention

XX Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1396 GAGGAGACTGTGAG 1409
 Db 3 GAGGAGACTGTGAG 16
 |||||

RESULT 1250

AAA29696
 ID AAA29696 standard; DNA; 16 BP.

XX AAA29696;

AC AAA29696;

DT 14-AUG-2000 (first entry)

XX CC83 heavy chain oligonucleotide primer SEQ ID NO:23.

XX Chimeric antibody; VHA1phaTAG; TAG-72; human; mouse; diagnosis;

KW tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma;

KW cancer; detection; therapy; primer; ds.

XX Homo sapiens.

OS Mus sp.

XX US6051225-A.

PN 18-APR-2000.

PD 31-MAR-1993; 93US-00040687.

XX 19-OCT-1988; 88US-00259943.

PR 24-OCT-1988; 88US-00261942.

PR 19-OCT-1989; 89US-00424362.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Kaplan DA, Schlom J, Gourlie BB, Mezes PS;

PI Rixon MW;

XX WPI; 2000-349294/30.

XX Novel family of chimeric antibodies for treating cancer with high

PT affinities to a high molecular weight tumor-associated sialylated

PT glycoprotein antigen of human origin.

XX Example; Col 34; 122pp; English.

XX The present invention describes an antibody (I) produced by one of the

CC following cell lines: CH44-1 (ATCC HB9884); CH44-2 (ATCC HB9880); CH44-4

CC (ATCC HB9877); CH88-1 (ATCC HB9882); CH88-2 (ATCC HB9881); CH88-3 (ATCC

CC HB9876); CH88-4 (ATCC HB9874); and CH84-1 (ATCC HB9883); CH84-2 (ATCC

CC HB9875); and CH84-3 (ATCC HB9878); and CH84-4 (ATCC HB9875), capable of binding to

CC tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at

CC least 25% greater than B72.3. (I) can be used for treating and diagnosing

CC cancer, and for the in situ detection of carcinoma lesions and for in

CC vivo therapy. AAA29682 to AAA29744, and AAA90714 to AAA90723, represent

CC sequences used in the exemplification of the present invention

XX Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1396 GAGGAGACTGTGAG 1409
 Db 3 GAGGAGACTGTGAG 16
 |||||

RESULT 1251

AAA29696
 ID AAA29696 standard; DNA; 16 BP.

XX AAA29696;

AC AAA29696;

DT 14-AUG-2000 (first entry)

XX CC83 heavy chain oligonucleotide primer SEQ ID NO:23.

XX Chimeric antibody; VHA1phaTAG; TAG-72; human; mouse; diagnosis;

KW tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma;

KW cancer; detection; therapy; primer; ds.

XX Homo sapiens.

OS Mus sp.

XX US6051225-A.

PN 18-APR-2000.

PD 31-MAR-1993; 93US-00040687.

XX 19-OCT-1988; 88US-00259943.

PR 24-OCT-1988; 88US-00261942.

PR 19-OCT-1989; 89US-00424362.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Kaplan DA, Schlom J, Gourlie BB, Mezes PS;

PI Rixon MW;

XX WPI; 2000-349294/30.

XX Novel family of chimeric antibodies for treating cancer with high

PT affinities to a high molecular weight tumor-associated sialylated

PT glycoprotein antigen of human origin.

XX Example; Col 34; 122pp; English.

XX The present invention describes an antibody (I) produced by one of the

CC following cell lines: CH44-1 (ATCC HB9884); CH44-2 (ATCC HB9880); CH44-4

CC (ATCC HB9877); CH88-1 (ATCC HB9882); CH88-2 (ATCC HB9881); CH88-3 (ATCC

CC HB9876); CH88-4 (ATCC HB9874); and CH84-1 (ATCC HB9883); CH84-2 (ATCC

CC HB9875); and CH84-3 (ATCC HB9878); and CH84-4 (ATCC HB9875), capable of binding to

CC tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at

CC least 25% greater than B72.3. (I) can be used for treating and diagnosing

CC cancer, and for the in situ detection of carcinoma lesions and for in

CC vivo therapy. AAA29682 to AAA29744, and AAA90714 to AAA90723, represent

CC sequences used in the exemplification of the present invention

XX Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1396 GAGGAGACTGTGAG 1409
 Db 3 GAGGAGACTGTGAG 16
 |||||

RESULT 1251

AAA29696
 ID AAA29696 standard; DNA; 16 BP.

XX AAA29696;

AC AAA29696;

DT 14-AUG-2000 (first entry)

XX CC83 heavy chain oligonucleotide primer SEQ ID NO:23.

XX Chimeric antibody; VHA1phaTAG; TAG-72; human; mouse; diagnosis;

KW tumour-associated sialylated glycoprotein antigen; cytostatic; carcinoma;

KW cancer; detection; therapy; primer; ds.

XX Homo sapiens.

OS Mus sp.

XX US6051225-A.

PN 18-APR-2000.

PD 31-MAR-1993; 93US-00040687.

XX 19-OCT-1988; 88US-00259943.

PR 24-OCT-1988; 88US-00261942.

PR 19-OCT-1989; 89US-00424362.

XX (DOWC) DOW CHEM CO.

XX Anderson WHK, Kaplan DA, Schlom J, Gourlie BB, Mezes PS;

PI Rixon MW;

XX WPI; 2000-349294/30.

XX Novel family of chimeric antibodies for treating cancer with high

PT affinities to a high molecular weight tumor-associated sialylated

PT glycoprotein antigen of human origin.

XX Example; Col 34; 122pp; English.

XX The present invention describes an antibody (I) produced by one of the

CC following cell lines: CH44-1 (ATCC HB9884); CH44-2 (ATCC HB9880); CH44-4

CC (ATCC HB9877); CH88-1 (ATCC HB9882); CH88-2 (ATCC HB9881); CH88-3 (ATCC

CC HB9876); CH88-4 (ATCC HB9874); and CH84-1 (ATCC HB9883); CH84-2 (ATCC

CC HB9875); and CH84-3 (ATCC HB9878); and CH84-4 (ATCC HB9875), capable of binding to

CC tumour-associated sialylated glycoprotein (TAG)-72 with an affinity at

CC least 25% greater than B72.3. (I) can be used for treating and diagnosing

CC cancer, and for the in situ detection of carcinoma lesions and for in

CC vivo therapy. AAA29682 to AAA29744, and AAA90714 to AAA90723, represent

CC sequences used in the exemplification of the present invention

XX Sequence 16 BP; 4 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.

PS Example; Fig 1C; 19pp; English.

CC The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is oligo dt
 CC PCR primer used to illustrate the method of the invention

XX Sequence 16 BP; 0 A; 0 C; 1 G; 14 T; 0 U; 1 Other;

SQ Query Match 0.8%; Score 14; DB 1; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
 Db 16 AAAAAAAAAAAAAA 3

RESULT 1254

AA44149/C
 ID AAD44149 standard; DNA; 16 BP.

XX AAD44149;

XX 13-DEC-2002 (first entry)

XX Oligo-dT PCR primer #9 used to illustrate the method of the invention.

XX Sequential consensus region-directed amplification; gene expression;
 KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
 KW primer; ss.

XX Unidentified.

XX US6277571-B1.

XX 21-AUG-2001.

XX 30-SEP-1998; 98US-00163485.

XX 03-OCT-1997; 97US-00943162.

XX 03-OCT-1997; 97US-0108152P.

XX (UVVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.

XX Fillmore H, Broadus W, Gillies G;

XX WPI; 2002-412824/44.

XX Sequential consensus region-directed amplification for sorting mixture of
 PT DNAs into 2 or more subsets or distinguishing gene expression patterns in
 PT 2 samples, useful for disease diagnosis and gene analysis.

XX Example; Fig 1C; 19pp; English.

XX The invention relates to a method of sequential consensus region-directed
 CC amplification for sorting a mixture of DNAs into 2 or more subsets or
 CC distinguishing gene expression patterns in 2 samples. The methods, kits
 CC and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
 CC more subsets or distinguishing gene expression patterns in 2 samples e.g.
 CC for disease diagnosis and gene analysis. The present sequence is oligo dt
 CC PCR primer used to illustrate the method of the invention

XX Sequence 16 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.8e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAA 1749
 Db 16 AAAAAAAAAAAAAA 3

RESULT 1255

AA69798/C
 ID AAX69798 standard; RNA; 17 BP.

XX AAX69798;

XX 28-JUL-1999 (first entry)

XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1093.

XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage; ocular disease;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.

XX Homo sapiens.

XX WO9715662-A2.

XX 01-MAY-1997.

XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.

XX 11-JAN-1996; 96US-00584040.

XX (RIBO-) RIBOZYME PHARM INC.

XX (CHIR) CHIRON CORP.

XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;

XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.

XX Claim 4; Page 79; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention

XX Sequence 17 BP; 1 A; 1 C; 0 G; 0 T; 15 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1749
 Db 17 AAAAAAAAAAAAAA 4

RESULT 1256

AA69803/C
 ID AAX69803 standard; RNA; 17 BP.

XX

AC AAX69803;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1098.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 XX 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, McSwiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 DR
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 79; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 1 A; 2 C; 0 G; 0 T; 14 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1749
 Db 14 AAAAAAAAAAAAAA 1
 RESULT 1257
 ID AAA18514/c
 ID AAA18514 standard; RNA; 17 BP.
 XX
 AC AAA18514;
 XX
 DT 19-JUN-2000 (first entry)
 XX
 DE Human TIE-2 substrate sequence SEQ ID NO:1740.
 XX
 KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;

KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberosus sclerosus; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 24-MAR-1999; 99WO-US006507.
 PR 27-MAR-1998; 98US-0079678P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Pavco PA, Roberts E, Jarvis T, Coeshott C, McSwiggen JA;
 XX WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 PS Claim 56; Page 100; 305pp; English.
 XX
 CC The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberosus sclerosus, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 2 A; 8 C; 2 G; 0 T; 5 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 768 AGGCGAGGTGAAG 781
 Db 14 AGGCGAGGTGAAG 1
 RESULT 1258
 ID AAA25447/c
 ID AAA25447 standard; DNA; 17 BP.
 XX
 AC AAA25447;
 XX
 DT 19-JUL-2000 (first entry)
 XX
 DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1945.
 XX

KW Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
KW gene expression modification; cancer; phosphothioate; endonuclease;
KW anticancer; breast cancer; endometrium cancer; ss.
XX
OS Homo sapiens.
XX WO9954459-A2.
FN
XX 28-OCT-1999.
PD
XX 19-APR-1999; 99WO-US008547.
PF
XX 20-APR-1998; 98US-0082404P.
PR
XX 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
DR MPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
PT used to treat cancer.
PT
XX
XX Claim 77; Page 79; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
CC with a target sequence and contain at least one phosphoro(dithioate
CC link, having endonuclease activity. (A), and more generally any catalytic
CC nucleic acid (A') that modulates expression of the oestrogen receptor
CC gene, are used to treat cancer (particularly of breast or endometrium),
CC in vivo or by transforming cells ex vivo and implanting treated cells, or
CC for other conditions associated with levels of oestrogen receptor.
CC Because of the high selectivity for targeted RNA, (A) can also be used to
CC correlate inhibition of gene expression with alterations in phenotype,
CC particularly for identification of therapeutic targets, and as research
CC reagents (for RNA, in the same way that restriction endonucleases are
CC used with DNA). The combination of modifications in (A) improves
CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
CC AAA24748 to AAA25992 represent their corresponding target sequences.
CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
CC sequences, and AAA26107 to AAA26218 represent their corresponding target
CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
CC antisense oligonucleotides used in the exemplification of the present
CC invention
XX
XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1736 AAAAAAAAAAAAAA 1749
DB 17 AAAAAAAAAAAAAA 4
RESULT 1259
ABK18191
ID ABK18191 standard; RNA; 17 BP.
XX
AC ABK18191;
XX
XX 09-APR-2002 (first entry)
DT
XX Human ERG hammerhead ribozyme target sequence, Seq ID No 838.
DE
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Oeller-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
KW amberzyme.
XX
XX Homo sapiens.
OS
XX WO200188124-A2.
FN
XX 22-NOV-2001.
PD
XX 16-MAY-2001; 2001WO-US015866.
PF
XX 16-MAY-2000; 2000US-00572021.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX (GLAX) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
PI
XX MPI; 2002-082995/11.
DR
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
XX Claim 4; Page 74; 149pp; English.
XX
XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Oeller-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
XX SQ Sequence 17 BP; 2 A; 12 C; 2 G; 0 T; 1 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 92.9%; Pred. No. 8.1e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 272 TCCAGCCCCACCCCC 285
DB 1 UCCAGCCCCACCCCC 14
RESULT 1260
ABV90789/c
ID ABV90789 standard; DNA; 17 BP.
XX
XX ABV90789;
AC

XX 23-DEC-2002 (first entry)
XX Human POSHL1 scanning oligonucleotide SEQ ID NO 1502.
DE
XX Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW Gene therapy; transgenic; ss.
XX Homo sapiens.
XX EP1239051-A2.
XX 11-SEP-2002.
XX 28-JAN-2002; 2002EP-00001165.
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1502; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 2 A; 4 C; 9 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0; Gaps 0;
QY 898 CCCTGAGCCAGCC 911
DB 17 CCCTGAGCCAGCC 4
RESULT 1261
ABV90793/c

ID ABV90793 standard; DNA; 17 BP.
XX
AC ABV90793;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1506.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW Gene therapy; transgenic; ss.
XX Homo sapiens.
XX OS
XX EP1239051-A2.
XX PN
XX 11-SEP-2002.
XX PD
XX 28-JAN-2002; 2002EP-00001165.
XX PF
XX 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 23-MAY-2001; 2001US-00864761.
PR 10-OCT-2001; 2001US-0328205P.
XX (AEOM-) AEOMICA INC.
XX Shannon M;
XX WPI; 2002-684061/74.
XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
PT -1, useful for treating disorders associated with decreased expression or
PT activity of human POSHL1.
XX Example 2; SEQ ID NO 1506; 60pp + Sequence Listing; English.
XX The invention relates to an isolated SH3 domain (POSH)-like signalling
CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
CC acids (S1, ABB83999), a sequence having 65% sequence identity to (S1),
CC (S1) having 95% deviations, especially conservative substitutions or a
CC fragment of the sequences comprising at least 8 contiguous amino acids.
CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
CC adaptor protein that interacts with Rho family small GTPases as well as
CC downstream components of the signal transduction pathway. (I) is useful
CC for identifying a specific binding partner. (I) and nucleic acids (II)
CC encoding (I) are useful for diagnosing, monitoring disease and treating
CC treating cancer, they are useful in the development of vaccines and (II) is
CC useful in gene therapy. (II) is useful for constructing microarrays which
CC are useful for measuring and for surveying gene expression and creating
CC transgenic non-human animals capable of producing the proteins. The
CC present sequence is that of a scanning oligonucleotide useful in examples
CC of the invention. Note: The present sequence did not form part of the
CC printed specification, but is based on sequence information supplied to
CC Derwent by the European Patent Office
XX Sequence 17 BP; 1 A; 5 C; 8 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02; Mismatches 0; Gaps 0;
Matches 14; Conservative 0; Indels 0; Gaps 0;
QY 897 GCCCTGAGCCAGC 910
DB 14 GCCCTGAGCCAGC 1

RESULT 1262
ADB04275/c
ID ADB04275 standard; DNA; 17 BP.
XX AC ADB04275;
XX DT 20-NOV-2003 (first entry)
XX DE Human MD27 scanning oligonucleotide SEQ ID 5261.
XX KW Cytostatic; immunostimulant; gene therapy; vaccine; human;
XX KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
XX KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
XX KW developmental disorder; ss.
XX OS Homo sapiens.
XX PN EP1281758-A2.
XX XX
XX PD 05-FEB-2003.
XX PF 30-JUL-2002; 2002EP-00016874.
XX PR 02-AUG-2001; 2001US-00922181.
XX PA (ABOM-) ABOMICA INC.
XX PI Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX XX
XX PT New zinc finger-containing proteins and nucleic acids, useful in
XX PT manufacturing a medicament for treating and preventing a disorder
XX PT associated with decreased or increased expression or activity of MD23,
XX PT MD24, MD27 or MD212, e.g. cancer.
XX PS Example 8; SEQ ID NO 5261; 103pp; English.
XX XX
XX CC The present invention relates to novel human zinc finger-containing
XX CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
XX CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
XX CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
XX CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
XX CC or in manufacturing a medicament for treating or preventing a disorder
XX CC associated with decreased or increased expression or activity of MD23,
XX CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
XX CC acids and proteins are also useful for diagnosing or monitoring a disease
XX CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
XX CC acids can also be used as probes to detect and characterize gross
XX CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
XX CC useful in constructing microarrays for measuring gene expression. The
XX CC proteins are useful as therapeutic agents for gene therapy or as
XX CC vaccines. The present sequence was used to illustrate the invention.
XX SQ Sequence 17 BP; 2 A; 0 C; 2 G; 13 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1735 CAAAAAAAAAAAAA 1748
Db 14 CAAAAAAAAAAAAA 1
RESULT 1263
ACC68542/c
ID ACC68542 standard; DNA; 17 BP.
XX AC ACC68542;
XX DT 01-JUL-2003 (first entry)
XX XX

XX XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5789.
XX DE
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX PN WO2003025176-A2.
XX XX
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001PR-00011979.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-333167/31.
XX XX
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 707; 738pp; French.
XX CC
XX CC The present invention relates to murine oligonucleotides (ACC62754-
XX CC ACC68806), which are associated with tumour suppression, tumour
XX CC reversion, apoptosis and virus resistance. The oligonucleotides are
XX CC useful as (1) as probes and primers for detecting, identifying,
XX CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
XX CC recombinant polypeptides. The oligonucleotides are useful for preparation
XX CC of pharmaceuticals for prevention and/or treatment of viral diseases that
XX CC are characterised by development of tumours or cell degeneration,
XX CC specifically cancer but also Alzheimer's disease and schizophrenia
XX SQ Sequence 17 BP; 6 A; 3 C; 5 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1286 CCTTCACAGTGGAT 1299
Db 15 CCTTCACAGTGGAT 2
RESULT 1264
ACC65056/c
ID ACC65056 standard; DNA; 17 BP.
XX AC ACC65056;
XX XX
XX DT 01-JUL-2003 (first entry)
XX DE Murine oligonucleotide associated with tumour suppression, SEQ ID 2303.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX KW tumour suppression; tumour reversion; apoptosis; virus resistance;
XX KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; ss.
XX OS Mus musculus.
XX PN WO2003025176-A2.
XX PD 27-MAR-2003.
XX XX

PF 17-SEP-2002; 2002WO-IB004210.
 PR 17-SEP-2001; 2001FR-00011979.
 XX (MOLE-) MOLECULAR ENGINES LAB.
 PA Telerman A, Amson R, Tuijnder M;
 PI WPI; 2003-333167/31.
 DR New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX
 PS Disclosure; Page 300; 738pp; French.
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 1 A; 7 C; 4 G; 5 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 336 GGGACCGGAGGATC 349
 DB 14 GGGACCGGAGGATC 1
 RESULT 1265
 ACC68607/C
 ID ACC68607 standard; DNA; 17 BP.
 XX
 AC ACC68607;
 XX
 DT 01-JUL-2003 (first entry)
 XX
 DE Murine oligonucleotide associated with tumour suppression, SEQ ID 5854.
 XX
 KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
 KW tumour suppression; tumour reversion; apoptosis; virus resistance;
 KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
 KW schizophrenia; ss.
 XX
 OS Mus musculus.
 XX
 PN WO2003025176-A2.
 XX
 PD 27-MAR-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004210.
 XX
 PR 17-SEP-2001; 2001FR-00011979.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-333167/31.
 XX
 PT New isolated nucleic acid, useful for treating viral diseases associated
 PT with tumors and cell degeneration, also related polypeptides, antibodies
 PT and transfected cells.
 XX

PS Disclosure; Page 715; 738pp; French.
 XX The present invention relates to murine oligonucleotides (ACC62754-
 CC ACC68806), which are associated with tumour suppression, tumour
 CC reversion, apoptosis and virus resistance. The oligonucleotides are
 CC useful as (1) as probes and primers for detecting, identifying,
 CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
 CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
 CC recombinant polypeptides. The oligonucleotides are useful for preparation
 CC of pharmaceuticals for prevention and/or treatment of viral diseases that
 CC are characterised by development of tumours or cell degeneration,
 CC specifically cancer but also Alzheimer's disease and schizophrenia
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 5 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1286 CTTTCACAGTGGAT 1299
 DB 15 CTTTCACAGTGGAT 2
 RESULT 1266
 ADB42903
 ID ADB42903 standard; DNA; 17 BP.
 XX
 AC ADB42903;
 XX
 DT 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 DE Tumour suppression/reversion associated nucleotide #3226.
 XX
 KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003040369-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-SEP-2002; 2002WO-IB004219.
 XX
 PR 17-SEP-2001; 2001FR-00011981.
 XX
 PA (MOLE-) MOLECULAR ENGINES LAB.
 XX
 PI Telerman A, Amson R, Tuijnder M;
 XX
 DR WPI; 2003-441574/41.
 XX
 PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 PS Disclosure; Page 409; 771pp; French.
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and

CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX Sequence 17 BP; 4 A; 6 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 620 CAGCCTCTTACACT 633
 Db ||||| ||||| ||||| 17
 4 CAGCCTCTTACACT

RESULT 1267
 ADB45468
 ID ADB45468 standard; DNA; 17 BP.

XX AC ADB45468;

XX DT 18-DEC-2003 (first entry)

XX DE Tumour suppression/reversion associated nucleotide #5791.

XX KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.

XX OS Homo sapiens.

XX PN WO2003040369-A2.

XX PD 15-MAY-2003.

XX PF 17-SEP-2002; 2002WO-IB004219.

XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;

XX DR WPI; 2003-441574/41.

XX PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.

XX PS Disclosure; Page 709; 771pp; French.

CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and/or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).

CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.

XX Sequence 17 BP; 4 A; 7 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 8.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1574 TCACCACTGACTGC 1587
 Db ||||| ||||| ||||| 16
 3 TCACCACTGACTGC

RESULT 1268
 ADE25221
 ID ADE25221 standard; DNA; 17 BP.

XX AC ADE25221;

XX DT 29-JAN-2004 (first entry)

XX DE Plant growth associated polynucleotide seq id 196.

XX KW plant growth; plant growth trait modulation; Brassicaceae; Arabidopsis;
 KW Brassica; Zea; Oryza; Triticum; Hordeum; Lolium; Sorghum; Glycine;
 KW Medicago; Helianthus; Lactuca; Beta; Vitis; Solanum; Lycopersicon;
 KW Capsicum; Gossypium; Hevea; Linum; Prunus; Citrus; Populus; Pinus;
 KW Quercus; ss.

XX OS Magnoliophyta.

XX PN US2003188343-A1.

XX PD 02-OCT-2003.

XX PF 07-JAN-2003; 2003US-00338777.

XX PR 09-JAN-2002; 2002US-0347288P.

XX PA (LYNX-) LYNX THERAPEUTICS INC.

XX PI Bowen BA, Haudenschild CD, Buckler ES;

XX DR WPI; 2003-803305/75.

XX PT New isolated or recombinant polypeptide for use in modulating a plant
 PT growth trait in a flowering plant e.g. in Arabidopsis, Brassica, Zea, or
 PT Oryza.

XX PS Example 2; SEQ ID NO 196; 81pp; English.

CC The invention describes an isolated or recombinant polypeptide (I)
 CC comprising a sequence: (a) comprising 1 of 30 sequences (S1), as given in
 CC the specification, or a conservative variant; (b) encoded by 1 of 30
 CC sequences (S2), as given in the specification, or a conservative variant;
 CC (c) encoded by a sequence that hybridizes under stringent conditions to
 CC S2; and (d) encoded by a sequence 70% identical to S2. The expression or
 CC activity of (I) is modulated to modulate a plant growth trait in a
 CC flowering plant, of the family Brassicaceae, preferably in a plant
 CC is Arabidopsis, Brassica, Zea, Oryza, Triticum, Hordeum, Lolium, Sorghum,
 CC Glycine, Medicago, Helianthus, Lactuca, Beta, Vitis, Solanum,
 CC Lycopersicon, Capsicum, Gossypium, Hevea, Linum, Prunus, Citrus, Populus,
 CC Pinus, or Quercus. A new method is used to detect genes for a plant
 CC growth trait. This sequence represents a polynucleotide isolated from the
 CC plant growth associated genes of the invention that can be used as a
 CC primer, probe or genetic marker.

XX Sequence 17 BP; 14 A; 1 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAAAAAA 1748
DB 4 CAAAAAAAAAAAAA 17

RESULT 1269

AAH74930
ID AAH74930 standard; DNA; 18 BP.

XX
AC AAH74930;

DT 29-OCT-2001 (first entry)

XX DNA sequence of cap adaptor.

DE Nucleotide sequence signature; nucleotide sequencing; ss.

XX Synthetic.

OS WO200161044-A1.

PN 23-AUG-2001.

XX 15-FEB-2001; 2001WO-US005032.

PF 15-FEB-2000; 2000US-0182454P.

PR 01-SEP-2000; 2000US-0654187P.

XX (LYNX-) LYNX THERAPEUTICS INC.

XX Corcoran KC, Eletr S;

PI WPI; 2001-522608/57.

DR Determining nucleotide sequence signature, by obtaining optical values for each nucleotide position in a group, adjusting them to get ratio of final highest values near predetermined factor, generating base call.

XX Disclosure; Page 19; 73pp; English.

XX The specification describes a method for determining a nucleotide sequence signature. The method comprises obtaining optical measurements with values indicating each nucleotide in a group of nucleotide positions, adjusting the values until the ratio of highest value in the set to next highest values in the set is at least a predetermined factor, and generating a base call for a position in the group based on results after the adjustment of values. The method is used for determining a signature of a nucleotide sequence, and for determining a nucleotide sequence of a polynucleotide from a series of optical measurements. The present sequence represents an adaptor, which is used in the course of the invention

XX Sequence 18 BP; 14 A; 0 C; 3 G; 0 T; 0 U; 1 Other;

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
DB 5 AAAAAAAAAAAAAA 18

RESULT 1270

AAH38930/c
ID AAH38930 standard; DNA; 18 BP.

XX
AC AAH38930;

XX

DT 14-AUG-2001 (first entry)

XX SNP specific lower PCR primer SEQ ID 1726.

XX Single nucleotide polymorphism; SNP; single nucleotide primer extension; SNPE; genotyping; agammaglobulinaemia; diabetes insipidus; cancer; Lesch-Nyhan syndrome; muscular dystrophy; familial hypercholesterolaemia; polycystic kidney disease; osteogenesis imperfecta; autoimmune disease; acute intermittent porphyria; rheumatoid arthritis; multiple sclerosis; inflammation; forensic investigation; paternity analysis; PCR primer; ss.

XX Homo sapiens.

OS WO200129262-A2.

PN 26-APR-2001.

XX 13-OCT-2000; 2000WO-US028436.

PF 15-OCT-1999; 99US-0160096P.

PR (ORCH-) ORCHID BIOSCIENCES INC.

XX Picoult-Newburg L, Pohl M;

PI WPI; 2001-290930/30.

DR New genotyping oligonucleotide, useful for detecting the presence, absence or identity of single polynucleotide polymorphism in a nucleic acid sample.

XX Claim 1; Page 58; 83pp; English.

XX Sequences AAH37205 - AAH40944 represent PCR primers, single nucleotide primer extension (SNPE) primers, and the sequences of regions flanking sites of single nucleotide polymorphisms SNPs. The present invention includes kits for determining the presence or absence of a SNP, using the oligonucleotides of the invention. The PCR primers are used to amplify a SNP flanking sequence, the SNPE primer is used as a genotyping primer. The oligonucleotides are useful for genotyping a nucleic acid sample by performing a single-nucleotide primer extension reaction. The oligonucleotides are useful for determining the presence, absence or identity of a SNP and for genotyping nucleic acid samples, for e.g. to assess by association analysis the genotype of an individual or group of individuals, having a pathological phenotypic trait suspected of being caused by one or more SNPs. Phenotypic traits include diseases e.g. agammaglobulinaemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, familial hypercholesterolaemia, polycystic kidney disease, osteogenesis imperfecta and acute intermittent porphyria. Phenotypic traits also include symptoms of or susceptibility to multifactorial disease of which a component is or may be genetic such as autoimmune diseases, including, rheumatoid arthritis, multiple sclerosis, inflammation, cancer, nervous system diseases and infection by pathogenic microorganism. The method is also useful in forensic investigations and paternity analysis. The present sequence represents a PCR primer specific for a human SNP containing DNA sequence

XX Sequence 18 BP; 4 A; 4 C; 8 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 278 CCCACCCCGGGTC 291
DB 18 CCCACCCCGGGTC 5

RESULT 1271

AAL49037/c
ID AAL49037 standard; DNA; 18 BP.

XX
AC AAL49037;

```

XX DT 29-OCT-2002 (first entry)
XX DE Drosophila ubx gene SNP analysis universal hybridisation tag #11.
XX KW Nucleic acid analysis; microarray; single nucleotide polymorphism; SNP;
XX KW Multiplex; expression analysis; hybridisation tag; ss.
XX OS Drosophila sp.
XX PN WO200261121-A2.
XX PD 08-AUG-2002.
XX PF 28-JAN-2002; 2002WO-EP000868.
XX PR 29-JAN-2001; 2001US-0264972P.
XX PR 02-FEB-2001; 2001US-0266186P.
XX PR 04-JUN-2001; 2001US-0295986P.
XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX PI Hinkel CA, Kimmerly WJ, Yang L;
XX WI WPI; 2002-636566/68.
XX PT Determining polynucleotide expression, useful for expressing profiling or
XX PT detecting single nucleotide polymorphisms, comprises hybridizing digested
XX PT cDNA to a capture probe coupled to a solid particle under stringent
XX PT conditions.
XX PS Example 2; Page 28; 63pp; English.
XX CC The present invention relates to a method of determining polynucleotide
XX CC expression, which comprises hybridising digested cDNA to a capture probe
XX CC coupled to a solid particle under stringent conditions, where the capture
XX CC probe is specific for the target polynucleotide and the particle
XX CC identifies the capture probe. The method is useful for expression
XX CC profiling, where the presence and/or the amount of a target
XX CC polynucleotide is simultaneously determined, for diagnosing a disease,
XX CC condition, disorder, or predisposition associated with a change in
XX CC expression patterns, in determining the developmental or physiological
XX CC state of a cell or tissue, for detecting SNPs, which may be used to
XX CC screen individuals for a genetic predisposition to a disease, condition,
XX CC or disorder, and in marker assisted selection. The present sequence is a
XX CC hybridisation tag described in the exemplification of the invention
XX SQ Sequence 18 BP; 3 A; 9 C; 1 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1122 CGTGAGAGGAGGG 1135
Db 15 CGTGAGAGGAGGG 2
|||||
RESULT 1272
ABL43331
ID ABL43331 standard; DNA; 18 BP.
XX AC ABL43331;
XX DT 11-APR-2002 (first entry)
XX DE Human chromosome lp36-35 PCR primer SEQ ID NO:375.
XX KW Human; chromosome lp36-35; chromosome 21q22.1; genetic analysis; genome;
XX KW PCR primer; ss.
XX OS Homo sapiens.
XX

```

```

PN JP2001321190-A.
XX 20-NOV-2001.
XX PF 12-MAR-2001; 2001JP-00068285.
XX PR 10-MAR-2000; 2000JP-00066716.
XX PA (RIKA ) RIKAGAKU KENKYUSHO.
XX PA (GENO-) GENOTEX YG.
XX DR WPI; 2002-144136/19.
XX PF Arraying genome clones.
XX PS Claim 4; Page 12; 528pp; Japanese.
XX CC The present invention describes a method of arraying genome clones. The
XX CC method comprises: (a) clones of the genomic libraries contained in
XX CC multiwell plates numbered for discrimination are mixed in each of the
XX CC multiwell plates; (b) a primer designed based on the chromosome marker
XX CC sequence is added to the mixture to carry out an amplification reaction;
XX CC (c) a signal corresponding to the marker is detected from the resultant
XX CC amplified product to specify the discrimination Nos. of the multiwell
XX CC plates containing the clones having said marker sequence; (d) the order
XX CC of the markers is changed so that the same discrimination Nos. succeed to
XX CC the maximum in the specified discrimination Nos. to array the multiwell
XX CC plates; (e) the clones in the multiwell plates of the specified
XX CC discrimination Nos. are mixed respectively in each wells of longitudinal
XX CC and lateral directions; (f) the mixed clones are cultured and the
XX CC resultant cultures are amplified by using the above primer; (g) signals
XX CC are detected from the amplified products; (h) the clones in the multiwell
XX CC plates are specified from the detected result; and (i) the clones are
XX CC reconstituted as the positions on the chromosome and arrayed. The
XX CC microarray is useful for gene analysis. ABL42957 to ABL45322 represent
XX CC PCR primers for human chromosome lp36-35 DNA, and ABL45323 to ABL45634
XX CC represent PCR primers for human chromosome 21q22.1, which are
XX CC specifically claimed for use in the present invention
XX SQ Sequence 18 BP; 5 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 14; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 383 TCCAGCACAGCGAG 396
Db 1 TCCAGCACAGCGAG 14
|||||
RESULT 1273
ADC64943/c
ID ADC64943 standard; DNA; 18 BP.
XX AC ADC64943;
XX DT 18-DEC-2003 (first entry)
XX DE Camellia sinensis L. (O.) Kuntze related PCR primer T11G.
XX KW Camellia sinensis L. (O.) Kuntze; tea tree; PCR primer; ss.
XX OS Synthetic.
XX OS Camellia sinensis.
XX PN CN1377966-A.
XX PD 06-NOV-2002.
XX PF 30-MAR-2001; 2001CN-00112459.
XX PR 30-MAR-2001; 2001CN-00112459.
XX

```

PA (SCIN-) SCI & IND RES COMMISSION.
 DR WPI; 2003-230959/23.
 XX
 PT Cloning of a new gene sequence expressed and inhibited during winter
 PT dormancy of a tea tree top plumlet, comprises identification, cloning
 PT and analysis of a new primer in the gene sequence.
 XX
 PS Example 3; Page 32; 66pp; Chinese.
 XX
 CC The present invention describes the cloning of a new gene sequence
 CC expressed and inhibited during hibernation of the top plumlet of a
 CC Camellia sinensis L.(O.) Kuntze tea tree. Also described is the
 CC identification, cloning and analysis of a primer terminal in the gene
 CC sequence expressed and inhibited during hibernation of the top plumlet
 CC of the tea tree. The present sequence represents a PCR primer which is
 CC used in an example from the present invention.
 XX
 SQ Sequence 18 BP; 2 A; 1 C; 2 G; 13 T; 0 U; 0 Other;
 Query Match 0.8%; Score 14; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAA AAAAAA 1748
 Db 18 CAAAAA AAAAAA 5
 |||||

RESULT 1274
 AAT81053/C
 ID AAT81053 standard; RNA; 17 BP.
 XX
 AC AAT81053;
 XX
 DT 26-SEP-1997 (first entry)
 XX
 DE Human c-myb hammerhead ribozyme target sequence (nt. position 55).
 XX
 KW Enzymatic nucleic acid; hammerhead; ribozyme; cleavage; human;
 KW smooth muscle cell; hyperproliferation; restenosis; cancer; c-myb;
 KW coronary angioplasty; ss.
 XX
 OS Homo sapiens.
 XX
 PN W09531541-A2.
 XX
 PD 23-NOV-1995.
 XX
 PF 18-MAY-1995; 95WO-US006368.
 XX
 PR 18-MAY-1994; 94US-00245466.
 PR 13-JAN-1995; 95US-00373124.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Stinchcomb DT, Draper K, Mcswiggen J, Jarvis T;
 XX WPI; 1996-010927/01.
 DR
 PT New enzymatic nucleic acid molecules - cleave RNA produced by e.g. c-myb,
 PT for treating restenosis or cancer.
 XX
 PS Claim 1; Page 64; 128pp; English.
 XX
 CC The present sequence represents the preferred target sequence for an
 CC enzymatic nucleic acid, especially a hammerhead ribozyme, which cleaves
 CC the human c-myb sequence at the base position indicated in the descriptor
 CC line. The c-myb sequence was screened for optimal ribozyme target sites
 CC using a computer folding algorithm, and regions of the mRNA which did not
 CC form secondary folding structures, and contained potential ribozyme
 CC cleavage sites were identified. Ribozymes were synthesised and their
 CC activities optimised by either varying the length of the binding arms or

CC by modification to prevent degradation by nucleases. The ribozymes cleave
 CC the c-myb sequence and can be used to prevent smooth muscle cell
 CC hyperproliferation in restenosis, especially after coronary angioplasty,
 CC and in cancers
 XX
 SQ Sequence 17 BP; 0 A; 9 C; 0 G; 0 T; 8 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 861 AGGAAGAGGAGAGAGAG 877
 Db 17 AGAAAGAGGAGGAGGAG 1
 |||||

RESULT 1275
 AAX75068/C
 ID AAX75068 standard; RNA; 17 BP.
 XX
 AC AAX75068;
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #596.
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX
 OS Mus sp.
 XX
 PN W09715662-A2.
 XX
 PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017480.
 XX
 PR 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX
 PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 XX WPI; 1997-259017/23.
 DR
 PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX
 PS Claim 4; Page 173; 218pp; English.
 XX
 CC The present invention describes nucleic acid molecules which modulate the
 CC synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX
 SQ Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752
DB 17 AACACAAACAAACAAA 1

RESULT 1276
AAX75073/C
ID AAX75073 standard; RNA; 17 BP.
XX
AC AAX75073;
XX
XX 28-JUL-1999 (first entry)
XX
DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #601.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
XX W09715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 173; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 0 A; 0 C; 3 G; 0 T; 14 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1734 AAAAAAAAAAAAAAAAAA 1750
DB 17 AACACAAACAAACAAA 1

RESULT 1277
AAX69804/C
ID AAX69804 standard; RNA; 17 BP.
XX
AC AAX69804;
XX
XX

DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1099.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX W09715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 79; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 2 A; 2 C; 0 G; 0 T; 13 U; 0 Other;
XX
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1732 TTACAAAAA 1748
DB 17 TTGAAAAA 1

RESULT 1278
AAX75070/C
ID AAX75070 standard; RNA; 17 BP.
XX
AC AAX75070;
XX
XX 28-JUL-1999 (first entry)
XX
DE Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #598.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.

XX WO9715662-A2.
 PN 01-MAY-1997.
 PD 25-OCT-1996; 96WO-US017480.
 XX 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 PI WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 173; 218pp; English.
 PS The present invention describes nucleic acid molecules which modulate the
 XX synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX Sequence 17 BP; 0 A; 0 C; 3 G; 0 T; 14 U; 0 Other;
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1735 CAATAAATAAATAAATAA 1751
 DB 17 CAATAAATAAATAAATAA 1
 ||||| ||||| ||||| ||||| |||||
 RESULT 1279
 AAX75069/C
 ID AAX75069 standard; RNA; 17 BP.
 XX AAX75069;
 AC AAX75069;
 XX 28-JUL-1999 (first entry)
 DT Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #597.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX Mus sp.
 OS WO9715662-A2.
 PN 01-MAY-1997.
 PD 25-OCT-1996; 96WO-US017480.
 XX 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 PI WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 173; 218pp; English.

PA (CHIR) CHIRON CORP.
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 PI WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 173; 218pp; English.
 PS The present invention describes nucleic acid molecules which modulate the
 XX synthesis, expression and/or stability of a mRNA encoding 1 or more
 CC receptors of vascular endothelial growth factor (VEGF). A patient
 CC (preferably human) having a condition associated with the level of the
 CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
 CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
 CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
 CC treated by administering the nucleic acid molecule or the expression
 CC vector to the patient. AAX67275 to AAX75752 represent specific examples
 CC of nucleic acid molecules from the present invention
 XX Sequence 17 BP; 0 A; 0 C; 2 G; 0 T; 15 U; 0 Other;
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1736 AAAAAAATAAATAAATAA 1752
 DB 17 AAAAAAATAAATAAATAA 1
 ||||| ||||| ||||| ||||| |||||
 RESULT 1280
 AAX69380/C
 ID AAX69380 standard; RNA; 17 BP.
 XX AAX69380;
 AC AAX69380;
 XX 28-JUL-1999 (first entry)
 DT Human flt1 VEGF receptor hammerhead ribozyme substrate #675.
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 XX Homo sapiens.
 OS WO9715662-A2.
 PN 01-MAY-1997.
 PD 25-OCT-1996; 96WO-US017480.
 XX 26-OCT-1995; 95US-0005974P.
 PR 11-JAN-1996; 96US-00584040.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (CHIR) CHIRON CORP.
 XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
 PI WPI; 1997-259017/23.
 XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
 PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
 PT rheumatoid arthritis, etc., in a human patient.
 XX Claim 4; Page 67; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX

SQ Sequence 17 BP; 5 A; 7 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 771 CCGAGGTGAGTCTGGG 787
Db 17 CCGAGTTGTAGTCTGGG 1

RESULT 1281
AAX75071/c
ID AAX75071 standard; RNA; 17 BP.
XX
AC AAX75071;
XX
DT 28-JUL-1999 (first entry)
XX
XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #599.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 173; 218pp; English.

The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX

XX SQ Sequence 17 BP; 0 A; 0 C; 3 G; 0 T; 14 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1734 ACAAAAAAAAAAAAAA 1750
Db 17 ACAAAACAAAAAACA 1

RESULT 1282
AAX69805/c
ID AAX69805 standard; RNA; 17 BP.
XX
AC AAX69805;
XX
DT 28-JUL-1999 (first entry)
XX
XX Human flt1 VEGF receptor hammerhead ribozyme substrate #1100.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
XX WO9715662-A2.
XX
PD 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 80; 218pp; English.

The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX

SQ Sequence 17 BP; 3 A; 2 C; 0 G; 0 T; 12 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1731 TTTACAAAAA 1747
Db 17 TTTGGA 1

```
RESULT 1283
AAAG3006/c
ID AAG3006 standard; RNA; 17 BP.
XX
AC AAG3006;
XX
DT 16-JUL-1999 (first entry)
XX
DE Delta-9 desaturase hamerhead ribozyme target SEQ ID NO:881.
XX
KW Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate;
KW granule bound starch synthase; hamerhead ribozyme; hairpin ribozyme;
KW modulation; gene expression; transgenic plant; cleavage; canola plant;
KW caffeine synthesis; coffee plant; nicotine production; tobacco;
KW fruit ripening; flower pigmentation; lignin production; ss.
XX
OS Zea mays.
XX
PN WO9710328-A2.
XX
PD 20-MAR-1997.
XX
PF 12-JUL-1996; 96WO-US011689.
XX
PR 13-JUL-1995; 95US-0001135P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (DOWC) DOWELANCO.
XX
PI Zwick MG, Edington BE, Mcswiggen JA, Merio PAO, Guo L, Skokut TA;
PI Young SA, Folkerts O, Merlo DJ;
XX
DR WPI; 1997-202224/18.
XX
PT Ribozyme which modulates plant gene expression - preferably modulates
PT expression of DELTA-9 desaturase or granule bound starch synthase in
PT maize or canola.
XX
PS Claim 38; Page 87; 155pp; English.
XX
CC The present invention describes an enzymatic nucleic acid molecule (I)
CC with RNA cleaving activity, which modulates the expression of a plant
CC gene. Also described is a gene comprising a cDNA sequence encoding maize
CC Delta-9 desaturase. (I) can be used to modulate expression of a gene.
CC Preferably Delta-9 desaturase or a granule bound starch synthase (GBSS)
CC gene, in a plant (preferably a maize or canola plant). (I) can be used to
CC modulate caffeine synthesis in a coffee plant, nicotine production in a
CC tobacco plant, fruit ripening processes in an apple, tomato, pear, plum
CC or peach plant, flower pigmentation in a rose, petunia, chrysanthemum or
CC marigold plant or lignin production in a tobacco, aspen, poplar or pine
CC plant
XX
SQ Sequence 17 BP; 2 A; 0 C; 2 G; 0 T; 13 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1733 TACAAAAAATAAAAAA 1749
DB 17 TACAAAAAATAAAAAA 1
RESULT 1284
AAA20382
ID AAA20382 standard; RNA; 17 BP.
XX
AC AAA20382;
XX
DT 19-JUN-2000 (first entry)
XX
DE Integrin alpha 6 subunit substrate sequence SEQ ID NO:3608.
```

```
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cycostatic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
OS Homo sapiens.
XX
PN WO9950403-A2.
XX
PD 07-OCT-1999.
XX
PF 24-MAR-1999; 99WO-US006507.
XX
PR 27-MAR-1998; 98US-0079678P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
PI WPI; 1999-591315/50.
XX
DR Novel ribozymes for modulating the synthesis, expression and/or stability
DR of an mRNA encoding an angiogenic factors.
XX
PS Claim 55; Page 142; 305pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules with RNA
CC cleaving activity, which specifically cleave RNA encoded by an aryl
CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
CC and AAA19155 to AAA19222 represent their corresponding target sequences;
CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
CC AAA21596 to AAA21688 represent their corresponding target sequences;
CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
CC AAA23422 represent their corresponding target sequences. The ribozymes of
CC the invention are used for modulating the synthesis, expression and/or
CC stability of an mRNA encoding angiogenic factor, especially ARNT,
CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
CC especially used to treat cancer, diabetic retinopathy, age related
CC macular degeneration (ARMD), inflammation, and arthritis, as well as
CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
CC angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
CC integrin subunit alpha-6, or integrin subunit beta-3
XX
SQ Sequence 17 BP; 1 A; 5 C; 6 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 8.6e+02;
Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 717 GGGAGCCTCTCAGGCTT 733
DB 1 GGGAGCCTCTCAGGCTT 17
RESULT 1285
AAA20383
ID AAA20383 standard; RNA; 17 BP.
XX
```

AC AAA20383;
 XX 19-JUN-2000 (first entry)
 DT Integrin alpha 6 subunit substrate sequence SEQ ID NO:3609.
 XX
 DE
 XX
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9950403-A2.
 XX 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US006507.
 XX
 XX 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 XX
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 XX Claim 55; Page 142; 305pp; English.
 XX
 XX The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 XX Sequence 17 BP; 1 A; 6 C; 4 G; 0 T; 6 U; 0 Other;
 SQ
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 58.8%; Pred. No. 8.6e-02;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Oy 719 GAGCCTCTCAGGCTTCT 735
 |||||:|:|:|:|:
 1 GAGCCUCUCGCGCUUCU 17
 Db

RESULT 1286
 AAA18807
 ID AAA18807 standard; RNA; 17 BP.
 XX
 AC AAA18807;
 XX
 XX 19-JUN-2000 (first entry)
 DT
 XX
 DE Human TIE-2 substrate sequence SEQ ID NO:2033.
 XX
 XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
 KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9950403-A2.
 XX 07-OCT-1999.
 XX
 XX 24-MAR-1999; 99WO-US006507.
 XX
 XX 27-MAR-1998; 98US-0079678P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 XX WPI; 1999-591315/50.
 XX
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 XX
 XX Claim 56; Page 118; 305pp; English.
 XX
 XX The present invention describes enzymatic nucleic acid molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberos scleriosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 XX Sequence 17 BP; 3 A; 0 C; 10 G; 0 T; 4 U; 0 Other;
 SQ
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 8.6e+02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Oy 719 GAGCCTCTCAGGCTTCT 735
 |||||:|:|:|:|:
 1 GAGCCUCUCGCGCUUCU 17
 Db

```
QY      1012 GATGTCGTTGGGAGCG 1028
DE      ||:|:|:|:|:|
XX      1 GAUGUGAUUGGGGAGGG 17

RESULT 1287
AAA36380
ID      AAA36380 standard; DNA; 17 BP.
XX
AC      AAA36380;
XX
DT      26-JUL-2000 (first entry)
XX
DE      Human genomic SNP allele specific oligonucleotide SEQ ID NO:414.
XX
KW      Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW      allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW      genomic classification; identification; DNA fingerprinting;
KW      tumour characterisation; hybridisation; ss.
XX
OS      Homo sapiens.
XX
PN      WO200018960-A2.
XX
PD      06-APR-2000.
XX
PF      24-SEP-1999; 99WO-US022283.
XX
PR      25-SEP-1998; 98US-0101757P.
XX
PA      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI      Landers JE, Jordan B, Housman DE, Charest A;
XX      WPI; 2000-293181/25.
XX
PT      Detection of single nucleotide polymorphisms in genomes by preparation
PT      and analysis of reduced complexity genomes, useful for genotyping,
PT      fingerprinting and determining allele frequency of SNPs.
XX
PS      Disclosure; Page 66; 11pp; English.
XX
CC      A method has been developed for detecting the presence or absence of a
CC      single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC      method comprises preparing a reduced complexity genome (RCG) from the
CC      genomic sample and analysing the RCG for the presence or absence of a SNP
CC      allele. The method can be used to characterise a tumour, to generate a
CC      genomic pattern for an individual genome or to generate a genomic
CC      classification code for a genome. The method can be used to assess
CC      whether a subject is at risk for developing a disease or to identify a
CC      set of SNP alleles associated with a disease. The method can also be used
CC      to perform linkage analysis. AAA35944 to AAA35947 represent sequences
CC      used in the exemplification of the present invention. AAA35948 to
CC      AAA36632 represent nucleotide sequences containing SNPs
XX
SQ      Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      720 AGCCTCTCAGGCTTCTG 736
DE      ||:|:|:|:|:|
XX      1 AGACTCTTAGGCTTCTG 17

RESULT 1288
AAA36382
ID      AAA36382 standard; DNA; 17 BP.
XX
AC      AAA36382;
XX
DT      26-JUL-2000 (first entry)
XX
DE      Human genomic SNP allele specific oligonucleotide SEQ ID NO:414.
XX
KW      Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW      allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW      genomic classification; identification; DNA fingerprinting;
KW      tumour characterisation; hybridisation; ss.
XX
OS      Homo sapiens.
XX
PN      WO200018960-A2.
XX
PD      06-APR-2000.
XX
PF      24-SEP-1999; 99WO-US022283.
XX
PR      25-SEP-1998; 98US-0101757P.
XX
PA      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI      Landers JE, Jordan B, Housman DE, Charest A;
XX      WPI; 2000-293181/25.
XX
PT      Detection of single nucleotide polymorphisms in genomes by preparation
PT      and analysis of reduced complexity genomes, useful for genotyping,
PT      fingerprinting and determining allele frequency of SNPs.
XX
PS      Disclosure; Page 66; 11pp; English.
XX
CC      A method has been developed for detecting the presence or absence of a
CC      single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC      method comprises preparing a reduced complexity genome (RCG) from the
CC      genomic sample and analysing the RCG for the presence or absence of a SNP
CC      allele. The method can be used to characterise a tumour, to generate a
CC      genomic pattern for an individual genome or to generate a genomic
CC      classification code for a genome. The method can be used to assess
CC      whether a subject is at risk for developing a disease or to identify a
CC      set of SNP alleles associated with a disease. The method can also be used
CC      to perform linkage analysis. AAA35944 to AAA35947 represent sequences
CC      used in the exemplification of the present invention. AAA35948 to
CC      AAA36632 represent nucleotide sequences containing SNPs
XX
SQ      Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      720 AGCCTCTCAGGCTTCTG 736
DE      ||:|:|:|:|:|
XX      1 AGACTCTTAGGCTTCTG 17

RESULT 1288
AAA36382
ID      AAA36382 standard; DNA; 17 BP.
XX
AC      AAA36382;
XX
```

```
DT      26-JUL-2000 (first entry)
XX
DE      Human genomic SNP allele specific oligonucleotide SEQ ID NO:416.
XX
KW      Human; single nucleotide polymorphism; SNP; genotyping; DNA analysis;
KW      allele specific oligonucleotide; ASO; reduced complexity genome; RCG;
KW      genomic classification; identification; DNA fingerprinting;
KW      tumour characterisation; hybridisation; ss.
XX
OS      Homo sapiens.
XX
PN      WO200018960-A2.
XX
PD      06-APR-2000.
XX
PF      24-SEP-1999; 99WO-US022283.
XX
PR      25-SEP-1998; 98US-0101757P.
XX
PA      (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
PI      Landers JE, Jordan B, Housman DE, Charest A;
XX      WPI; 2000-293181/25.
XX
PT      Detection of single nucleotide polymorphisms in genomes by preparation
PT      and analysis of reduced complexity genomes, useful for genotyping,
PT      fingerprinting and determining allele frequency of SNPs.
XX
PS      Disclosure; Page 66; 11pp; English.
XX
CC      A method has been developed for detecting the presence or absence of a
CC      single nucleotide polymorphism (SNP) allele in a genomic sample. The
CC      method comprises preparing a reduced complexity genome (RCG) from the
CC      genomic sample and analysing the RCG for the presence or absence of a SNP
CC      allele. The method can be used to characterise a tumour, to generate a
CC      genomic pattern for an individual genome or to generate a genomic
CC      classification code for a genome. The method can be used to assess
CC      whether a subject is at risk for developing a disease or to identify a
CC      set of SNP alleles associated with a disease. The method can also be used
CC      to perform linkage analysis. AAA35944 to AAA35947 represent sequences
CC      used in the exemplification of the present invention. AAA35948 to
CC      AAA36632 represent nucleotide sequences containing SNPs
XX
SQ      Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
XX
Query Match      0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      720 AGCCTCTCAGGCTTCTG 736
DE      ||:|:|:~|:|:|
XX      1 AGACTCTTAGGCTTCTG 17

RESULT 1289
AAZ44068/C
ID      AAZ44068 standard; DNA; 17 BP.
XX
AC      AAZ44068;
XX
DT      23-MAR-2000 (first entry)
XX
DE      L. delbruekii insertion sequences ISL6 and ISL7 PCR primer 1.
XX
KW      Insertion sequence; IS element; yoghurt; secondary metabolite;
KW      beta-galactosidase; cell wall protease; catabolite control protein A;
KW      lactate dehydrogenase; glycosyltransferase; lysogenic prophage;
KW      lac operon permease; ISL6; ISL7; PCR primer; ss.
XX
OS      Lactobacillus delbrueckii.
XX
PN      EP965643-A1.
```

XX PD 22-DEC-1999.
 XX PF 17-JUN-1998; 98EP-00202028.
 XX PR 17-JUN-1998; 98EP-00202028.
 XX PA (NEST) SOC PROD NESTLE SA.
 XX PI Mollet B, Germond JE, Lapierre L;
 XX DR WPI; 2000-074582/07.
 XX PT Use of insertion sequence elements for modifying the genomes of
 XX PT Lactobacillus bacteria, useful for screening and integration experiments.
 XX PS Example 1; Page 11; 19pp; English.
 XX CC This invention describes a novel use of insertion sequences (IS) elements
 CC (I) as tools for genetically modifying the genome of Lactobacillus
 CC delbrueckii (II) or Lactobacillus helveticus (III). (I) are used as tools
 CC for genetically modifying the genome of (II) and (III). This has
 CC applications in screening experiments to identify relevant genetic
 CC functionalities, for integration experiments or for gene expression onto
 CC the bacterial genome of (II) or (III). (II) and (III) are used for the
 CC preparation of a fermented product, secondary metabolites, beta-
 CC galactosidase, cell wall protease, catabolite control protein A, lactate
 CC dehydrogenase, glycosyltransferase, a restriction system, a lysogenic
 CC prophage or the permease of the lac operon, where the gene is inactivated
 CC by insertion of at least 1 IS element. (I) are also useful for gene
 CC tagging, gene inactivation and integration and/or gene expression on a
 CC plasmid and/or genomic level. Prior art IS elements were not used for
 CC modifying Lactobacilli, as this species, used for yoghurt production,
 CC were difficult to modify. (I) provide new genetic tools for Lactobacilli
 CC species which can be used for many processes such as gene tagging, unlike
 CC prior art Lactobacilli IS elements, which are very limited. The modified
 CC bacterial strains are useful for producing a yoghurt in which post-
 CC acidification and bitter taste which occurs during storage, is
 CC significantly reduced. This sequence represents a PCR primer used in the
 CC detection of the insertion sequence elements ISL6 and ISL7
 XX SQ Sequence 17 BP; 3 A; 4 C; 4 G; 6 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. NO. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1672 GACCTTGTCCACCAATG 1688
 Db 17 GACATTGTCCACCAAGG 1
 RESULT 1290
 AAA25445/C
 ID AAA25445 standard; DNA; 17 BP.
 XX AC AAA25445;
 XX DT 19-JUL-2000 (first entry)
 XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1943.
 XX KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX OS Homo sapiens.
 XX PN WO9954459-A2.
 XX PD 28-OCT-1999.
 XX PF 28-OCT-1999.

PF 19-APR-1999; 99WO-US0008547.
 XX 20-APR-1998; 98US-0082404P.
 PR 23-JUN-1998; 98US-00103636.
 XX (RIBO-) RIBOZYME PHARM INC.
 XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX WPI; 2000-013248/01.
 XX New nucleic acids that interact, and optionally cleave, target sequences,
 PT used to treat cancer.
 XX Claim 77; Page 79; 148pp; English.
 XX CC The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(di)thioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium), or
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA25503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences.
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. NO. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 1291
 AAA25182/C
 ID AAA25182 standard; DNA; 17 BP.
 XX AC AAA25182;
 XX DT 19-JUL-2000 (first entry)
 XX DE Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1680.
 XX KW Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX OS Homo sapiens.
 XX PN WO9954459-A2.
 XX PD 28-OCT-1999.
 XX PF 19-APR-1999; 99WO-US0008547.
 XX

```

PR 20-APR-1998; 98US-0082404P.
PR 23-JUN-1998; 98US-00103636.
PA (RIBO-) RIBOZYME PHARM INC.
PI Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
PI Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
XX used to treat cancer.
XX
XX Claim 77; Page 71; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX AAA24748 to AAA25992 represent their corresponding target sequences.
XX AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1734 ACAAAAAAAAAAAAAA 1750
Db 17 ACATAAATAAACAA 1
RESULT 1292
AAA25180/c
ID AAA25180 standard; DNA; 17 BP.
XX
XX AC AAA25180;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1678.
XX
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US008547.
XX
XX 20-APR-1998; 98US-0082404P.
XX
XX 23-JUN-1998; 98US-00103636.

```

```

XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
XX Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
XX Matulic-Adamic J;
XX
XX WPI; 2000-013248/01.
XX
XX New nucleic acids that interact, and optionally cleave, target sequences,
XX used to treat cancer.
XX
XX Claim 77; Page 71; 148pp; English.
XX
XX The present invention describes nucleic acids (A) that interact stably
XX with a target sequence and contain at least one phosphorodithioate
XX link, having endonuclease activity. (A), and more generally any catalytic
XX nucleic acid (A') that modulates expression of the oestrogen receptor
XX gene, are used to treat cancer (particularly of breast or endometrium),
XX in vivo or by transforming cells ex vivo and implanting treated cells, or
XX for other conditions associated with levels of oestrogen receptor.
XX Because of the high selectivity for targeted RNA, (A) can also be used to
XX correlate inhibition of gene expression with alterations in phenotype,
XX particularly for identification of therapeutic targets, and as research
XX reagents (for RNA, in the same way that restriction endonucleases are
XX used with DNA). The combination of modifications in (A) improves
XX resistance to nucleases, binding affinity and/or activity. AAA23503 to
XX AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
XX AAA24748 to AAA25992 represent their corresponding target sequences.
XX AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
XX sequences, and AAA26107 to AAA26218 represent their corresponding target
XX sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
XX antisense oligonucleotides used in the exemplification of the present
XX invention
XX
XX Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1752
Db 17 AAAAAATAAACAA 1
RESULT 1293
AAA25446/c
ID AAA25446 standard; DNA; 17 BP.
XX
XX AC AAA25446;
XX
XX 19-JUL-2000 (first entry)
XX
XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1944.
XX
XX Oestrogen receptor; c-ras; bcl-2; ribozyme; cleavage;
XX hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
XX gene expression modification; cancer; phosphorothioate; endonuclease;
XX anticancer; breast cancer; endometrium cancer; ss.
XX
XX Homo sapiens.
XX
XX WO954459-A2.
XX
XX 28-OCT-1999.
XX
XX 19-APR-1999; 99WO-US008547.
XX
XX 20-APR-1998; 98US-0082404P.
XX
XX 23-JUN-1998; 98US-00103636.
XX
XX (RIBO-) RIBOZYME PHARM INC.

```


XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;
 PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX WPI; 2000-013248/01.
 DR New nucleic acids that interact, and optionally cleave, target sequences,
 XX used to treat cancer.
 PT Claim 77; Page 79; 148pp; English.
 XX The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(di)thioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences,
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX SQ Sequence 17 BP; 1 A; 0 C; 1 G; 15 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1736 AAAAAAAAAAAAAAAAAA 1752
 |||||
 Db 17 AAAAAAAAAAAAAAAAAA 1
 RESULT 1294
 AAA25181/c
 ID AAA25181 standard; DNA; 17 BP.
 XX AAA25181;
 AC
 XX 19-JUL-2000 (first entry)
 DT
 XX Oestrogen receptor hammerhead ribozyme target sequence SEQ ID NO:1679.
 DE
 XX Oestrogen receptor; c-raf; k-ras; bcl-2; ribozyme; cleavage;
 KW hammerhead ribozyme; hairpin ribozyme; antisense oligonucleotide;
 KW gene expression modification; cancer; phosphorothioate; endonuclease;
 KW anticancer; breast cancer; endometrium cancer; ss.
 XX Homo sapiens.
 OS
 XX WO9954459-A2.
 FN
 XX 28-OCT-1999.
 PD
 XX 19-APR-1999; 99WO-US008547.
 PF
 XX 20-APR-1998; 98US-0082404P.
 PR
 XX 23-JUN-1998; 98US-00103636.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Thompson JD, Beigelman L, Mcswiggen JA, Karpeisky A, Bellon L;

PI Reynolds M, Zwick M, Jarvis T, Woolf T, Haerberli P;
 PI Matulic-Adamic J;
 XX WPI; 2000-013248/01.
 DR New nucleic acids that interact, and optionally cleave, target sequences,
 XX used to treat cancer.
 PT Claim 77; Page 71; 148pp; English.
 XX The present invention describes nucleic acids (A) that interact stably
 CC with a target sequence and contain at least one phosphoro(di)thioate
 CC link, having endonuclease activity. (A), and more generally any catalytic
 CC nucleic acid (A') that modulates expression of the oestrogen receptor
 CC gene, are used to treat cancer (particularly of breast or endometrium),
 CC in vivo or by transforming cells ex vivo and implanting treated cells, or
 CC for other conditions associated with levels of oestrogen receptor.
 CC Because of the high selectivity for targeted RNA, (A) can also be used to
 CC correlate inhibition of gene expression with alterations in phenotype,
 CC particularly for identification of therapeutic targets, and as research
 CC reagents (for RNA, in the same way that restriction endonucleases are
 CC used with DNA). The combination of modifications in (A) improves
 CC resistance to nucleases, binding affinity and/or activity. AAA23503 to
 CC AAA24747 represent oestrogen receptor hammerhead ribozyme sequences, and
 CC AAA24748 to AAA25992 represent their corresponding target sequences,
 CC AAA25993 to AAA26105 represent oestrogen receptor hairpin ribozyme
 CC sequences, and AAA26107 to AAA26218 represent their corresponding target
 CC sequences. AAA26219 to AAA26271 represent other ribozyme sequences and
 CC antisense oligonucleotides used in the exemplification of the present
 CC invention
 XX SQ Sequence 17 BP; 1 A; 0 C; 2 G; 14 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1735 CAAAAAAAAAAAAAAAAA 1751
 |||||
 Db 17 CAAAAAAAAAAAAAAAAA 1
 RESULT 1295
 AAF02549
 ID AAF02549 standard; DNA; 17 BP.
 XX AAF02549;
 AC
 XX 16-FEB-2001 (first entry)
 DT
 XX Hammerhead ribozyme substrate #844.
 DE
 XX Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 KW
 XX Homo sapiens.
 OS
 XX WO200061729-A2.
 FN
 XX 19-OCT-2000.
 PD
 XX 11-APR-2000; 2000WO-US009721.
 PF
 XX 12-APR-1999; 99US-0129390P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Blatt L, Zwick M, Pavco P, Mcswiggen J;
 PI WPI; 2000-647423/62.
 DR
 XX Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,

PT interferon alpha and erythropoietin.
 PS Claim 37; Page 75; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 1 A; 6 C; 5 G; 5 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1239 TGGCTGCTTCACCTGCG 1255
 DB 1 TGGCTGCTTCACCTGCG 17
 RESULT 1296
 AAF06382/C
 ID AAF06382 standard; DNA; 17 BP.
 XX
 AC AAF06382;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #3179.
 XX
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 42; Page 128; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1239 TGGCTGCTTCACCTGCG 1255
 DB 1 TGGCTGCTTCACCTGCG 17
 RESULT 1296
 AAF06382/C
 ID AAF06382 standard; DNA; 17 BP.
 XX
 AC AAF06382;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #3179.
 XX
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 42; Page 128; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 3 A; 0 C; 1 G; 0 T; 13 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1733 TACAAAAA 1749
 DB 17 TACAAATTA 1
 RESULT 1297
 AAF06381/C
 ID AAF06381 standard; DNA; 17 BP.
 XX
 AC AAF06381;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #3178.
 XX
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200061729-A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 11-APR-2000; 2000WO-US009721.
 XX
 PR 12-APR-1999; 99US-0129390P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 XX
 PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
 XX
 DR WPI; 2000-647423/62.
 XX
 CC Enzymatic and antisense nucleic acid inhibition of repressor genes,
 PT useful for producing e.g. granulocyte colony stimulating factor protein,
 PT interferon alpha and erythropoietin.
 XX
 PS Claim 42; Page 128; 164pp; English.
 XX
 CC The present invention relates to enzymatic and antisense nucleic acid
 CC molecules that act as inhibitors of the expression of repressor genes
 CC encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
 CC factor gene, IRF-2 and/or the CAAT Displacement Protein (CDP).
 CC Inhibition of the repressors removes prevents inhibition (and
 CC consequently increases expression of) genes involved in the production of
 CC erythropoietin, granulocyte colony stimulating factor protein and
 CC interferon alpha
 XX
 SQ Sequence 17 BP; 2 A; 0 C; 1 G; 0 T; 14 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1734 ACAAAAAA 1750
 DB 17 ACAAAATTA 1
 RESULT 1298
 AAF03345/C
 ID AAF03345 standard; DNA; 17 BP.
 XX
 AC AAF03345;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Hammerhead ribozyme substrate #1640.
 XX
 DE Ribozyme; erythropoietin; granulocyte colony stimulating factor;
 KW interferon alpha; ss.


```
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1731 TTTACAAAAA 1747
Db 17 TTTACAAAAATGAAAA 1

RESULT 1301
AAF02205
ID AAF02205 standard; DNA; 17 BP.
XX AC AAF02205;
XX DT 16-FEB-2001 (first entry)
XX DE Hammerhead ribozyme substrate #500.
XX KW Ribozyme; erythropoietin; granulocyte colony stimulating factor;
interferon alpha; ss.
XX OS Homo sapiens.
XX PN WO200061729-A2.
XX PD 19-OCT-2000.
XX PF 11-APR-2000; 2000WO-US009721.
XX PR 12-APR-1999; 99US-0129390P.
XX PA (RIBO-) RIBOZYME PHARM INC.
XX PI Blatt L, Zwick M, Pavco P, Mcswiggen J;
XX DR WPI; 2000-647423/62.
XX PT Enzymatic and antisense nucleic acid inhibition of repressor genes,
useful for producing e.g. granulocyte colony stimulating factor protein,
interferon alpha and erythropoietin.
XX PS Claim 37; Page 67; 164pp; English.
XX CC The present invention relates to enzymatic and antisense nucleic acid
molecules that act as inhibitors of the expression of repressor genes
encoding the TR2 Orphan receptor, EAR3/COUP-TF-1, the GATA transcription
factor gene, IRF-2 and/or the CAAAT Displacement Protein (CDP).
XX CC Inhibition of the repressors removes prevents inhibition (and
consequently increases expression of) genes involved in the production of
erythropoietin, granulocyte colony stimulating factor protein and
interferon alpha
XX SQ Sequence 17 BP; 1 A; 9 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 231 CCGCGGCACCCGGGCG 247
Db 1 CCACGGCTCCCGGGCG 17

RESULT 1302
AAC67367/C
ID AAC67367 standard; DNA; 17 BP.
XX AC AAC67367;
XX DT 14-FEB-2001 (first entry)
XX DE Alzheimer's disease-linked mitochondrial SNP PCR primer #67.
XX KW Human; mitochondrial genome; single nucleotide polymorphism; SNP;
```

```
KW Alzheimer's disease; mtDNA; PCR primer; ss.
XX Homo sapiens.
XX PN WO200063441-A2.
XX PD 26-OCT-2000.
XX PF 19-APR-2000; 2000WO-US010906.
XX PR 20-APR-1999; 99US-0130447P.
XX PR 22-OCT-1999; 99US-0160901P.
XX PA (MITO-) MITOKOR.
XX PI Herrnstadt C, Davis RE;
XX DR WPI; 2000-672748/65.
XX PT Diagnosing a subject at the risk for or having Alzheimer's disease
comprises determining at least one single nucleotide polymorphism in
mitochondrial DNA associated with the disease in the sample from the
subject.
XX PS Example 4; Page 39; 89pp; English.
XX CC The present invention describes a novel method for determining the risk
of or diagnosing Alzheimer's disease using single nucleotide
polymorphisms (SNPs) present in an individual's mitochondrial DNA
(mtDNA). In addition, the SNPs identified can be used to identify agents
suitable for use in treating Alzheimer's disease. Sequences AAC67301-
C67610 are PCR primers used to demonstrate the method of the invention
XX SQ Sequence 17 BP; 3 A; 9 C; 1 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1450 AAGTCCGAGGAGTGTCG 1466
Db 17 AAGCGCGATGAGTGTCG 1

RESULT 1303
ABK01375/C
ID ABK01375 standard; RNA; 17 BP.
XX AC ABK01375;
XX DT 12-MAR-2002 (first entry)
XX DE Human NOGO Inozyme #645.
XX KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
DNazyme; inozyme; G-cleaver; amberzyme; zinczyme; lymphoma; leukaemia;
B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
inflammatory arthropathy; central nervous system injury;
cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
Parkinson's disease; ataxia; Huntington's disease;
Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200159103-A2.
XX PD 16-AUG-2001.
```

[illegible]

CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention
XX
SQ Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 861 AGGAGAGGAGGAGGAG 877
DB 1 AGGAGAGGAGGAGGAG 17
RESULT 1305
ABK02357
ID ABK02357 standard; RNA; 17 BP.
XX
AC ABK02357;
DT 12-MAR-2002 (first entry)
XX
DE Human NOGO Amberzyme #29.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
OS
OS Homo sapiens.
OS Synthetic.
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 88; Page 131; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention
XX
SQ Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 861 AGGAGAGGAGGAGGAG 877
DB 1 AGGAGAGGAGGAGGAG 17
RESULT 1306
ABK03744
ID ABK03744 standard; RNA; 17 BP.
XX
AC ABK03744;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human CD20 Amberzyme #93.
XX
KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
OS
OS Homo sapiens.
OS Synthetic.
PN WO200159103-A2.
XX
PD 16-AUG-2001.
XX
PF 09-FEB-2001; 2001WO-US004273.
XX
PR 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX

PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
PI Blatt L, Mcswiggen J, Chowrira BM;
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
XX Claim 30; Page 168; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a NYN motif) or
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention
XX
XX Sequence 17 BP; 10 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 860 CAGGAAGAGGAAGGA 876
Db 1 CAAGAAGAGGAAGA 17
RESULT 1307
ABK02367
ID ABK02367 standard; RNA; 17 BP.
XX
XX AC ABK02367;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NOGO Amberzyme #39.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;
KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW DNzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;

KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW inflammatory arthropathy; central nervous system injury;
KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW Parkinson's disease; ataxia; Huntington's disease;
KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
OS
OS Synthetic.
XX
XX W0200159103-A2.
PN
XX
XX 16-AUG-2001.
PD
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
PR
XX 28-FEB-2000; 2000US-0185516P.
PR
XX 06-MAR-2000; 2000US-0187128P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGGEN J.
PA (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
PI
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
XX Claim 88; Page 131; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOGO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNzyme) an inozyme (an endolytic nucleic acid cleaving a NYN motif) or
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an amberzyme molecule of the invention
XX
XX Sequence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;

```
Best Local Similarity 88.2%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

QY 861 AGGAGAGGAGGAGGAG 877
DB 1 AGGAGAGGAGGAGGAG 17

RESULT 1308
ABL46642
ID ABL46642 standard; RNA; 17 BP.
XX
AC ABL46642;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human GRID NCH ribozyme substrate oligonucleotide #96.
XX
KW Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200162911-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005957.
XX
PR 24-FEB-2000; 2000US-0184594P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.
XX
PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX
PS Claim 4; Page 64; 108pp; English.
XX
CC The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention
XX
SQ Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 202 GCCAGAGCCCTCAGGG 218
DB 1 GCCAGAGCCCTCAGGG 17

RESULT 1309
ABL46740/c
ID ABL46740 standard; RNA; 17 BP.
XX
AC ABL46740;
XX
DT 27-JUN-2003 (first entry)
XX
```

```
DE Human GRID NCH ribozyme substrate oligonucleotide #194.
XX
KW Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200162911-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005957.
XX
PR 24-FEB-2000; 2000US-0184594P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX ) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
XX WPI; 2001-550088/61.
XX
PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX
PS Claim 4; Page 66; 108pp; English.
XX
CC The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention
XX
SQ Sequence 17 BP; 3 A; 8 C; 3 G; 0 T; 3 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1133 GGGCATATTGGGAGGC 1149
DB 17 GGGCATATTGGGAGGC 1

RESULT 1310
ABL46643
ID ABL46643 standard; RNA; 17 BP.
XX
AC ABL46643;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human GRID NCH ribozyme substrate oligonucleotide #97.
XX
KW Human; Grb2-related with Insert Domain; GRID; T-cell;
KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukaemia; cytostatic; ss.
XX
OS Homo sapiens.
XX
PN WO200162911-A2.
XX
PD 30-AUG-2001.
XX
PF 23-FEB-2001; 2001WO-US005957.
XX
PR 24-FEB-2000; 2000US-0184594P.
XX
```


PA (RIBO-) RIBOZYME PHARM INC.
 XX (GLAX) GLAXO GROUP LTD.
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 64; 108pp; English.
 XX
 CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 4 A; 6 C; 6 G; 0 T; 1 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 204 CAGAGCCCCCTCAGGGGA 220
 DB ||||| ||||| ||||| |||||
 1 CAGAGCUCCCCCAGGGGA 17
 RESULT 1311
 ABL46459
 ID ABL46459 standard; RNA; 17 BP.
 XX
 AC ABL46459;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID hammerhead ribozyme substrate oligonucleotide #92.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; 8s.
 XX
 OS Homo sapiens.
 XX
 XX WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 60; 108pp; English.
 XX
 CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful

CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 203 CCAGAGCCCCCTCAGGGG 219
 DB ||||| ||||| ||||| |||||
 1 CCAGAGCUCCCCCAGGGG 17
 RESULT 1312
 ABL46888/C
 ID ABL46888 standard; RNA; 17 BP.
 XX
 AC ABL46888;
 XX
 DT 27-JUN-2003 (first entry)
 XX
 DE Human GRID G-cleaver ribozyme substrate oligonucleotide #29.
 XX
 KW Human; Grb2-related with Insert Domain; GRID; T-cell;
 KW co-stimulatory adaptor protein; tissue rejection; graft rejection;
 KW leukaemia; cytostatic; 8s.
 XX
 OS Homo sapiens.
 XX
 XX WO200162911-A2.
 XX
 PD 30-AUG-2001.
 XX
 PF 23-FEB-2001; 2001WO-US005957.
 XX
 PR 24-FEB-2000; 2000US-0184594P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
 XX WPI; 2001-550088/61.
 DR
 XX New nucleic acid(s) for regulating the Grb2-related with Insert Domain
 PT (GRID) gene comprises using antisense and enzymatic nucleic acid
 PT molecules such as hammerhead ribozymes.
 XX
 XX Claim 4; Page 69; 108pp; English.
 XX
 CC The present invention relates to oligonucleotides that downregulate the
 CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
 CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
 CC for modulating the expression of GRID, to treat conditions such as
 CC tissue/graft rejection and leukaemia. The oligonucleotides can also be
 CC administered in conjunction with other therapies such as radiation,
 CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
 CC used to illustrate the invention
 XX
 SQ Sequence 17 BP; 4 A; 7 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1135 GCATATTGCGAGGCGCTG 1151
 DB ||||| ||||| ||||| |||||
 17 GCATATTGCGAGGCGCTG 1

```
RESULT 1313
AAC89333/c
ID AAC89333 standard; DNA; 17 BP.
XX
XX AC AAC89333;
XX
XX DT 07-MAR-2001 (first entry)
XX
XX DE First conventional primer.
XX
XX KW Hairpin oligonucleotide; amplification; primer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200071562-A1.
XX
XX PD 30-NOV-2000.
XX
XX PF 03-MAY-2000; 2000WO-US011979.
XX
XX PR 24-MAY-1999; 99US-00317350.
XX
XX PA (PUBL-) PUBLIC HEALTH RES INST NEW YORK.
XX
XX PI Tyagi S, Kramer FR, Vartikian R;
XX
XX DR WPI; 2001-032015/04.
XX
XX PT Novel primers for nucleic acid amplification, comprise a hairpin
PT structure in which a single-stranded loop separates complementary 3' and
PT 5' arms and the loop and the 3' arm are complementary to target nucleic
PT acid.
XX
XX PS Example 4; Page 23; 40pp; English.
XX
XX CC The present invention relates to a hairpin oligonucleotide primer for
CC extension by a DNA polymerase, comprising a stem formed by complementary
CC 3' and 5' arm sequences and a single-stranded loop sequence separating
CC the arm sequences, where the 3' arm sequence and the loop sequence are
CC both complementary to a selected priming region of a target nucleic acid
CC strand. The invention is useful for nucleic acid amplification by a
CC polymerase chain reaction (PCR), a strand displacement reaction (SDA), a
CC nucleic acid sequence-based amplification (NASBA), transcription-mediated
CC amplification (TMA), and a rolling-circle amplification (RCA). The
CC process includes real-time detection of intended amplification products
CC utilizing separate detector probes having interactive labels, at least
CC one of which is a fluorophore
XX
XX SQ Sequence 17 BP; 0 A; 6 C; 9 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 8.6e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 242 CGGGGCCACCCGCC 258
XX |||||
XX Db 17 CGGGGCCACCCGCC 1
XX
XX RESULT 1314
ABN10512
ID ABN10512 standard; DNA; 17 BP.
XX
XX AC ABN10512;
XX
XX DT 29-MAY-2002 (first entry)
XX
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10504.
XX
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
```

```
XX OS Homo sapiens.
XX
XX PN WO200192524-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 25-MAY-2001; 2001WO-US016981.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
XX
XX PR 21-SEP-2000; 2000US-0234687P.
XX
XX PR 07-SEP-2000; 2000US-0236359P.
XX
XX PR 04-OCT-2000; 2000GB-00024263.
XX
XX PR 30-JAN-2001; 2001WO-US000661.
XX
XX PR 30-JAN-2001; 2001WO-US000662.
XX
XX PR 30-JAN-2001; 2001WO-US000663.
XX
XX PR 30-JAN-2001; 2001WO-US000664.
XX
XX PR 30-JAN-2001; 2001WO-US000665.
XX
XX PR 30-JAN-2001; 2001WO-US000666.
XX
XX PR 30-JAN-2001; 2001WO-US000667.
XX
XX PR 30-JAN-2001; 2001WO-US000668.
XX
XX PR 30-JAN-2001; 2001WO-US000669.
XX
XX PR 05-FEB-2001; 2001WO-US000670.
XX
XX PR 05-FEB-2001; 2001US-0266860P.
XX
XX PA (AEOM-) AROMICA INC.
XX
XX PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX DR WPI; 2002-179446/23.
XX
XX PT New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX PS Disclosure; SEQ ID NO 10504; 214pp; English.
XX
XX CC The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption/ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX SQ Sequence 17 BP; 5 A; 3 C; 9 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 8.6e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX Qy 807 GAGAGACCCAGGCCAG 823
XX |||||
XX Db 1 GAGAGACCCAGGCCAG 17
XX
XX RESULT 1315
ABN07887
```

ID ABN07887 standard; DNA; 17 BP.
AC ABN07887;
XX
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7879.
DE
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
PT
XX
XX Disclosure; SEQ ID NO 7879; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 2 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. NO. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 835 GAAGCTGCTGGGTCTC 851
Db 1 GGAGCTGCTGGGTCTC 17
RESULT 1316
ABN00904
ID ABN00904 standard; DNA; 17 BP.
XX
XX AC ABN00904;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:4 sequence SEQ ID NO:896.
DE
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
PT
XX
XX Disclosure; SEQ ID NO 896; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The

PF 25-MAY-2001; 2001WO-US016981.
XX
PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
DR
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX
PS Disclosure; SEQ ID NO 10502; 214pp; English.
XX
CC The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 5 A; 4 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 805 CAGAGAGAGCCAGGGCC 821
DB 1 CGGAGAGAGCCAGGGAC 17
RESULT 1321
AAD33183/c
ID AAD33183 standard; DNA; 17 BP.
XX
XX AAD33183;
AC
XX
DT 01-JUL-2002 (first entry)
XX
DE LDLR cDNA amplifying RT-PCR primer, LDLR/p1.

XX
KW Phytanic acid; non-insulin dependent diabetes mellitus; NIDDM; obesity;
KW glucose tolerance; food supplement; feed supplement; hyperinsulinaemia;
KW hyperlipidaemia; hypertension; insulin therapy; hypercholesterolaemia;
KW hypertriglyceridaemia; primer; RT-PCR; LDLR; reverse transcription PCR;
XX low-density lipoprotein receptor; ss.
OS Unidentified.
XX
XX EP1177789-A2.
PN
XX 06-FEB-2002.
XX
PF 30-JUL-2001; 2001EP-00118230.
XX
PR 04-AUG-2000; 2000EP-00116848.
XX
XX (HOFF) ROCHE VITAMINS AG.
XX
PI Fluehmann B, Heim M, Hunziker W, Weber P;
XX
XX WPI; 2002-270864/32.
DR
XX
XX New composition comprising phytanic acid or its derivatives, useful for
PT treating or preventing non-insulin dependent diabetes mellitus, impaired
PT glucose tolerance and related obesity.
XX
PS Example 3; Page 9; 29pp; English.
XX
CC The invention relates to the use of phytanic acid or its derivatives for
CC the treatment or prevention of diabetes mellitus. The invention also
CC relates to a method for treating or preventing non-insulin dependent
CC diabetes mellitus (NIDDM) or other conditions associated with impaired
CC glucose tolerance such as obesity using phytanic acid or its derivatives.
CC The phytanic acid, their derivatives or their precursors are useful as
CC pharmaceutical compounds or supplements to foods or feeds for the
CC treatment or prevention of type II or NIDDM, hyperlipidaemia,
CC hypercholesterolaemia, hyperinsulinaemia, syndrome X, hypertension,
CC hypertriglyceridaemia, impaired glucose tolerance and related obesity.
CC They are also useful in insulin therapy in combination with known active
CC compounds. The present sequence is low-density lipoprotein receptor
CC (LDLR) cDNA amplifying reverse transcription PCR (RT-PCR) primer used in
CC the exemplification of the invention
XX
SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 694 AGGGGCTGGGGCCACC 710
DB 17 AGGGGCTGCTGACCACC 1
RESULT 1322
ABV85236/c
ID ABV85236 standard; DNA; 17 BP.
XX
XX ABV85236;
AC
XX
DT 11-DEC-2002 (first entry)
XX
DE Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:229.
XX
XX Human; UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10;
KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
KW ss.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX EP1243660-A2.

```
XX 25-SEP-2002.
XX 25-JAN-2002; 2002EP-00001161.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 30-JAN-2001; 2001WO-US000671.
XX 23-MAY-2001; 2001US-00864761.
XX 30-AUG-2001; 2001US-0315984P.
XX (AEOM-) AEOMICA INC.
XX Zhang J, Gu Y, Nguyen C;
XX WPI; 2002-724954/79.
XX Nucleic acid encoding human UDP-GalNAC:polypeptide N-
XX cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
XX PT and treat disorders associated with reduced or over expression of the
XX PT encoded protein.
XX Example 2; SEQ ID NO 229; 59pp; English.
XX The present invention describes an isolated nucleic acid (I) encoding a
XX human UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10 (pp-
XX GanTase 10, EC 2.4.1.41) protein. Human pp-GanTase 10 is located to
XX chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
XX present invention can be used in therapy, particularly to prevent or
XX treat a disorder associated with decreased expression or activity of pp-
XX GanTase. The sequences given in ABV85011 to ABV8689 and ABP53502 to
XX ABP53504 are given in the exemplification of the present invention. N.B.
XX The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied by the
XX European Patent Office
XX SQ Sequence 17 BP; 4 A; 9 C; 3 G; 1 T; 0 U; 0 Other;
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. NO. 8.6e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX Qy 1024 GATGGGCTGGGTTGT 1040
XX Db 17 GATGGGCTGGGCTGT 1
XX RESULT 1323
XX ABV85235/C
XX ID ABV85235 standard; DNA; 17 BP.
XX AC ABV85235;
XX XX 11-DEC-2002 (first entry)
XX DT
XX DE Human pp-GanTase 10 scanning 17-mer SEQ ID NO:228.
XX KW Human; UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10;
XX KW pp-GanTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX KW ss.
XX XX Homo sapiens.
XX OS Synthetic.
XX XX EP1243660-A2.
XX FN
XX XX
XX XX EP1243660-A2.
XX PD
XX XX
XX XX 25-SEP-2002.
XX PF
```

```
XX 25-JAN-2002; 2002EP-00001161.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 23-MAY-2001; 2001US-00864761.
XX 30-AUG-2001; 2001US-0315984P.
XX (AEOM-) AEOMICA INC.
XX Zhang J, Gu Y, Nguyen C;
XX WPI; 2002-724954/79.
XX Nucleic acid encoding human UDP-GalNAC:polypeptide N-
XX cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
XX PT and treat disorders associated with reduced or over expression of the
XX PT encoded protein.
XX Example 2; SEQ ID NO 228; 59pp; English.
XX The present invention describes an isolated nucleic acid (I) encoding a
XX human UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10 (pp-
XX GanTase 10, EC 2.4.1.41) protein. Human pp-GanTase 10 is located to
XX chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
XX present invention can be used in therapy, particularly to prevent or
XX treat a disorder associated with decreased expression or activity of pp-
XX GanTase. The sequences given in ABV85011 to ABV8689 and ABP53502 to
XX ABP53504 are given in the exemplification of the present invention. N.B.
XX The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied by the
XX European Patent Office
XX SQ Sequence 17 BP; 4 A; 9 C; 3 G; 1 T; 0 U; 0 Other;
XX Query Match 0.8%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. NO. 8.6e+02;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX Qy 1025 ATGGGGCTGGGTTGTG 1041
XX Db 17 ATGGGGCTGGGCTGTG 1
XX RESULT 1324
XX ABV85237/C
XX ID ABV85237 standard; DNA; 17 BP.
XX AC ABV85237;
XX XX 11-DEC-2002 (first entry)
XX DT
XX DE Human pp-GanTase 10 scanning 17-mer SEQ ID NO:230.
XX KW Human; UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10;
XX KW pp-GanTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
XX KW ss.
XX XX Homo sapiens.
XX OS Synthetic.
XX XX EP1243660-A2.
XX FN
XX XX
XX XX 25-SEP-2002.
XX XX 25-JAN-2002; 2002EP-00001161.
XX XX 30-JAN-2001; 2001WO-US000663.
```

PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 30-AUG-2001; 2001US-0315984P.
 XX (AEOM-) AEOMICA INC.
 XX Zhang J, Gu Y, Nguyen C;
 PI WPI; 2002-724954/79.
 DR Nucleic acid encoding human UDP-GalNAC:polypeptide N-
 XX cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
 PT and treat disorders associated with reduced or over expression of the
 PT encoded protein.
 XX Example 2; SEQ ID NO 230; 59pp; English.
 XX The present invention describes an isolated nucleic acid (I) encoding a
 CC human UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10 (pp-
 CC GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
 CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
 CC present invention can be used in therapy, particularly to prevent or
 CC treat a disorder associated with decreased expression or activity of pp-
 CC GaNTase. The sequences given in ABV85011 to ABV8689 and ABP3502 to
 CC ABP3504 are given in the exemplification of the present invention. N.B.
 CC The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office
 XX Sequence 17 BP; 3 A; 10 C; 3 G; 1 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1023 GGATGGGCTGGGGTGTG 1039
 DB 17 GGATGGGCTGGCGCTG 1
 RESULT 1325
 ABV85264
 ID ABV85264 standard; DNA; 17 BP.
 XX AC ABV85264;
 XX 11-DEC-2002 (first entry)
 DT Human pp-GaNTase 10 scanning 17-mer SEQ ID NO:257.
 XX Human; UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10;
 KW pp-GaNTase 10; EC 2.4.1.41; chromosome 7q11.2; gene therapy; scanning;
 KW ss.
 XX Homo sapiens.
 OS Synthetic.
 XX EP1243660-A2.
 PN 25-SEP-2002.
 PD 25-JAN-2002; 2002EP-00001161.
 PF 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 23-MAY-2001; 2001US-00864761.
 PR 30-AUG-2001; 2001US-0315984P.
 XX (AEOM-) AEOMICA INC.
 XX Zhang J, Gu Y, Nguyen C;
 PI WPI; 2002-724954/79.
 DR Nucleic acid encoding human UDP-GalNAC:polypeptide N-
 XX cetylalactosaminyltransferase 10 protein is useful to diagnose, prevent
 PT and treat disorders associated with reduced or over expression of the
 PT encoded protein.
 XX Example 2; SEQ ID NO 257; 59pp; English.
 XX The present invention describes an isolated nucleic acid (I) encoding a
 CC human UDP-GalNAC:polypeptide N-acetylalactosaminyltransferase 10 (pp-
 CC GaNTase 10, EC 2.4.1.41) protein. Human pp-GaNTase 10 is located to
 CC chromosome 7q11.2. (I) can be used in gene therapy. Molecules of the
 CC present invention can be used in therapy, particularly to prevent or
 CC treat a disorder associated with decreased expression or activity of pp-
 CC GaNTase. The sequences given in ABV85011 to ABV8689 and ABP3502 to
 CC ABP3504 are given in the exemplification of the present invention. N.B.
 CC The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied by the
 CC European Patent Office
 XX Sequence 17 BP; 2 A; 7 C; 5 G; 3 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1535 CCTGACGGCTGGCGC 1551
 DB 1 CCTGACGGCTGGCGC 17
 RESULT 1326
 ABV79401/c
 ID ABV79401 standard; DNA; 17 BP.
 XX AC ABV79401;
 XX 03-JAN-2003 (first entry)
 DT Human HTPL scanning oligonucleotide SEQ ID 647.
 DE Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
 XX Homo sapiens.
 OS EP1229046-A2.
 PN 07-AUG-2002.
 PD 28-JAN-2002; 2002EP-00001167.
 PF 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.


```

PR 09-OCT-2001; 2001US-0327898P.
XX (AEOM-) AEOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX Example 2; Page 148; 718pp; English.
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB898519 to AB898520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 852 TGGCCCTGCAGAGAG 868
Db 17 TGGCCCTGCAGAGCG 1
RESULT 1327
ID ABV79138
XX ABV79138 standard; DNA; 17 BP.
XX AC ABV79138;
XX DT 03-JAN-2003 (first entry)
XX DE Human HTPL scanning oligonucleotide SEQ ID 384.
XX Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
XX human testis expressed Patched like protein; testis; adrenal; liver;
XX male germ cell development; bone marrow; brain; kidney; lung; placenta;
XX prostate; skeletal muscle; colon; male infertility; cancer; ss.
XX OS Homo sapiens.
XX EP1229046-A2.
XX PN EP1229046-A2.
XX PD 07-AUG-2002.
XX 28-JAN-2002; 2002EP-00001167.
XX 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
PR 09-OCT-2001; 2001WO-US000669.
XX 23-MAY-2001; 2001US-00864761.
XX PR 09-OCT-2001; 2001US-0327898P.
XX (AEOM-) AEOMICA INC.
XX Zhan J;
XX WPI; 2002-676582/73.
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX Example 2; Page 114; 718pp; English.
XX The present invention relates to human testis expressed Patched like
CC protein (HTPL, see ABV78759 to ABV78762 and AB898519 to AB898520). HTPL
CC has two isoforms, with a few single base pair differences between the
CC two. One of the single base pair changes introduces a premature stop
CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
CC shares an overall structure organisation with the Patched protein. The
CC shared structural features strongly imply that HTPL plays a role similar
CC to that of Patched, and is a potential tumour suppressor. HTPL is
CC important in regulating male germ cell development, and the HTPL gene was
CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
CC useful for diagnosing a disorder caused by mutation in HTPL, and in
CC therapy and manufacture of a medicament for treatment or prevention of
CC such disorder associated with decreased expression or activity of human
CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
CC clinically useful diagnostic markers and potential therapeutic agents for
CC male infertility and cancer. The present oligonucleotide was used in an
CC example from the invention
XX Sequence 17 BP; 4 A; 5 C; 7 G; 1 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 855 CCCTGCAGGAGAGGAA 871
Db 1 CCCTGCAGGAGAGGAA 17
RESULT 1328
ABK18613
ID ABK18613 standard; RNA; 17 BP.
XX AC ABK18613;
XX DT 09-APR-2002 (first entry)
XX DE Human ERG G-cleaver ribozyme target sequence Seq ID No 1260.
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
XX ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
XX vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
XX tumour angiogenesis; diabetic retinopathy; macular degeneration;
XX neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
XX angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
XX Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
XX Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNAzyme; inozyme;
XX amberzyme.
XX OS Homo sapiens.
XX WO2001188124-A2.
XX PN WO2001188124-A2.
XX PD 22-NOV-2001.
XX

```

```
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX ) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
PI WPI; 2002-082995/11.
XX
DR Novel polynucleotide which down regulates expression of Ets-related gene,
XX useful for treating cancer, diabetic retinopathy, macular degeneration,
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 83; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK2719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 10 A; 1 C; 5 G; 0 T; 1 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 31 AGAGGAAAAAAAAAAGC 47
DB 1 AGAGGAAUGAAAAAGC 17
RESULT 1329
ABK18870
ID ABK18870 standard; RNA; 17 BP.
XX
XX ABK18870;
AC
XX
XX 09-APR-2002 (first entry)
DT
XX
XX Human ERG DNAzyme target sequence Seq ID No 1517.
DE
XX
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
KW amberzyme.
```

```
XX Homo sapiens.
OS
XX WO200188124-A2.
XX
XX 22-NOV-2001.
XX
XX 16-MAY-2001; 2001WO-US015866.
XX
XX 16-MAY-2000; 2000US-00572021.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX ) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Mclaughlin F, Randi AM;
PI WPI; 2002-082995/11.
XX
DR Novel polynucleotide which down regulates expression of Ets-related gene,
XX useful for treating cancer, diabetic retinopathy, macular degeneration,
XX arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 94; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK2719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 8 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 861 AGGAGAGGAGAGAGAG 877
DB 1 AGGAGAGGCAGAGAAG 17
RESULT 1330
ABK18192
ID ABK18192 standard; RNA; 17 BP.
XX
XX ABK18192;
AC
XX
XX 09-APR-2002 (first entry)
DT
XX
XX Human ERG hammerhead ribozyme target sequence, Seq ID No 839.
DE
XX Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
```

KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
KW amberyze.
XX
OS Homo sapiens.
XX
PN WO200108124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX
XX WPI; 2002-082995/11.
DR
XX
XX Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
XX Claim 4; Page 74; 149pp; English.
XX
XX The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 2 A; 12 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 273 CCAGCCCCCACCACCGG 289
DB 1 CCAGCCCCCACCACCGG 17

RESULT 1331
ABS74958
ID ABS74958 standard; DNA; 17 BP.
XX
AC ABS74958;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 273 CCAGCCCCCACCACCGG 289
DB 1 CCAGCCCCCACCACCGG 17

RESULT 1332
ABV90794/c
ID ABV90794 standard; DNA; 17 BP.
XX
AC ABV90794;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1507.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
PN EP1239051-A2.

XX 24-DEC-2002 (first entry)
DT Human PAPP-Ea associated 17-mer SEQ ID 484.
XX
DE PAPP-E; human; pregnancy associated plasma protein E; abortive;
XX contraceptive; gene therapy; vaccine; pregnancy; antenatal; diagnosis;
KW dysgenetic pregnancy; primer; ss.
KW
XX
OS Homo sapiens.
XX
PN US2002102252-A1.
XX
PD 01-AUG-2002.
XX
PF 06-APR-2001; 2001US-00827998.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PA (GUYY/) GU Y.
PA (SHAN/) SHANNON M E.
XX
XX Gu Y; Shannon ME;
XX
XX WPI; 2002-697817/75.
DR
XX
XX New isolated nucleic acid encoding an isoform of human pregnancy
PT associated plasma protein E, for preventing or aborting pregnancy.
PT
XX
XX Example 2; Page 138; 353pp; English.
XX
XX This invention describes a novel isolated nucleic acid that encodes one
CC of three new isoforms of human pregnancy associated plasma protein E,
CC hPAPP-E. The products of the invention have abortive and contraceptive
CC activity and can be used for gene therapy or in a vaccine. The nucleic
CC acid, polypeptide encoded by it, or antibody to the polypeptide can be
CC used in pharmaceutical compositions or vaccines for preventing or
CC aborting pregnancy. PAPP-E is used in the antenatal diagnosis of
CC dysgenetic pregnancies. The nucleic acids are used as probes to assess
CC the level of PAPP-E isoform mRNA in chorionic villus samples, and the
CC antibodies can be used to assess the expression levels of PAPP-E isoform
CC proteins in chorionic villus samples, to diagnose dysgenetic pregnancies
CC antenatally. This sequence represents an oligomer used in scanning the
CC human PAPP-E genes described in the disclosure of the invention
XX
SQ Sequence 17 BP; 15 A; 0 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 37 AAAAAAAAAAGCCAGAAA 53
DB 1 AAAAAAAAAAGAGAGAAA 17

RESULT 1332
ABV90794/c
ID ABV90794 standard; DNA; 17 BP.
XX
AC ABV90794;
XX
DT 23-DEC-2002 (first entry)
XX
DE Human POSHL1 scanning oligonucleotide SEQ ID NO 1507.
XX
KW Human; POSHL 1; SH3 domain; POSH-like signalling protein 1; oncogene;
KW Rho GTPase; signal transduction; gene expression; cancer; vaccine;
KW gene therapy; transgenic; ss.
XX
OS Homo sapiens.
XX
PN EP1239051-A2.

```

XX PD 11-SEP-2002.
XX PN
XX PD 28-JAN-2002; 2002EP-00001165.
XX PF
XX PD 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 23-MAY-2001; 2001US-00864761.
XX PR 10-OCT-2001; 2001US-0328205P.
XX PA (AEOM-) AEOMICA INC.
XX PI
XX PI Shannon M;
XX PD WPI; 2002-684061/74.
XX DR
XX XX Novel human SH3 domain (POSH)-like signaling protein 1 polypeptide, POSHL
XX PT -1, useful for treating disorders associated with decreased expression or
XX PT activity of human POSHL1.
XX PS
XX PS Example 2; SEQ ID NO 1507; 60pp + Sequence Listing; English.
XX XX
XX CC The invention relates to an isolated SH3 domain (POSH)-like signalling
XX CC protein 1 (POSHL 1) polypeptide (I), comprising a sequence of 730 amino
XX CC acids (S1, AB883999), a sequence having 65% sequence identity to (S1),
XX CC (S1) having 95% deviations, especially conservative substitutions or a
XX CC fragment of the sequences comprising at least 8 contiguous amino acids.
XX CC Human POSHL 1 is a proto-oncogene/oncogene product that functions as an
XX CC adaptor protein that interacts with Rho family small GTPases as well as
XX CC downstream components of the signal transduction pathway. (I) is useful
XX CC for identifying a specific binding partner. (II) and nucleic acids (II)
XX CC encoded by (I) are useful for diagnosing, monitoring disease and treating
XX CC caused by altered expression of human POSHL1 including diagnosing and
XX CC treating cancer, they are useful in the development of vaccines and (II) is
XX CC useful in gene therapy. (III) is useful for constructing microarrays which
XX CC are useful for measuring and for surveying gene expression and creating
XX CC transgenic non-human animals capable of producing the proteins. The
XX CC present sequence is that of a scanning oligonucleotide useful in examples
XX CC of the invention. Note: The present sequence did not form part of the
XX CC printed specification, but is based on sequence information supplied to
XX CC Derwent by the European Patent Office
XX SQ Sequence 17 BP; 1 A; 5 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 893 AGGTGCCCCCTGAGCCAG 909
DB 17 AGACGCCCTGAGCCAG 1

RESULT 1333
ACCS9531/c
ID ACCS9531 standard; DNA; 17 BP.
XX AC
XX AC ACCS9531;
XX XX
XX DT 08-SEP-2003 (first entry)
XX DE Human HER-2 gene PCR primer #3.
XX KW Genetic expression detection; transcriptional activity;
XX KW run-on transcription; PCR; primer; probe; ss.
XX XX
XX OS Homo sapiens.

```

```

XX PN WO2003018832-A1.
XX PD 06-MAR-2003.
XX PF
XX PR 30-AUG-2002; 2002WO-AU001182.
XX PR 31-AUG-2001; 2001US-0316308P.
XX PA (BENI-) BENITEC AUSTRALIA LTD.
XX PI Rice RN, Harrison BT;
XX DR WPI; 2003-393249/37.
XX XX
XX PT Determining the activity of a transcriptional unit(s) in a cell comprises
XX PT simultaneously or sequentially detecting and amplifying the transcripts
XX PT including nascent RNA molecules to measure the presence of a detectable
XX PT product.
XX PS Example 23; Page 78; 114pp; English.
XX XX
XX CC The present invention relates to a method of determining the activity of
XX CC a transcriptional unit(s) in a cell, which comprises simultaneously or
XX CC sequentially subjecting the population of transcripts including nascent
XX CC RNA molecules comprising one or more labeled ribonucleotides to
XX CC detection, and optionally to amplification to measure the appearance of a
XX CC detectable product. The method can be used for determining the activity
XX CC of transcriptional unit(s) in a cell, determining changes in activity of
XX CC a transcriptional unit(s) in a eukaryotic cell or cell lineage and
XX CC monitoring the transcriptional activity of genetic elements including
XX CC genes in a cell, particularly determining at a quantitative, semi-
XX CC quantitative or qualitative level the transcriptional activity of
XX CC selected genetic elements in a cell. The method may also be used to
XX CC determine the level of expression of the same gene under different
XX CC conditions and to provide a fingerprint of genetic expression and
XX CC transcriptional activity in a cell. The present sequence is an
XX CC oligonucleotide used to demonstrate the method of the invention
XX SQ Sequence 17 BP; 3 A; 10 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1357 TCAGTGTGCGGTGGGC 1373
DB 17 TCAGTGTGCGGTGGGC 1

RESULT 1334
ABQ80178/c
ID ABQ80178 standard; DNA; 17 BP.
XX AC
XX AC ABQ80178;
XX DT 13-JUN-2003 (first entry)
XX DE Variant primer DBM0195B amplifies IL4R amplicon of 413 bp for SNP #6.
XX KW Human; interleukin 4 receptor; IL4R; type 1; diabetes; allele;
XX KW insulin dependent diabetes mellitus; IDDM; myasthenia gravis; PCR;
XX KW single nucleotide polymorphism; SNP; autoimmune disease; amplif;
XX KW T helper type 1 mediated disease; rheumatoid arthritis; primer;
XX KW multiple sclerosis; inflammatory bowel disease; systemic sclerosis;
XX KW systemic lupus erythematosus; psoriasis; scleroderma; Grave's disease;
XX KW Guillain-Barre syndrome; Hashimoto's thyroiditis; ss.
XX OS Homo sapiens.
XX PN WO2003010335-A2.
XX XX
XX PD 06-FEB-2003.

```

XX PP 17-JUL-2002; 2002WO-EP007956.
XX PR 20-JUL-2001; 2001US-0306912P.
XX PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX PI Mirel DB, Erlich HA, Bugawan TL, Noble JA, Valdez AM;
XX DR WPI; 2003-248086/24.
XX XX
XX PT Determining an individual's risk for type 1 diabetes, comprises detecting
XX PT the presence of an insulin dependent diabetes mellitus-associated
XX PT interleukin 4 receptor allele in a nucleic acid sample of the individual.
XX PS Example 5; Page 39; 79pp; English.
XX XX
XX CC The sequences given in ABQ80170-78 represent primers which were used to
XX CC identify wild type and variant loci in the human interleukin 4 receptor
XX CC (IL4R). These primer sequences were used in the method of the invention
XX CC for determining an individual's risk for type 1 diabetes. The method
XX CC comprises detecting the presence of an insulin dependent diabetes
XX CC mellitus (IDDM)-associated interleukin 4 receptor allele in a nucleic
XX CC acid sample of the individual, where the presence of the allele indicates
XX CC the individual's risk for type 1 diabetes. The method identifies one or
XX CC more single nucleotide polymorphism (SNP) within the IL4R gene listed in
XX CC the specification. The method and the SNP's are useful for determining an
XX CC individual's risk for type 1 diabetes. The IL4R SNP's are also useful for
XX CC determining an individual's risk for any autoimmune disease or condition
XX CC or any T helper type 1 mediated disease, e.g. rheumatoid arthritis,
XX CC multiple sclerosis, inflammatory bowel disease, systemic lupus
XX CC erythematosus, psoriasis, scleroderma, Grave's disease, systemic
XX CC sclerosis, myasthenia gravis, Guillain-Barre syndrome, or Hashimoto's
XX CC thyroiditis
XX SQ Sequence 17 BP; 2 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 898 CCCCTGAGCCAGCTCC 914
| | | | | | | | | | | | | | | | | | | | | |
Db 17 CCCCTGAGCCAGCTCACC 1
RESULT 1335
ABT36841
ID ABT36841 standard; DNA; 17 BP.
XX AC ABT36841;
XX XX
XX DT 12-JUN-2003 (first entry)
XX DE Tumour suppression related human fukutin oligo SEQ ID No 2478.
XX KW Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; gene chip;
XX KW antisense; sense; tumour; cell degeneration; cancer; Alzheimer's disease;
XX KW schizophrenia; protein chip; gene therapy; tumour suppression;
XX KW human fukutin; ds.
XX OS Homo sapiens.
XX XX
XX FN WO2003025175-A2.
XX XX
XX PD 27-MAR-2003.
XX XX
XX PF 17-SEP-2002; 2002WO-IB004208.
XX PR 17-SEP-2001; 2001FR-00011978.
XX PA (MOLE-) MOLECULAR ENGINES LAB.

XX PI Telerman A, Amson R, Tuijnder M;
XX DR WPI; 2003-313353/30.
XX XX
XX PT New isolated nucleic acid, useful for treating viral diseases associated
XX PT with tumors and cell degeneration, also related polypeptides, antibodies
XX PT and transfected cells.
XX PS Disclosure; Page 322; 720pp; French.
XX XX
XX CC The invention relates to a novel isolated 17 mer nucleic acid sequence,
XX CC given in the specification, a sequence containing at least 15 consecutive
XX CC nucleotides from the 17 mer sequence, a sequence with, after optimal
XX CC alignment, at least 80 % identity to the 17 mer sequence, a sequence that
XX CC hybridizes to them under highly stringent conditions, or the complement
XX CC of any of them, or the corresponding RNA. The novel isolated nucleic
XX CC acids of the invention are useful as probes and primers for detecting,
XX CC identifying, quantifying and/or amplifying a nucleic acid, e.g. as one
XX CC component of a gene chip, in vitro as (anti)sense reagents, and for
XX CC production of recombinant polypeptides. Any of the nucleic acids,
XX CC polypeptides, vectors containing the nucleic acids, cells containing the
XX CC vector or antibodies directed against the polypeptides are useful for
XX CC preparation of pharmaceuticals for prevention and/or treatment of viral
XX CC diseases that are characterised by development of tumours or cell
XX CC degeneration, specifically cancer but also Alzheimer's disease and
XX CC schizophrenia. Analysis of the expression of the 17 mer nucleic acids in
XX CC patient samples is useful for diagnosis and/or prognosis of these
XX CC diseases. The polypeptides can also be used to generate antibodies, and
XX CC both the polypeptide and antibodies are useful as components of protein
XX CC chips. The nucleic acid sequences of the invention can be used in gene
XX CC therapy. This polynucleotide sequence represents a tumour suppression
XX CC related human fukutin oligonucleotide of the invention
XX SQ Sequence 17 BP; 3 A; 8 C; 3 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 263 GAGCAGCAGCTCCAGCCC 279
| | | | | | | | | | | | | | | | | | | | | |
Db 1 GATCTGCAGCTCCAGCCC 17
RESULT 1336
ACA08326/C
ID ACA08326 standard; DNA; 17 BP.
XX AC ACA08326;
XX XX
XX DT 03-JUN-2003 (first entry)
XX DE Necrosis factor kappa B (NFkB) sub-unit modulating DNzyme #95.
XX KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
XX KW G-cleaver; amberyzyme; cancer; REL-A activity; breast cancer; lung cancer;
XX KW prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
XX KW stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
XX KW head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
XX KW multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;
XX KW paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;
XX KW doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;
XX KW radiation therapy; inflammatory disease; asthma; diabetes;
XX KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
XX KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
XX KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
XX KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX OS Synthetic.
XX XX
XX FN US2002177568-A1.
XX XX

PD XX 23-MAY-2001; 2001US-00864785.
XX
XX
PR 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-00777916.
XX
XX (STIN/) STINCHOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX WPI; 2003-340953/32.
DR
XX
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
XX Claim 3; Page 48; 72pp; English.
XX
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/grft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents an enzymatic nucleic acid used to
CC modulate the function of a necrosis factor kappa B sub-unit
XX
SQ Sequence 17 BP; 9 A; 3 C; 3 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1634 TCCTTTGATGATCACT 1650
Db 17 TCGTTTGATGTTCACT 1
RESULT 1337
ADB00093
ID ADB00093 standard; DNA; 17 BP.
XX
AC ADB00093;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human MDZ3 scanning oligonucleotide SEQ ID 1079.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.

XX OS Homo sapiens.
XX
XX EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MDZ3,
PT MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1079; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC encoded at chromosome 7q22.1. MDZ4 is encoded at chromosome 6p21.3-22.2.
CC MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC 15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MDZ3,
CC MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
SQ Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 852 TGGCCCTTCAGGAGAG 868
Db 1 TGGCCCTTCAGGAGTG 17
RESULT 1338
ASZ64549/C
ID ABZ64549 standard; RNA; 17 BP.
XX
XX ABZ64549;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human HER2 DNazyme substrate #6.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX

PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
XX PA (RIBO-) RIBOZYME PHARM INC.
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 4; Page 133; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
SQ Sequence 17 BP; 1 A; 8 C; 8 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 232 CGCGGACCCCGGGGCC 248
Db 17 CGCGGCTCCCGGGGCC 1
RESULT 1339
ABZ61439
ID ABZ61439 standard; RNA; 17 BP.
XX
XX AC ABZ61439;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human H-Ras DNzyme target #230.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX
XX 06-JUN-2001; 2001US-0296249P.
XX
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 115; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX ribozymes of the invention
XX
SQ Sequence 17 BP; 0 A; 9 C; 3 G; 0 T; 5 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 64.7%; Pred. No. 8.6e+02;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 730 GCTTCTGGGCCCTCC 746
Db 1 GCUUCUGGCCCTUCC 17
RESULT 1340
ABZ61374/c
ID ABZ61374 standard; RNA; 17 BP.
XX
XX AC ABZ61374;
XX
XX 21-MAR-2003 (first entry)
XX
XX Human H-Ras DNzyme target #165.
XX
XX Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
XX Homo sapiens.
XX
XX WO200297114-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-US016840.
XX
XX 29-MAY-2001; 2001US-0294140P.
XX
XX 06-JUN-2001; 2001US-0296249P.
XX
XX 10-SEP-2001; 2001US-0318471P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
XX Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
XX Claim 58; Page 114; 185pp; English.
XX
XX The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing

CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 0 A; 6 C; 11 G; 0 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 736 GGGCCCTCCCGGCC 752
DB 17 GGGCCCCCGCGGCC 1
RESULT 1341
ID ABZ65369
XX ABZ65369 standard; RNA; 17 BP.
AC ABZ65369;
XX
DT 21-MAR-2003 (first entry)
XX
DE Human HER2 DNazyme substrate #826.
XX
KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
KW anti-rheumatic; cancer; AIDS; ss.
XX
OS Homo sapiens.
XX
PN WO200297114-A2.
XX
PD 05-DEC-2002.
XX
PF 29-MAY-2002; 2002WO-US016840.
XX
PR 29-MAY-2001; 2001US-0294140P.
PR 06-JUN-2001; 2001US-0296249P.
PR 10-SEP-2001; 2001US-0318471P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J;
XX
XX WPI; 2003-140484/13.
XX
PT Novel short interfering RNA and enzymatic nucleic acid useful for
PT treating cancer, modulates the expression of a nucleic acid encoding
PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
XX
PS Claim 4; Page 148; 185pp; English.
XX
CC The invention relates to a novel short interfering RNA (siRNA) nucleic
CC acid molecule or an enzymatic nucleic acid molecule, that modulates
CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
CC rheumatic activity. The nucleic acid molecules are useful for reducing
CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
CC also useful for treating breast, ovarian, colorectal, lung, prostate,
CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
CC ribozymes of the invention
XX
SQ Sequence 17 BP; 1 A; 8 C; 4 G; 0 T; 4 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 70.6%; Pred. No. 8.6e+02;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1151 GCTAGTGGCCACCTG 1167
DB 1 GCUACGUUGCCCCCUG 17
RESULT 1342
ACD62029
ID ACD62029 standard; RNA; 17 BP.
XX
AC ACD62029;
XX
DT 23-SEP-2003 (first entry)
XX
DE HCV minus strand DNazyme substrate sequence #340.
XX
KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; substrate; ss.
XX
OS Hepatitis C virus.
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009187.
XX
PR 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.
PR 05-DEC-2001; 2001US-0337055P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LSEP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
PI Blatt L, Macejak D, Mcswiggen J, Morrissey J, Pavco P, Lee P;
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
PT Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
PS Claim 1; Page 281; 387pp; English.
XX
CC The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNzyme or minus strand DNzyme sequences disclosed in the present
 CC invention
 XX Sequence 17 BP; 2 A; 2 C; 9 G; 0 T; 4 U; 0 Other;
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 64.7%; Pred. No. 8.6e+02;
 Matches 11; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 1005 CGGAGAGATGCTTG 1021
 DB 1 CGGAGCGAUGGUGUUG 17
 RESULT 1343
 ACD62960/c
 ID ACD62960 standard; RNA; 17 BP.
 XX AC ACD62960;
 XX DT 24-SEP-2003 (first entry)
 XX DE HCV minus strand DNzyme substrate sequence #823.
 XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX OS Hepatitis C virus.
 XX PN WO200281494-A1.
 XX PD 17-OCT-2002.
 XX PF 26-MAR-2002; 2002WO-US009187.
 XX PR 26-MAR-2001; 2001US-00817879.
 XX PR 08-JUN-2001; 2001US-00877478.
 XX PR 08-JUN-2001; 2001US-0296876P.
 XX PR 24-OCT-2001; 2001US-0335059P.
 XX PR 05-DEC-2001; 2001US-0337055P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (BLAT/) BLATT L.
 XX PA (MACE/) MACEJAK D.
 XX PA (MCSW/) MCSWIGGEN J.
 XX PA (MORR/) MORRISSEY D.
 XX PA (PVC/) PAVCO P.
 XX PA (LEEP/) LEE P.
 XX PA (DRAP/) DRAPER K.
 XX PA (ROBE/) ROBERTS E.
 XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;
 XX WPI; 2003-229207/22.
 XX Novel compound useful for treating cirrhosis, liver failure,
 PT hepatocellular carcinoma, or condition associated with hepatitis C virus
 PT infection.
 XX Claim 1; Page 289; 387pp; English.
 XX The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
 CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
 CC and enzymatic nucleic acids such as hammerhead ribozymes, DNzymes,
 CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
 CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
 CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
 CC as oligonucleotides that specifically bind the Enhancer I region of HBV
 CC DNA. The nucleic acids may be used to modulate the expression of HBV
 CC genes and HBV viral replication. Also disclosed is a method for screening
 CC compounds and/or potential therapies directed against HBV, and compounds
 CC that modulate the expression and/or replication of HCV. The compounds and
 CC methods of the invention are useful for the treatment of degenerative and
 CC disease states related to HBV and HCV infection, replication and gene
 CC expression such as cirrhosis, liver failure, and hepatocellular
 CC carcinoma. The present sequence represents a substrate for one of the HCV
 CC DNzyme or minus strand DNzyme sequences disclosed in the present
 CC invention
 XX Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;
 SQ Query Match 0.8%; Score 13.8; DB 1; Length 17;
 Best Local Similarity 88.2%; Pred. No. 8.6e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1212 GCGGGCTATGCGGAGG 1228
 DB 17 GCGGGCTATGCGAGCAGG 1
 RESULT 1344
 ACD56960
 ID ACD56960 standard; RNA; 17 BP.
 XX AC ACD56960;
 XX DT 23-SEP-2003 (first entry)
 XX DE HCV DNzyme substrate sequence #106.
 XX KW Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
 KW RNA stability; RNA expression; RNA synthesis; antisense;
 KW enzymatic nucleic acid; hammerhead ribozyme; DNzyme; inozyme; zinzyme;
 KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
 KW HBV reverse transcriptase; Enhancer I region; viral replication;
 KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
 KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
 KW virucide; antiinflammatory; substrate; ss.
 XX OS Hepatitis C virus.
 XX PN WO200281494-A1.
 XX PD 17-OCT-2002.
 XX PF 26-MAR-2002; 2002WO-US009187.
 XX PR 26-MAR-2001; 2001US-00817879.
 XX PR 08-JUN-2001; 2001US-00877478.
 XX PR 08-JUN-2001; 2001US-0296876P.
 XX PR 24-OCT-2001; 2001US-0335059P.
 XX PR 05-DEC-2001; 2001US-0337055P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (BLAT/) BLATT L.
 XX PA (MACE/) MACEJAK D.
 XX PA (MCSW/) MCSWIGGEN J.
 XX PA (MORR/) MORRISSEY D.
 XX PA (PVC/) PAVCO P.
 XX PA (LEEP/) LEE P.
 XX PA (DRAP/) DRAPER K.
 XX PA (ROBE/) ROBERTS E.
 XX PI Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
 PI Draper K, Roberts E;

```
PI Draper K, Roberts E;
XX
XX WPI; 2003-229207/22.
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Claim 1; Page 235; 387pp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, ambezymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents a substrate for one of the HCV
CC DNazyme or minus strand DNazyme sequences disclosed in the present
CC invention
XX
XX Sequence 17 BP; 2 A; 6 C; 8 G; 0 T; 1 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 8.6e+02;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 880 GAGCAGCGGCCCCAGGT 896
DB 1 GCGCAGGGGCCCCAGGU 17
RESULT 1345
ACC68140
ID ACC68140 standard; DNA; 17 BP.
XX
XX ACC68140;
XX
XX 01-JUL-2003 (first entry)
XX
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 5387.
XX
XX Cytostatic; virucide; neuroprotective; nontropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX
XX Mus musculus.
OS
XX WO2003025176-A2.
PN
XX 27-MAR-2003.
PD
XX 17-SEP-2002; 2002WO-IB004210.
PF
XX 17-SEP-2001; 2001PR-00011979.
PR
XX (MOLE-) MOLECULAR ENGINES LAB.
PA
XX Telerman A, Amson R, Tuijnder M;
PI
XX WPI; 2003-333167/31.
DR
XX
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT
```

```
PT and transfected cells.
XX
XX Disclosure; Page 660; 738pp; French.
XX
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC6806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of a
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 5 A; 4 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
Best Local Similarity 88.2%; Pred. No. 8.6e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 801 GAGCCAGAGAGCCAG 817
DB 1 GATCCAGTGAGAGCCAG 17
RESULT 1346
ADD42044
ID ADD42044 standard; DNA; 17 BP.
XX
XX ADD42044;
XX
XX 15-JAN-2004 (first entry)
XX
XX Rice acetolactate synthase related oligonucleotide 4-83-1 SEQ ID NO:25.
DE ss; rice; acetolactate synthase; ALS; pyrimidinyl carboxy herbicide;
KW herbicide-resistance; herbicide.
KW
XX Synthetic.
OS
XX WO2003083118-A1.
PN
XX 09-OCT-2003.
PD
XX 21-FEB-2003; 2003WO-JP001917.
PF
XX 29-MAR-2002; 2002JP-00095721.
PR
XX (TSUB ) KUMIAI CHEM IND CO LTD.
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.
XX
XX Kaku K, Shimizu T, Kawai K, Nagayama K, Fukuda A, Tanaka Y;
PI
XX WPI; 2003-902935/82.
DR
XX Genes of rice origin encoding pyrimidinyl carboxy herbicide resistant
PT acetolactate synthase for production of herbicide resistant strains or
PT rice and other plants.
XX
XX Example 4; SEQ ID NO 25; 96pp; Japanese.
PS
XX The invention relates to novel mutant forms of the rice acetolactate
CC synthase (ALS) gene encoding ALS resistant to pyrimidinyl carboxy
CC herbicides. Plants which may be transformed with the mutant gene include
CC rice, and also maize, barley, wheat, soya, cotton and tobacco. The mutant
CC gene may be useful in the production of herbicide-resistant plants which
CC can be cultivated in the presence of the herbicide. The present sequence
CC is used in the exemplification of the invention.
XX
XX Sequence 17 BP; 3 A; 0 C; 9 G; 5 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 17;
```

```

Best Local Similarity 88.2%; Pred. No. 8.6e+02; Mismatches 2; Indels 0; Gaps 0;
Matches 15; Conservative 0;

Qy 1011 AGATGTGTTGGGATG 1027
Db 1 AGAGGTGTTGGTGATG 17

RESULT 1347
AAT31547/c
ID AAN97167 standard; DNA; 18 BP.
XX
AC AAN97167;
XX
DT 25-MAR-2003 (revised)
DT 03-FEB-1995 (first entry)
XX
DE Mutagenic oligonucleotide TG566 to introduce SmaI restriction site.
XX
KW Transgenic animal; stable cell line; tumour cell line; polylinker;
KW human alpha-antitrypsin; Arg variant; 3'-UTR; Homo sapiens;
KW immunoglobulin light chain; promoter; ss.
XX
OS Synthetic.
XX
PN EP298807-A.
XX
PD 11-JAN-1989.
XX
PF 17-JUN-1988; 88EP-00401520.
XX
PR 19-JUN-1987; 87FR-00008623.
XX
PA (TRGE ) TRANSGENE SA.
XX
PI Skern T, Courtney M, Lecocq JP;
XX
DR WPI; 1989-009862/02.
XX
PT Stable eucaryotic cell lines for expressing specific protein - are tumour
PT or hybridoma cells derived from animals which develop from vector
PT transformed ova.
XX
PS Example 1; Fig 7; 31pp; French.
XX
CC The sequence coding for alpha-antitrypsin was fused to an Ig light chain
CC signal sequence. Part of the cloning procedure involved introducing a
CC SmaI restriction site downstream of the stop codon of the alpha-
CC antitrypsin coding region. The mutation was created using oligonucleotide
CC TG566 (AAN97167). The SV40 polyadenylation site could then be inserted
CC into the restriction site. Subsequent manipulations eventually produced
CC plasmid pTG1999, for expression of human alpha-antitrypsin (Arg358
CC variant) under the control of mouse Ig light chain regulatory sequences.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 18 BP; 3 A; 3 C; 11 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 740 CCCTCCGGGCCCCAC 756
Db 17 CCATCCGGGCCCCCTC 1

RESULT 1348
AAT31547/c
ID AAT31547 standard; DNA; 18 BP.
XX
AC AAT31547;
XX
DT 18-SEP-1996 (first entry)

```

```

XX Vaccinia virus thymidine kinase 5' primer.
DE
XX Anti-idiotype; monoclonal antibody; MAb; 3H1; CEA;
KW carcinoembryonic antigen; cancer; gene therapy; immunotherapy; vaccine;
KW genetic immunisation; vaccinia virus; thymidine kinase; PCR; primer;
KW polymerase chain reaction; ss.
XX
OS Synthetic.
XX
PN WO9620277-A2.
XX
PD 04-JUL-1996.
XX
PF 28-DEC-1995; 95WO-US017103.
XX
PR 28-DEC-1994; 94US-00365484.
XX
PA (KENT ) UNIV KENTUCKY.
XX
PI Chatterjee M, Kohler H, Chatterjee SK, Foon KA;
XX
DR WPI; 1996-321850/32.
XX
PT Recombinant monoclonal anti-idiotype antibody 3H1 sequences - used to
PT develop prods. for the detection and treatment of carcinoembryonic
PT antigen-associated diseases, partic. cancers.
XX
PS Example 4; Page 85; 121pp; English.
XX
CC A PCR primer (AAT31547) corresponds to nucleotides 22-39 of the thymidine
CC kinase (TK) gene of the wild-type WR strain of vaccinia virus. It was
CC used with a primer (AAT31548) complementary to nucleotides 708-727 of TK
CC for the PCR amplification of the TK gene. The TK gene was used in the
CC construction of a recombinant vaccinia virus vector encoding a VL or VH
CC polypeptide (see also AAR98410 and AAR98411) of monoclonal anti-idiotype
CC antibody 3H1. This was used as a vaccine to protect mice against tumour
CC challenge
XX
SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 297 TTGCCCTTCCATCTG 313
Db 17 TTGGGCTTCCATCTG 1

RESULT 1349
AAT31397/c
ID AAT31397 standard; DNA; 18 BP.
XX
AC AAT31397;
XX
DT 07-FEB-2000 (first entry)
XX
DE TK gene specific forward primer.
XX
KW Monoclonal antibody; MAb; 1A7; GD2; immune response; melanoma;
KW neuroblastoma; glioma; soft tissue carcinoma; small cell carcinoma;
KW tumor-associated antigen; TK gene; PCR primer; ss.
XX
OS Synthetic.
XX
PN US5977316-A.
XX
PD 02-NOV-1999.
XX
PF 16-JAN-1996; 96US-00591196.
XX
PR 17-JAN-1995; 95US-00372676.

```

XX (KENT) UNIV KENTUCKY.
 XX PA Foon KA, Chatterjee SK, Chatterjee M;
 XX PI WPI; 1996-354530/35.
 XX DR Monoclonal antibody 1A7 and related polynucleotide(s) and polypeptide(s)
 XX PT - useful to treat or palliate a GD2-associated disease, e.g. melanoma and
 XX PT glioma.
 XX PS Example 6; Col 56; 74pp; English.
 XX CC The invention provides a monoclonal antibody (mAb) designated 1A7, which
 CC elicits an anti-GD2 (tumor-associated antigen) immunological response in
 CC humans. MAb 1A7 has defined light and heavy chain variable region
 CC sequences. The MAb 1A7 and polypeptides can be used for eliciting an anti
 CC -GD2 immune response. The polypeptides can also be used for detecting or
 CC purifying anti-GD2 antibody. The products can be used for treating GD2 -
 CC associated diseases, e.g. melanoma, neuroblastoma, glioma, soft tissue
 CC carcinoma, and small cell carcinoma. They can be used for palliating the
 CC disease or for reducing the risk of recurrence. Sequences AA231197-100
 CC represent primers used for constructing a recombinant vaccinia vector
 CC encoding a 1A7 polypeptide fragment
 XX CC
 SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 297 TTGGCCCTTCCATCTG 313
 ||| |||||
 DB 17 TTGGCCCTTCCATCTG 1
 ||| |||||
 RESULT 1350
 AAT96696/c
 ID AAT96696 standard; DNA; 18 BP.
 XX AC AAT96696;
 XX DT 14-APR-1998 (first entry)
 XX DE Hereditary haemochromatosis gene 24d1 allele OLA oligonucleotide.
 XX KW Hereditary haemochromatosis; metal toxicity; diagnosis; gene therapy;
 XX KW prenatal screening; human; oligonucleotide ligation assay; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT misc_feature 1
 FT /*tag= a
 FT /*note= "5'-phosphorylated"
 FT 18
 FT misc_feature
 FT /*tag= a
 FT /*note= "3' digoxigenin"
 FT 1
 XX PN WO9738137-A1.
 XX PD 16-OCT-1997.
 XX PF 04-APR-1997; 97WO-US006254.
 XX PR 04-APR-1996; 96US-00630912.
 XX PR 16-APR-1996; 96US-00632673.
 XX PR 23-MAY-1996; 96US-00652265.
 XX PA (MERC-) MERCATOR GENETICS INC.
 XX Thomas WJ, Drayna DT, Feder JN, Gnirke A, Ruddy D, Tauchihashi Z;

PI Wolff RK;
 XX DR WPI; 1997-512743/47.
 XX PT Hereditary haemochromatosis gene and variants - useful for diagnosis and
 XX PT treatment of hereditary haemochromatosis disease.
 XX PS Example 1; Fig 5; 115pp; English.
 XX CC Upstream oligonucleotides 24d1.A (AAT96694) for the common allele, 24d1.B
 CC (see AAT96695) for the haemochromatosis allele, and downstream
 CC oligonucleotide 24d1.X (see AAT96696) are used in an oligonucleotide
 CC ligation assay (OLA) to detect the 24d1 mutation in the gene (see
 CC AAT96690) associated with hereditary haemochromatosis (HH). The 24d1
 CC mutation appears responsible for the majority of HH disease. It comprises
 CC a G to A substitution that is present in 86% of affected chromosomes and
 CC in 4% of unaffected chromosomes. The mutation results in a Cys to Tyr
 CC substitution in the encoded protein (see AAW36499) at a critical
 CC disulphide bridge important for secondary structure. OLA allows the
 CC differentiation between homozygous and heterozygous individuals for the
 CC 24d1 allele, and provides rapid determination of the risk of an
 CC individual developing HH
 XX CC
 SQ Sequence 18 BP; 4 A; 6 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1237 CCTGGCTGCTTCACCTG 1253
 ||||| |||||
 DB 18 CCTGGCTGCTTCACCTG 2
 ||||| |||||
 RESULT 1351
 AAV01515
 ID AAV01515 standard; DNA; 18 BP.
 XX AC AAV01515;
 XX DT 27-APR-1998 (first entry)
 XX DE Antisense primer for human SR-p70e gene.
 XX KW SR-p70; transcription factor; tumour suppressor gene; human; p53;
 XX KW homology; differential splicing; diagnosis; cancer; neuroblastoma;
 XX KW gene therapy; apoptosis; primer; PCR; amplification; ss.
 XX OS Synthetic.
 XX OS Homo sapiens.
 XX PN WO9728186-A1.
 XX PD 07-AUG-1997.
 XX PF 03-FEB-1997; 97WO-FR000214.
 XX PR 02-FEB-1996; 96FR-00001309.
 XX PA (SNFI) SANOFI SA.
 XX PI Caput D, Ferrara P, Kaghad A;
 XX DR WPI; 1997-402550/37.
 XX CC New polypeptide(s) encoded by the SR-p70 tumour suppressor gene - and
 XX PT related nucleic acid, useful for diagnosis and treatment of tumours.
 XX PS Claim 16; Page 81; 136pp; French.
 XX CC Primers AAV01514-V01515 were used to PCR amplify the gene encoding the
 CC human SR-p70e protein (AAV01503). SR-p70 are transcription factors which
 CC may control the activity of p53-regulated genes, and are expressed by

CC tumour suppressor genes related to the p53 gene family. SR-p70 sequences
CC (see AAV01496-V01505) can be used in the diagnosis and monitoring of
CC cancer, especially neuroblastoma. The nucleic acid sequences and
CC corresponding antisense sequences, are also useful in gene therapy, e.g.
CC to regulate apoptosis
XX
SQ Sequence 18 BP; 1 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 838 GCTGCTGGGGTCTCTGG 854
DB 2 GCAGCTTGGGTCTCTGG 18

RESULT 1352
AAV75622/c
ID AAX75622 standard; RNA; 18 BP.
XX
AC AAX75622;
XX
XX
DT 28-JUL-1999 (first entry)
XX
DE Mouse flt-1 VEGF receptor hairpin ribozyme substrate #81.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammarhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Mus sp.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 188; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AAX67275 to AAX75752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
SQ Sequence 18 BP; 6 A; 9 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC tumour suppressor genes related to the p53 gene family. SR-p70 sequences
CC (see AAV01496-V01505) can be used in the diagnosis and monitoring of
CC cancer, especially neuroblastoma. The nucleic acid sequences and
CC corresponding antisense sequences, are also useful in gene therapy, e.g.
CC to regulate apoptosis
XX
SQ Sequence 18 BP; 1 A; 4 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 773 GAGGTGAAGTCTGGGG 789
DB 18 GAGTTAGTCTGGGG 2

RESULT 1353
AAT85157/c
ID AAT85157 standard; cDNA; 18 BP.
XX
AC AAT85157;
XX
XX 25-MAR-2003 (revised)
DT 04-JAN-1998 (first entry)
XX
DE Vaccinia virus thymidine kinase gene forward PCR primer.
XX
KW Monoclonal antibody 11D10; anti-idiotype antibody; mucin;
KW human milk fat globule; HMPG; tumour; breast cancer; vaccine;
KW polymerase chain reaction; PCR; primer; vaccinia virus; thymidine kinase;
KW vector; ss.
XX
OS Synthetic.
XX
XX WO9722699-A2.
XX
XX 26-JUN-1997.
XX
XX 19-DEC-1996; 96WO-US020757.
XX
XX 20-DEC-1995; 95US-00575762.
XX 26-JAN-1996; 96US-00591965.
XX 13-DEC-1996; 96US-00766350.
XX
XX (KENT) UNIV KENTUCKY.
XX
XX Chatterjee M, Foon KA, Chatterjee SK;
XX WPI; 1997-341690/31.
XX
XX Monoclonal anti-idiotype antibody 11D10 - elicits immune response against
XX human milk fat globule disease associated tumours, especially breast
XX cancer.
XX
XX Example 6; Page 84; 130pp; English.
XX
XX This synthetic oligonucleotide comprises a forward PCR primer
XX corresponding to nucleotides 22-39 of the thymidine kinase (TK) gene of
XX the wild-type WR strain of vaccinia virus (GenBank J02425). It contains
XX an ApaI site. It was used with a reverse primer (see T85158) to amplify
XX the TK gene. The TK gene was incorporated into recombinant vaccinia virus
XX vectors encoding monoclonal anti-idiotype 11D10 polypeptides (see also
XX W27119-20). 11D10 elicits an immune response to human milk fat globule in
XX patients with HMPG-associated tumours such as breast cancer. (Updated on
XX 25-MAR-2003 to correct PR field.)
XX
XX Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 297 TTGCCCCCTTCATCTG 313
DB 17 TTGGCCCTTCATCTG 1

RESULT 1354
AAV12805
ID AAV12805 standard; DNA; 18 BP.
XX
XX AAV12805;
XX

DT 03-JUN-1998 (first entry)
 XX Clonotypic IgH CDR3 sequences from the joining (J) gene pool segment.
 DE Rearrangement; gene; immunoglobulin H; IgH; T cell receptor; TCR;
 XX Clonotypic rearrangement; haematopoietic cell; monitor; response;
 KW haematological cancer; multiple myeloma; Hodgkin's disease;
 KW acute lymphoblastic leukaemia; test; bone marrow; autologous transplant;
 KW detection; clonotypic cell; premalignant; autoimmune; PCR primer; ss.
 XX Homo sapiens.
 OS
 XX WO9746706-A1.
 PN
 XX 11-DEC-1997.
 PD
 XX 03-JUN-1997; 97WO-US009534.
 PF
 XX 03-JUN-1996; 96US-0019106P.
 PR
 XX (UYAL-) UNIV ALBERTA.
 PA
 XX Pilsarski LM, Belch AR, Szczepek AJ;
 PI
 XX WPI; 1998-042212/04.
 DR
 XX Detecting specific clonotypic nucleic acid rearrangement in
 XX haematopoietic cells - used to monitor treatment of haematological cancer
 PT or to screen bone marrow transplants.
 PT
 XX Example 3; Page 49; 74pp; English.
 PS
 XX V127805-22 represent clonotypic immunoglobulin H (IgH) complementarity
 CC determining region 3 (CDR3) rearrangements. The rearrangement of
 CC immunoglobulin (Ig) H genes or the rearrangement of T cell receptor (TCR)
 CC genes in a clone is called its clonotypic rearrangement. The sequences
 CC are derived from BM plasma cells of patients suffering from multiple
 CC myeloma. A novel method is described that identifies clonotypic nucleic
 CC acid rearrangements in haematopoietic cells from a patient with (or at
 CC risk of) a haematological neoplastic disease. This method comprises
 CC isolating a neoplastic haematopoietic cell containing a target clonotypic
 CC rearrangement and amplifying a specific segment of the target. The
 CC amplified product is sequenced to determine if the clonotypic
 CC rearrangement is present. The method is especially used to monitor a
 CC patients' response to treatment of haematological cancer (e.g. multiple
 CC myeloma, Hodgkin's disease or acute lymphoblastic leukaemia). The method
 CC can also be used to test bone marrow samples, including stem cells,
 CC intended for autologous transplant. Other applications include detecting
 CC clonotypic cells in premalignant and autoimmune states, identifying cell
 CC types representative of the different stages in a malignant clone and
 CC development of therapies
 XX
 SQ Sequence 18 BP; 3 A; 4 C; 6 G; 5 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 982 TACTTTGGCCAGTGTGG 998
 Db 1 TACTTTGACGAGTGGG 17
 RESULT 1355
 AAX89560/c
 ID AAX89560 standard; DNA; 18 BP.
 XX
 AC AAX89560;
 XX
 XX 06-OCT-1999 (first entry)
 DT
 XX Forward PCR primer for Thymidine kinase gene amplification.
 DE
 XX

KW PCR primer; TK; thymidine kinase; vaccinia virus; melanoma;
 XX recombinant vector; carcinoma; ss.
 OS Synthetic.
 OS Mus sp.
 XX US5935821-A.
 PN
 XX 10-AUG-1999.
 PD
 XX 21-NOV-1996; 96US-00752844.
 PF
 XX 17-JAN-1995; 95US-00372676.
 PR
 XX 16-JAN-1996; 96US-00591196.
 XX
 PA (KENT) UNIV KENTUCKY.
 XX Chatterjee SK, Foon KA, Chatterjee M;
 PI
 XX WPI; 1999-457600/38.
 DR
 XX Anti-GD2 immunological peptides useful for the treatment of tumors
 PT especially melanomas and small cell carcinomas.
 XX
 PS Example 6; Col 59; 84pp; English.
 XX
 CC The sequence is the forward PCR primer for the amplification of the
 CC vaccinia virus TK (thymidine kinase) gene. The sequence corresponds to
 CC nucleotides 22-39 of the TK sequence. The reverse primer AAX89561
 CC corresponds to nucleotides 727-708 of the TK gene. The amplified sequence
 CC is used in the construction of a recombinant vaccinia vector encoding a
 CC 1A7 polypeptide fragment. The 1A7 antibody can be used to produce an anti
 CC -GD2 T cell or antibody response. The 1A7 peptides and antibodies may be
 CC useful for the modulation of ganglioside GD2, and particularly for the
 CC treatment of GD2-associated tumours e.g. melanoma, neuroblastoma, glioma,
 CC soft tissue sarcoma, and small cell carcinoma (including small cell lung
 CC cancer)
 XX
 SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 297 TTGCCCCCTTCATCTG 313
 Db 17 TTGGCCCTTCATCTG 1
 RESULT 1356
 AAX06978
 ID AAX06978 standard; DNA; 18 BP.
 XX
 AC AAX06978;
 XX
 XX 10-MAY-1999 (first entry)
 DT
 XX Secretory peptide-9 (Zsig9) antisense primer.
 DE
 XX Secretory peptide-9; Zsig9; human; tumour marker; cancer; therapy;
 KW diagnosis; growth enhancer; PCR; primer; ss.
 KW
 XX Synthetic.
 OS Homo sapiens.
 OS
 XX WO9901554-A1.
 PN
 XX 14-JAN-1999.
 PD
 XX 02-JUL-1998; 98WO-US013859.
 PF
 XX 03-JUL-1997; 97US-0051704P.
 PR
 XX 03-JUL-1997; 97US-0088088.
 PR

PR 19-MAY-1998; 98US-00081338.
 PR 19-MAY-1998; 98US-0085983P.
 PR 17-JUN-1998; 98US-00099005.
 PR 17-JUN-1998; 98US-0089899P.
 XX
 PA (ZYMO) ZYMOGENETICS INC.
 XX
 PI Sheppard PO, Jelinek LJ, Jaspers SR, Whitmore TE;
 XX
 DR WPI; 1999-106055/09.
 XX
 PT New mammalian secretory peptide-9 (Zsig9) - used as a growth enhancer for
 PT placenta, liver and heart, and as an indicator of cancer.
 XX
 PS Example 4; Page 72; 85pp; English.
 XX
 CC This antisense primer, and a sense primer (see AAX06977), were used in a
 CC PCR designed to determine the chromosomal assignment of Zsig9 (see
 CC AAX06968), a gene encoding new secretory peptide-9 (see AAW88469). Zsig9
 CC was mapped to chromosome 12. The invention provides polynucleotides (see
 CC AAX06968-70) encoding Zsig9 polypeptides (see AAW88469-77). Zsig9 can
 CC used as a growth enhancer for placenta, liver and heart, and as an
 CC indicator of cancer. Antisense nucleotides derived from Zsig9 cDNA, and
 CC anti-Zsig9 antibodies, can be used to inhibit the growth of tumour cells
 CC that express Zsig9
 XX
 SQ Sequence 18 BP; 4 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1570 ACCGTCACCACTGACTG 1586
 Db 2 ACCTCCACCACTGACTG 18
 RESULT 1357
 AAX08679
 ID AAX08679 standard; DNA; 18 BP.
 XX
 AC AAX08679;
 XX
 DT 27-SEP-1999 (first entry)
 XX
 DE Oligonucleotide derived from pinene synthase.
 XX
 KW Myrcene synthase; limonene synthase; pinene synthase; flavour;
 KW monoterpene synthase; aroma; defense; plant seed; oil; meal; primer; PCR;
 KW ss.
 XX
 XX Synthetic.
 OS
 XX WO9902030-A1.
 PN
 XX 21-JAN-1999.
 PD
 XX 10-JUL-1998; 98WO-US014528.
 PF
 XX 11-JUL-1997; 97US-0052249P.
 PR
 XX (UNIW) UNIV WASHINGTON STATE RES FOUND.
 PA
 XX Bohlmann J, Steele CL, Croteau RB;
 PI
 XX WPI; 1999-120396/10.
 DR
 DR P-PSDB; AAW85714.
 XX
 XX New isolated gymnosperm monoterpene synthase DNA - obtained from Grand
 PT fir (Abies grandis), used to provide plants with modified production of
 PT monoterpenes, e.g. myrcene, limonene or pinene.
 XX
 PS Example 11; Page 116; 121pp; English.

XX Nucleotide sequences encoding myrcene synthase, limonene synthase and
 CC pinene synthase from Grand fir may be incorporated into any organism
 CC (e.g. intact plant, animal, microbe), or derived cell culture that
 CC produces geranyl diphosphate for the production of the aforementioned
 CC enzymes or their products. The sequences when expressed in transfected
 CC cells may also be used for the production or modification of flavour and
 CC aroma properties, improvement of defense capability, and the alteration
 CC of other ecological interactions mediated by myrcene, limonene, pinene,
 CC or their derivatives. In particular they can be used for the production
 CC of plant seeds for the extraction of oil or meal. Peptides derived from
 CC conserved regions of the synthase sequences can be used to create
 CC degenerate primers which can be used for screening/amplification
 XX
 SQ Sequence 18 BP; 2 A; 10 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 749 GCCCCCACCTTCTCTC 765
 Db 1 GCCACCACCTTCTCTC 17
 RESULT 1358
 AAZ08292
 ID AAZ08292 standard; DNA; 18 BP.
 XX
 AC AAZ08292;
 XX
 DT 07-FEB-2000 (first entry)
 XX
 DE Antisense PCR primer used for mapping of human Zsig9 gene.
 XX
 KW Secretory protein-9; Human Zsig9; antisense PCR primer; mapping;
 KW chromosomal assignment; chromosome 12q15 region; ss.
 XX
 OS Synthetic.
 XX
 XX WO9960405-A1.
 PN
 XX 25-NOV-1999.
 PD
 XX 19-MAY-1999; 99WO-US011107.
 PF
 XX 19-MAY-1998; 98US-00081183.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 PA
 XX Moore EE, Taft DW;
 PI
 XX WPI; 2000-039447/03.
 DR
 XX Detecting tumors using antibodies, antagonists and antisense nucleotides
 PT to secretory protein-9 (Zsig9).
 XX
 PS Example 4; Page 33; 45pp; English.
 XX
 CC The present DNA sequence is the antisense PCR primer, that is used for
 CC the chromosomal assignment and placement of Zsig9 gene. The gene was
 CC mapped to chromosome 12q15 region, on the integrated LDB chromosome 12
 CC map
 XX
 SQ Sequence 18 BP; 4 A; 8 C; 2 G; 4 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1570 ACCGTCACCACTGACTG 1586
 Db 2 ACCTCCACCACTGACTG 18

```

RESULT 1359
AAZ30195
ID AAZ30195 standard; DNA; 18 BP.
XX
XX AAZ30195;
AC
XX
XX 11-FEB-2000 (first entry)
DT
XX
XX PCR primer Mkl7 used to amplify the mvk gene 5' adjacent region.
DE
XX
XX mvk gene; mevalonate kinase; mevalonate pathway; carotenogenic yeast;
KW isopentenyl pyrophosphate; farnesyl pyrophosphate; isoprenoid;
KW carotenoid; astaxanthin; cancer; antioxidant; colouring reagent;
KW farmed fish industry; PCR primer; ss.
XX
XX Synthetic.
OS
XX Xanthophyllomyces dendrorhous.
OS
XX
XX BP955363-A2.
PN
XX
XX 10-NOV-1999.
PD
XX
XX 26-APR-1999; 99EP-00107413.
PF
XX
XX 06-MAY-1998; 98EP-00108210.
PR
XX
XX (HOFF ) HOFFMANN LA ROCHE & CO AG F.
PA
XX
XX Hoshino T, Ojima K, Setoguchi Y;
PI
XX
XX WPI; 2000-001086/01.
DR
XX
XX Isolated DNA sequences encoding enzymes, useful for the production of
PT isoprenoids and carotenoids.
PT
XX
XX Example 10; Page 15; 58pp; English.
PS
XX
XX PCR primers AAZ30195-96 were used to amplify the mvk gene 5' adjacent
CC region. The mvk gene encodes a mevalonate kinase enzyme. The enzyme is
CC involved in the mevalonate pathway in the carotenogenic yeast Phaffia
CC rhodozyma. The specification also describes enzymes that are involved in
CC the pathway from isopentenyl pyrophosphate to farnesyl pyrophosphate. The
CC enzymes of the invention are used in the production of isoprenoids and
CC carotenoids, especially astaxanthin. Astaxanthin is useful for the
CC pharmaceutical industry, to protect cells against cancer as it has a
CC strong antioxidant property. Astaxanthin is also useful as a colouring
CC reagent in the farmed fish industry, e.g. salmon
XX
XX Sequence 18 BP; 10 A; 0 C; 8 G; 0 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 28 GGAAGAGGAAAAA 44
DB 1 GGAAGAGGAGAGAAA 17
RESULT 1360
AAAZ2592
ID AAA92592 standard; DNA; 18 BP.
XX
XX AAA92592;
AC
XX
XX 04-JAN-2001 (first entry)
DT
XX
XX Antisense oligonucleotide ISIS# 30411.
DE
XX
XX Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;
KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
KW

```

```

XX
OS Synthetic.
XX
XX US6107092-A.
PN
XX
XX 22-AUG-2000.
PD
XX
XX 29-MAR-1999; 99US-00280409.
PF
XX
XX 29-MAR-1999; 99US-00280409.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX
XX Cowser LM, Bennett CF, O'malley BW;
PI
XX
XX WPI; 2000-586211/55.
DR
XX
XX Antisense compounds targeted to steroid receptor RNA activator useful for
PT diagnosis, prophylaxis and treatment of diseases associated with the
PT steroid activator, such as infection, inflammation or tumor formation.
XX
XX Claim 3; Col 42; 47pp; English.
PS
XX
XX The present sequence is one of a large number of antisense
CC oligonucleotides which is directed against one of four human steroid
CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
CC antisense oligonucleotides were synthesised. The first series comprised 8
CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second
CC series comprised chimeric oligonucleotides composed of a central gap
CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
CC sides by four-nucleotide wings. The wings were composed of 2'-
CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
CC nucleotide sequences. The antisense compounds are useful for research,
CC diagnosis, treatment and prophylaxis to prevent or delay infection,
CC inflammation or tumour formation. Therapeutically the oligonucleotides
CC are highly safe and are effectively administered to humans
XX
XX Sequence 18 BP; 5 A; 5 C; 6 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 768 AGGCCGAGGTCAAGTCT 784
DB 1 AGGCCGAGGAGAGTCT 17
RESULT 1361
AAA92513
ID AAA92513 standard; DNA; 18 BP.
XX
XX AAA92513;
AC
XX
XX 04-JAN-2001 (first entry)
DT
XX
XX Antisense oligonucleotide ISIS# 30180.
DE
XX
XX Human; SRA; steroid receptor RNA activator; cytostatic; antiinflammatory;
KW SRA inhibitor; cancer; infection; antisense oligonucleotide; ss.
XX
XX Synthetic.
OS
XX
XX US6107092-A.
PN
XX
XX 22-AUG-2000.
PD
XX
XX 29-MAR-1999; 99US-00280409.
PF
XX
XX 29-MAR-1999; 99US-00280409.
PR
XX
XX (ISIS-) ISIS PHARM INC.
PA

```


PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX Cowser LM, Bennett CF, O'malley BW;
 XX WPI; 2000-586211/55.
 XX Antisense compounds targeted to steroid receptor RNA activator useful for
 PT diagnosis, prophylaxis and treatment of diseases associated with the
 PT steroid activator, such as infection, inflammation or tumor formation.
 XX
 PS Claim 3; Col 40; 47pp; English.
 XX
 CC The present sequence is one of a large number of antisense
 CC oligonucleotides which is directed against one of four human steroid
 CC receptor RNA activator (SRA) nucleic acid sequences. Two series of
 CC antisense oligonucleotides were synthesised. The first series comprised 8
 CC -30 oligodeoxynucleotides with a phosphorothioate backbone. The second
 CC series comprised chimeric oligonucleotides composed of a central gap
 CC region, consisting of ten 2'-deoxynucleotides, which was flanked on both
 CC sides by four-nucleotide wings. The wings were composed of 2'-
 CC methoxyethyl (2'-MOE) nucleotides. Both series contained the same
 CC nucleotide sequences. The antisense compounds are useful for research,
 CC diagnosis, treatment and prophylaxis to prevent or delay infection,
 CC inflammation or tumour formation. Therapeutically the oligonucleotides
 CC are highly safe and are effectively administered to humans
 XX
 SQ Sequence 18 BP; 5 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 768 AGGCCGAGGTGAAGTCT 784
 Db 2 AGGCCGAGGAGTCT 18
 RESULT 1362
 AAH27102
 ID AAH27102 standard; DNA; 18 BP.
 XX
 AC AAH27102;
 XX
 DT 06-AUG-2001 (first entry)
 XX
 DE Heltest4 cleavage fragment.
 XX
 KW Cleavage structure; target sequence detection; flap endonuclease; FEN;
 KW Heltest4; ss.
 XX
 OS Synthetic.
 XX
 PN WO200132922-A2.
 XX
 PD 10-MAY-2001.
 XX
 XX 27-OCT-2000; 2000WO-US029663.
 PF
 XX 29-OCT-1999; 99US-00430692.
 PR
 XX (STRA-) STRATAGENE.
 PA
 PI Sorge JA;
 XX
 XX WPI; 2001-328805/34.
 DR
 XX The labelling of nucleic acids for their detection and quantification
 PT comprises the formation of a cleavage structure and its cleavage with a
 PT five' exonuclease-1 or flap endonuclease-1.
 XX
 XX Example 3; Page 22; 81pp; English.
 PS
 XX This invention relates to a method for generating a signal indicative of

CC the presence of a target nucleic acid sequence in a sample. The method
 CC comprises the formation of a cleavage structure through the incubation of
 CC a sample comprising a target nucleic acid sequence and a nucleic acid
 CC polymerase and cleaving the cleavage structure with a 5' exonuclease-1 or
 CC flap endonuclease (FEN) to generate the signal. The method is used for
 CC the detection and quantification of a target nucleic acid sequence. The
 CC present sequence represents a fragment of oligonucleotide Heltest4, which
 CC is used in an assay to evaluate the activity of a FEN endonuclease. This
 CC sequence is the fragment of Heltest4 which is cleaved off by FEN
 XX
 SQ Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAAAAAA 1752
 Db 1 AAAAAAAAAAAAAAAAAA 17
 RESULT 1363
 AAH62882
 ID AAH62882 standard; DNA; 18 BP.
 XX
 AC AAH62882;
 XX
 XX 06-AUG-2003 (revised)
 DT
 DT 11-SEP-2001 (first entry)
 XX
 DE Shrimp white spot Bacilliform virus (WSBV) oligonucleotide 43.
 XX
 KW Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
 KW antiviral agent; gene expression; antisense construct; probe; primer;
 KW transgenic viral resistant shrimp; ss.
 XX
 OS Shrimp white spot syndrome virus.
 XX
 PN WO200138351-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 08-NOV-2000; 2000WO-US028888.
 XX
 XX 24-NOV-1999; 99CN-00124717.
 PR
 XX (PENY-) PE CORP NY.
 PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
 PA (SINO-) SINOGENOMAX CO LTD.
 XX
 PI Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
 XX
 XX WPI; 2001-355877/37.
 DR
 XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
 PT (WSBV), useful for producing viral polypeptides that can be used to
 PT screen for agents that are useful for treating WSBV infection.
 XX
 PS Disclosure; Fig 3; 626pp; English.
 XX
 CC The invention provides the primary nucleotide sequence of the WSBV genome
 CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
 CC encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
 CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
 CC molecules and proteins of the invention are useful for diagnosis and
 CC monitoring viral infection, in screens for antiviral agents and for
 CC monitoring viral gene expression or activity during a treatment regimen.
 CC The nucleic acid molecules are also useful as antisense constructs to
 CC control viral gene expression in infected cells and tissues and to create
 CC transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 18 BP; 5 A; 8 C; 4 G; 1 T; 0 U; 0 Other;

```
Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 380 TACTCAGCAGCAGGCGAG 396
DB 1 TACCCAGCAGCAGGCGAG 17

RESULT 1364
AAAF73407
ID AAF73407 standard; DNA; 18 BP.
XX AC
XX AAF73407;
XX 30-APR-2001 (first entry)
DE Grand fir monoterpene synthase conserved coding sequence SEQ ID NO: 60.
XX KW Monoterpene synthase; grand fir; cancer; (-)-camphene synthase;
XX KW myrcene synthase; (-)-limonene synthase; (-)-pinene synthase;
XX KW terpinolene synthase; insect resistance; nutrition; ss.
XX OS Abies grandis.
XX PN WO200107565-A2.
XX PD 01-FEB-2001.
XX PF 24-JUL-2000; 2000WO-US020264.
XX PR 26-JUL-1999; 99US-00360545.
XX PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX PI Steele CL, Bohlmann J, Croteau RB, Phillips MA;
XX DR WPI; 2001-182782/18.
XX PT New nucleic acid encoding monoterpene synthases, for increasing terpene
XX PT synthesis in plants, e.g. for increasing resistance to pests or for
XX PT treatment of cancer.
XX PS Example 10; Page 146; 175pp; English.
XX CC The present invention provides the protein and coding sequences of
XX CC monoterpene synthases from the grand fir. These include (-)-camphene
XX CC synthase, (-)-beta-phellandrene synthase, terpinolene synthase, (-)-
XX CC limonene/(-)-alpha-pinene synthase, limonene synthase, myrcene synthase
XX CC and pinene synthase. The sequences can be used to produce transgenic
XX CC plants expressing high levels of the enzymes, resulting in levels which
XX CC are useful in protecting against and treating cancers, and to confer
XX CC insect resistance on plants
XX SQ Sequence 18 BP; 2 A; 10 C; 2 G; 4 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 749 GCCCCACCTTCTCTCTC 765
DB 1 GCCACCACCTTCTCTCTC 17

RESULT 1365
AAH45239/C
ID AAH45239 standard; DNA; 18 BP.
XX AC AAH45239;
XX 06-SEP-2001 (first entry)
DE
```

```
XX DE Human fibronectin PCR primer #2.
XX KW Human; fibronectin; cytostatic; metastasis inhibition; cancer;
XX KW actin-based cytoskeleton; melanoma; PCR primer; ss.
XX OS Homo sapiens.
XX PN WO200141815-A2.
XX PD 14-JUN-2001.
XX PF 11-DEC-2000; 2000WO-US033631.
XX PR 10-DEC-1999; 99US-0170233P.
XX PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX PA (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX PA (DAND ) DANA FARBER CANCER INST INC.
XX PI Clark EA, Golub TR, Hynes RO, Lander ES;
XX DR WPI; 2001-381502/40.
XX PT Inhibiting metastasis in humans by administering an agent which inhibits
XX PT activity of genes which function in regulation of tumor cell metastasis,
XX PT particularly genes which alter actin-based cytoskeleton of tumor cells.
XX PS Example; Page 26; 48pp; English.
XX CC The invention relates to a method for inhibiting metastasis in a mammal.
XX CC The method comprises administering an agent which alters the actin-based
XX CC cytoskeleton of one or more tumour cells in the mammal. It is useful for
XX CC inhibiting metastatic conditions, such as melanoma and ovarian, prostate,
XX CC lung, bone, throat, brain, testicular, liver, stomach and pancreatic
XX CC cancer. The present sequence is a primer used to clone human fibronectin
XX CC in an example illustrating the invention. The fibronectin gene is one of
XX CC a group of genes whose activity may be inhibited by the agent of the
XX CC invention
XX SQ Sequence 18 BP; 8 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1010 AAGATGCTGTTGGGAT 1026
DB 17 AAGATTTGCTTTGGGAT 1

RESULT 1366
ABK72460
ID ABK72460 standard; DNA; 18 BP.
XX AC ABK72460;
XX DT 13-AUG-2002 (first entry)
XX DE Sample originonucleotide #22 for analysing nucleic acid base sequence.
XX KW Nucleic acid base sequence analysis; DNA diagnosis; probe; ss.
XX OS Synthetic.
XX PN WO200233068-A1.
XX PD 25-APR-2002.
XX PF 18-OCT-2000; 2000WO-JP007244.
XX PR 18-OCT-2000; 2000WO-JP007244.
XX
```

PA (CANO) CANON KK.
XX Yamamoto N, Okamoto T, Suzuki T;
XX WPI; 2002-372310/40.
XX
XX Screening an unknown base sequence at a defined site of a target single-
PT stranded nucleic acid for use in DNA diagnosis and therapy, comprises a
PT DNA chip, fluorescence yield and pattern-based method.
XX
XX Example 1; Page 13; 53pp; Japanese.
XX
XX The present invention relates to a method of analysing an unknown nucleic
CC acid base sequence. The method comprises preparing a probe array,
CC hybridising with the probe array, measuring the fluorescence yield in the
CC reaction, obtaining a template pattern, producing a sample pattern, and
CC comparing the sample pattern with the template pattern. The method is
CC useful for specifying an unknown base sequence at a defined site of a
CC target single-stranded nucleic acid, which is useful for analysing a
CC nucleic acid base sequence. The method is applicable in DNA diagnosis and
CC therapy, and is useful in medicine and biology. Measuring the
CC fluorescence yield allows the detection of a one-base mismatch which can
CC be considered to produce high detection accuracy. The hybrid pattern of
CC the DNA probe is used so the difference in thermostability is less
CC important, and the judgement on each spot can be reliably carried out.
CC ABK72439-ABK72502 represent sample orignucleotides used in the present
CC invention
XX
XX Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
SQ

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 482 ATGGGGGTCGGGTCAT 498
Db 2 ATGGGGGTCGGGTCAT 18

RESULT 1367
ABLS4126
ID ABL54126 standard; DNA; 18 BP.
XX
XX ABL54126;
XX
XX 12-JUL-2002 (first entry)
XX
XX Cleavage product of FEN nuclease template Heltest4.
XX
XX FEN; endonuclease; nuclease; template; Heltest4; nucleic acid detection;
KW ss.
XX
XX Synthetic.
OS
XX US6350580-B1.
PN
XX 26-FEB-2002.
PD
XX 11-OCT-2000; 2000US-00686179.
PF
XX 11-OCT-2000; 2000US-00686179.
PR
XX (STRA-) STRATAGENE.
PA
XX Sorage JA;
PI
XX WPI; 2002-380832/41.
XX
XX Detecting a target nucleic acid in a polymerase chain reaction process
PT comprises forming a cleavage structure by incubating with a probe having
PT secondary structure that changes upon binding and cleaving with a
PT nuclease to release a fragment.
XX

PS Example 6; Col 66; 62pp; English.
XX
XX The present sequence is the 18-nucleotide cleavage product of FEN
CC nuclease template 1 oligonucleotide, Heltest4 (see ABL54126), which was
CC used in a method for determining FEN endonuclease activity. Heltest4
CC binds to M13 to produce a complementary double-stranded domain and a non-
CC complementary 5' overhang. This duplex forms template 2. Template 3 has
CC an additional primer, FENAS (see ABL54127), bound to M13 and is directly
CC adjacent to Heltest4. In the presence of template 3, FENAS binds the free
CC 5' terminus of Heltest4, migrates to the junction and cleaves Heltest4 to
CC produce the present 18-nucleotide fragment. FEN nuclease is preferred for
CC use in the method of the invention, which relates to generating a signal
CC to detect the presence of a target nucleic acid in a sample. In this
CC method, a nucleic acid is treated with a probe that has a secondary
CC structure which changes upon binding of the probe to a target nucleic
CC acid sequence, and a nuclease. The invention also provides a process for
CC detecting or measuring a nucleic acid that allows for concurrent
CC amplification, cleavage and detection of a target nucleic acid sequence
CC in a sample
XX
XX Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
SQ

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Oy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1368
ABN99768
ID ABN99768 standard; DNA; 18 BP.
XX
XX ABN99768;
AC
XX 20-AUG-2002 (first entry)
XX
XX DNA probe #22 for use in an oligonucleotide array.
XX
XX Human; probe; array; oligonucleotide detection; ss.
XX
XX Synthetic.
OS
XX JP2002065274-A.
PN
XX 05-MAR-2002.
PD
XX 31-AUG-2000; 2000JP-00263395.
PF
XX 31-AUG-2000; 2000JP-00263395.
PR
XX (CANO) CANON KK.
PA
XX WPI; 2002-474199/51.
DR
XX
XX Detection of an object component in a sample using an oligonucleotide as
PT detecting probe.
XX
XX Example 3; Page 19; 25pp; Japanese.
XX
XX The invention relates to a novel method for detecting a complex formed
CC between a probe and its complement. The method is used for detecting a
CC complex formed between an oligonucleotide of known base sequence and a
CC complementary probe, and for evaluating if the sequence is contained in
CC liquid samples, or the level of binding by using the oligonucleotide as
CC the detecting probe. The sequence represents a probe used in the
CC invention
XX
XX Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
SQ

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Query Match

```

Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGCTCGGGTTCAT 498
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 1369
ABL54922
ID ABL54922 standard; DNA; 18 BP.
XX
AC ABL54922;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human tumour suppressor gene p53 probe #22.
XX
KW Human; p53; probe; variation detection; DNA array; ss.
XX
OS Homo sapiens.
XX
PN EP1184467-A2.
XX
PD 06-MAR-2002.
XX
PF 31-AUG-2001; 2001EP-00307415.
XX
PR 31-AUG-2000; 2000JP-00263396.
XX
PA (CANO ) CANON KK.
XX
PI Yamamoto N, Okamoto T, Tanaka S, Suzuki T;
XX
DR WPI; 2002-271043/32.
XX
PT Screening for gene variation by using DNA array in which probes giving
PT strong signals forming hybrids with normal sequence, and probes having
PT sequences expected to form hybrids with variants are separately arranged.
XX
PS Example 2; Page 6; 22pp; English.
XX
CC The sequence represents a two-base mismatch probe designed to detect a
CC variation a specific base in the p53 gene sequence. The invention relates
CC to a novel method for screening for a variation in a nucleic acid
CC sequence. The method involves using a DNA array in which a group of
CC probes which will give strong signals forming hybrids with a normal gene
CC sequence, and a group of probes having sequences expected to form hybrids
CC with gene variants are separately arranged. The method is useful for
CC screening for the presence or absence of variation in a nucleic acid
CC sequence. The method is also useful for mass screening to determine
CC rapidly the presence or absence of a gene variation without need of an
CC expensive apparatus and a complex analysis
XX
SQ Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGCTCGGGTTCAT 498
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 1370
ABT04715
ID ABT04715 standard; DNA; 18 BP.
XX
AC ABT04715;
XX
DT 27-SEP-2002 (first entry)
XX
XX

```

```

DE End-labelled probe array production method-related oligonucleotide 22.
XX
KW End-labelled probe array production; probe; ss; target substance capture.
XX
OS Unidentified.
XX
PN JP2002153284-A.
XX
PD 28-MAY-2002.
XX
PF 24-NOV-2000; 2000JP-00357446.
XX
PR 24-NOV-2000; 2000JP-00357446.
XX
PA (CANO ) CANON KK.
XX
DR WPI; 2002-552742/59.
XX
PT Preparation of an end-labelled probe array, for capturing a target
PT substance.
XX
PS Example 1; Page 5; 25pp; Japanese.
XX
CC The invention comprises a method for the synthesis of an end-labelled
CC probe array - in which part of a probe for capturing a target substance
CC is fixed at a plural of the matrix sites on the surface of a probe array
CC substrate. In the method of the invention the units for constituting the
CC probe are combined successively and, at the final stage of the successive
CC synthesis, a labelling substance is combined to the end of the probe and
CC extended to a desired chain length. The method of the invention is useful
CC for the production of a probe array. The present DNA sequence represents
CC an oligonucleotide that was used in an example of the invention
XX
SQ Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGCTCGGGTTCAT 498
Db 2 ATGGGGCTCGGGTTCAT 18

RESULT 1371
ABK43380
ID ABK43380 standard; DNA; 18 BP.
XX
AC ABK43380;
XX
DT 05-JUN-2002 (first entry)
XX
DE Siglec-BMS, PCR primer #5.
XX
KW Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;
KW immune system disease; leukaemia; allergy; inflammatory disease;
KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;
KW psoriasis; rheumatoid arthritis; conjunctivitis; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200208257-A2.
XX
PD 31-JAN-2002.
XX
PF 20-JUL-2001; 2001WO-US023082.
XX
PR 21-JUL-2000; 2000US-0220139P.
XX
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
PI Longphre M, Chang H, Whitney G;
XX

```

DR WPI; 2002-241565/29.

XX Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein

PT molecules useful for treating immune system diseases such as asthma,

PT leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

XX Example 2; Page 69; 209pp; English.

XX The invention relates to an isolated SIGLEC (sialic acid-binding Ig-

CC related lectin) protein (I). Pharmaceutical compositions comprising (I)

CC are useful for treating immune system diseases such as asthma, leukaemia

CC or other allergic or inflammatory diseases. Extracellular domains of (I)

CC represent potential markers for screening, diagnosis, prognosis, follow-

CC up assays, and imaging methods. (I) is useful as a target for drugs which

CC inhibit inflammation, tissue damage and remodeling in asthma, and

CC inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's

CC disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is

CC also useful for monitoring the course of disease or disorders, and for

CC identifying agents that bind with and/or modulate the biological activity

CC of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are

CC useful in diagnosis and/or prognosis methods, and to detect the presence

CC and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS

CC proteins in a biological sample. (II) are useful as nucleic acid probes

CC are useful for screening genomic library to isolate a genomic clone of

CC SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting

CC diseases or disorders associated with SIGLEC-BMS transcripts or proteins.

CC The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells

CC expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

CC ABK43360-ABK43411 represent human SIGLEC coding sequences and PCR primers

CC of the invention

XX Sequence 18 BP; 0 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 8.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 CTTCTGGGCCCCCTCCG 747

DB 1 CTGCTGGGCCCCCTCTG 17

RESULT 1372

ABK43392

ID ABK43392 standard; DNA; 18 BP.

XX AC ABK43392;

XX 05-JUN-2002 (first entry)

DE Siglec-BMS, PCR primer #17.

XX Human; sialic acid-binding Ig-related lectin; SIGLEC; asthma;

KW immune system disease; leukaemia; allergy; inflammatory disease;

KW tissue damage; allergic rhinitis; osteoarthritis; Crohn's disease;

XX psoriasis; rheumatoid arthritis; conjunctivitis; primer; ss.

OS Homo sapiens.

XX WO200208257-A2.

PN 31-JAN-2002.

XX 20-JUL-2001; 2001WO-US023082.

PF 21-JUL-2000; 2000US-0220139P.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Longphre M, Chang H, Whitney G;

PI WPI; 2002-241565/29.

XX

PT Novel isolated SIGLEC (sialic acid-binding Ig-related lectin) protein

PT molecules useful for treating immune system diseases such as asthma,

XX leukemia, allergic rhinitis, psoriasis, conjunctivitis, Crohn's disease.

XX Example 4; Page 73; 209pp; English.

XX The invention relates to an isolated SIGLEC (sialic acid-binding Ig-

CC related lectin) protein (I). Pharmaceutical compositions comprising (I)

CC are useful for treating immune system diseases such as asthma, leukaemia

CC or other allergic or inflammatory diseases. Extracellular domains of (I)

CC represent potential markers for screening, diagnosis, prognosis, follow-

CC up assays, and imaging methods. (I) is useful as a target for drugs which

CC inhibit inflammation, tissue damage and remodeling in asthma, and

CC inflammatory diseases such as allergic rhinitis, osteoarthritis, Crohn's

CC disease, psoriasis, rheumatoid arthritis, conjunctivitis, etc. (I) is

CC also useful for monitoring the course of disease or disorders, and for

CC identifying agents that bind with and/or modulate the biological activity

CC of SIGLEC-BMS proteins. The nucleic acid molecules (II) encoding (I) are

CC useful in diagnosis and/or prognosis methods, and to detect the presence

CC and/or amount of SIGLEC-BMS nucleotide sequences and/or SIGLEC-BMS

CC proteins in a biological sample. (II) are useful as nucleic acid probes

CC are useful for screening genomic library to isolate a genomic clone of

CC SIGLEC gene. SIGLEC-BMS gene copy number is determined for detecting

CC diseases or disorders associated with SIGLEC-BMS transcripts or proteins.

CC The SIGLEC-BMS antibodies are also used to detect, sort or isolate cells

CC expressing SIGLEC-BMS proteins and in diagnostic imaging technology.

CC ABK43360-ABK43411 represent human SIGLEC coding sequences and PCR primers

CC of the invention

XX Sequence 18 BP; 0 A; 9 C; 5 G; 4 T; 0 U; 0 Other;

SQ Query Match 0.8%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 8.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 731 CTTCTGGGCCCCCTCCG 747

DB 1 CTGCTGGGCCCCCTCTG 17

RESULT 1373

ABQ78689

ID ABQ78689 standard; DNA; 18 BP.

XX AC ABQ78689;

XX 05-DEC-2002 (first entry)

DE Cleavage product of Heitest4 after cleavage with FEN nuclease.

XX hairpin probe; safety pin probe; assay; nucleic acid detection;

KW FEN nuclease; ss.

XX Synthetic.

XX US2002102591-A1.

PN 01-AUG-2002.

XX 17-OCT-2001; 2001US-00981621.

PF 11-OCT-2000; 2000US-00686179.

PR (SORG/) SORGE J A.

PA SORGE JA;

XX WPI; 2002-682018/73.

XX Generating a signal indicating presence of a target nucleic acid, for use

PT in a polymerase chain reaction, comprises incubating target nucleic acid

PT with a probe to form a cleavage structure that is cleaved with nuclease.

XX

PS Example 6; Page 37; 62pp; English.

XX The present sequence represents the cleavage product of an oligonucleotide

CC used to test FEN nuclease activity. FEN nucleases are used in the course

CC of the invention. The specification describes a method for generating a

CC signal indicative of the presence of a target nucleic acid sequence in a

CC sample. The method comprises forming a cleavage structure comprising

CC duplex and single-stranded nucleic acid, by incubating the target nucleic

CC acid sequence with a probe having a secondary structure that changes upon

CC binding of the probe to the target nucleic acid sequence, and cleaving

CC the cleavable structure with a nuclease to release a nucleic acid

CC fragment. The method is useful for generating a signal indicative of the

CC presence of target nucleic acid sequence in a sample. It is useful in a

CC polymerase chain reaction (PCR)-based assay or non-PCR based assay for

CC detecting naturally occurring target nucleic acid sequences in a solution

CC including RNA and DNA that is isolated and purified from cells, tissues,

CC single cell organisms, bacteria or viruses, and for detecting synthetic

CC targets in solution, including RNA or DNA oligonucleotides, and peptide

XX nucleic acids

SQ Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 8.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAAAAAA 1752

DB 1 AAAAAAAAAAAAAAAAAA 17

RESULT 1374

ABL59657

ID ABL59657 standard; DNA; 18 BP.

XX ABL59657;

XX 18-JUL-2002 (first entry)

DE Oligonucleotide probe SEQ ID NO:22.

XX Simultaneous determination; probe; ss.

XX Synthetic.

XX JP2002065299-A.

XX 05-MAR-2002.

XX 31-AUG-2000; 2000JP-00263505.

XX 31-AUG-2000; 2000JP-00263505.

XX (CANO) CANON KK.

XX WPI; 2002-398978/43.

XX Simultaneous testing of the reactivity of a sample with other different

PT samples, comprises applying to the two samples to a substrate comprising

PT divided matrices.

XX Example 1; Page 11; 24pp; Japanese.

XX The present invention describes a method for determining simultaneously

CC the reactivity of a first sample with other samples, in which the second

CC to the 2 plus nth (n is not less than 1) samples having different

CC properties are arranged independently on a substrate, on whose surface

CC the first sample is already present, and the reactivities between the

CC first sample and each of the second to the 2 plus n-th samples are

CC determined. Also described is a tissue sample matrix in which several

CC samples from different sources are present on each matrix divided on a

CC substrate. The method is used for determining simultaneously the

CC reactivity of a first sample with several other differing samples.

CC ABL59636 to ABL59701 represent oligonucleotide probes used in an example

CC from the present invention

SQ Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 8.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498

DB 2 ATGGGGGTCGGGGTCAT 18

RESULT 1375

ABT06236

ID ABT06236 standard; DNA; 18 BP.

XX ABT06236;

XX 24-OCT-2002 (first entry)

DE Synthetic DNA selling system - related oligonucleotide 41.

XX Synthetic DNA selling system; internet; ss; purchase order menu;

KW major histocompatibility complex; MHC.

XX Synthetic.

XX JP2002074089-A.

XX 12-MAR-2002.

XX 29-AUG-2000; 2000JP-00259715.

XX 29-AUG-2000; 2000JP-00259715.

XX (CANO) CANON KK.

XX WPI; 2002-492955/53.

XX Synthetic DNA selling system using the Internet, displays purchase order

PT menu to orderer's terminal and initiates production of selected DNA for

PT the successful bidder.

XX Disclosure; Fig 5; 22pp; Japanese.

XX The invention comprises a synthetic DNA selling system using the

CC internet. The system displays a purchase order menu display, with the

CC number of base sequences of DNA from which the orderer selects a DNA. The

CC order information is transmitted to a successful bidder side server which

CC orders for production and delivery of selected synthetic DNA. The system

CC of the invention is useful for marketing synthetic DNAs of different base

CC sequences and concentrations according to the desire of the user,

CC especially genes concerned with human major histocompatibility complex

CC (MHC). Oligonucleotides ABT06196 - ABT06278 are used in the invention

XX Sequence 18 BP; 2 A; 3 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;

Best Local Similarity 88.2%; Pred. No. 8.9e+02;

Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 482 ATGGGGGTCGGGGTCAT 498

DB 2 ATGGGGGTCGGGGTCAT 18

RESULT 1376

ABK87302

ID ABK87302 standard; DNA; 18 BP.

XX ABK87302;

AC ABK87302;

```

XX DT 24-SEP-2002 (first entry)
XX DE FEN 1 nuclease cleavage product.
XX KW ss; nucleic acid detection; FEN nuclease.
XX OS Synthetic.
XX PN WO200244326-A2.
XX PD 06-JUN-2002.
XX PF 26-NOV-2001; 2001WO-US044215.
XX PR 30-NOV-2000; 2000US-00728574.
XX PA (STRA-) STRATAGENE.
XX PI Sorge JA, Whalen AM;
XX DR WPI; 2002-508503/54.
XX
XX Detecting/measuring target nucleic acid, by forming cleavage structure by
XX incubating target nucleic acid with probe having binding moiety, cleaving
XX structure to release nucleic acid and detecting released fragments.
XX
XX Disclosure; Page 38; 157pp; English.
XX
XX This invention relates to a novel method for detecting/measuring a target
XX nucleic acid. The method comprises forming a cleavage structure by
XX incubating the target sequence with a probe comprising a binding moiety
XX and a secondary structure that changes upon binding of the probe to the
XX target, cleaving the cleavage structure to release a nucleic acid
XX fragment, and detecting and/or measuring the fragment captured by binding
XX of the binding moiety to a capture element on a solid support. The method
XX of the invention is useful for detecting or measuring a target nucleic
XX acid and are useful for generating a signal indicative of the presence of
XX the target nucleic acid in a sample. Another method of the invention is
XX useful for simultaneously forming a cleavage structure, amplifying the
XX target nucleic acid in a sample and cleaving the cleavage structure. The
XX method does not require multiple steps, subsequent amplification process,
XX and allows for concurrent amplification and detection of target nucleic
XX acid in a sample. The present sequence represents a cleavage product
XX generated by FEN 1 nuclease shown in an example of the method of the
XX invention
XX
XX Sequence 18 BP; 15 A; 0 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAAAAAA 1752
Db 1 AAAAAATAATAAAAAAAAAA 17
RESULT 1377
ADA14814/C
ID ADA14814 standard; DNA; 18 BP.
XX AC ADA14814;
XX
XX 06-NOV-2003 (first entry)
XX DE Vaccinia virus TK gene PCR primer #1.
XX
XX ss; PCR; ganglioside GD2-associated tumour; melanoma; antibody;
XX anti-idiotype; monoclonal antibody; 1A7; neuroblastoma; glioma; sarcoma;
XX small cell lung cancer; primer.
XX OS Vaccinia virus.

```

```

XX PN US6509016-B1.
XX PD 21-JAN-2003.
XX PF 15-APR-1999; 99US-00293533.
XX PR 17-JAN-1995; 95US-00372676.
XX PR 16-JAN-1996; 96US-00591196.
XX PR 21-NOV-1996; 96US-00752844.
XX PA (KENT ) UNIV KENTUCKY.
XX
XX Chatterjee M, Foon KA, Chatterjee SK;
XX WPI; 2003-401117/38.
XX
XX Delaying recurrence and/or development of ganglioside GD2-associated
XX tumor in individual, by administering antibody containing light and heavy
XX chain variable region sequences contained in sequence of specified amino
XX acids.
XX
XX Example 6; Col 59; 82pp; English.
XX
XX The invention relates to the recurrence and/or development of a
XX ganglioside GD2-associated tumour, e.g. melanoma, in an individual which
XX is delayed by administration of an antibody comprising light and heavy
XX chain variable region sequences of the anti-idiotype monoclonal antibody
XX 1A7. The antibody is used for delaying recurrence and/or development of
XX GD2-associated tumour, e.g. melanoma, neuroblastoma, glioma, sarcoma, or
XX small cell lung cancer, in individual, and for treating individual with
XX GD2-associated tumour. The present sequence is a PCR primer used to clone
XX vaccinia virus sequences in order to construct an expression vector for
XX the cDNA encoding the anti-idiotype antibody 1A7.
XX
XX Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.8; DB 1; Length 18;
Best Local Similarity 88.2%; Pred. No. 8.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 297 TTGCCCCCTTCCATCTG 313
Db 17 TTGGGCCCCCTCCATCTG 1
RESULT 1378
ABZ59705
ID ABZ59706 standard; DNA; 18 BP.
XX AC ABZ59706;
XX DT 04-APR-2003 (first entry)
XX
XX Humanin-like protein related DNA fragment # SEQ ID 8.
XX
XX Humanin; neuroprotective; cerebroprotective; cytostatic; immunomodulator;
XX antimetabolic; cardiant; gene therapy; neurodegenerative disease; cancer;
XX brain dysfunction; immune disease; infection; digestive disease;
XX circulatory disease; endocrine disease; cell death; ds.
XX OS Homo sapiens.
XX PN WO2002103018-A1.
XX PD 27-DEC-2002.
XX PF 14-JUN-2002; 2002WO-JP005941.
XX PR 15-JUN-2001; 2001JP-00182275.
XX PR 01-AUG-2001; 2001JP-00233532.
XX PA (TAKE ) TAKEDA CHEM IND LTD.

```


CC polynucleotide consisting of a variable region encoding sequence
 CC appearing as ADC35321 - ADC35370, a host cell comprising the
 CC polynucleotide, a fusion polypeptide comprising IA7, a humanised antibody
 CC comprising 5 consecutive amino acids from the IA7 variable regions and a
 CC vaccine comprising the antibodies. The antibodies are useful for
 CC eliciting an immune response in an individual, and for treating a GD2-
 CC associated disease in an individual. The GD2-associated diseases is
 CC chosen from melanoma, neuroblastoma, glioma, soft tissue sarcoma, and
 CC small cell carcinoma. The individual has a clinically detectable tumour,
 CC and the method is for palliating the GD2-associated disease. IA7 is
 CC preferably useful for treating a tumour that was previously detected in
 CC the individual and has been treated and is clinically undetectable at the
 CC time of the administering of IA7, or for reducing the risk of recurrence
 CC of a clinically detectable tumour. IA7 and the humanised antibody are
 CC useful for detecting the presence of an anti-GD2 antibody bound to a
 CC tumour cell. The present sequence represents a PCR primer used in the
 CC construction of a vaccinia virus vector expressing the light or heavy
 CC chain variable regions of monoclonal antibody IA7.

XX
 SQ Sequence 18 BP; 6 A; 5 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 297 TTGGCCCTTCATCTG 313
 Db 17 TTGGCCCTTCATCTG 1

RESULT 1381
 ADE15136/C
 ID ADE15136 standard; DNA; 18 BP.

AC ADE15136;

DT 29-JAN-2004 (first entry)

DE Beer spoilage-associated primer SEQ ID 331.

ss: primer; detection: beer-spoilage; lactic acid bacteria;
 Gram-negative bacteria; spoilage bacteria.

OS Lactobacillus perolens.

PN WO2002103043-A2.

PD 27-DEC-2002.

PP 19-JUN-2002; 2002WO-EP006808.

PR 19-JUN-2001; 2001DE-01029410.

PA (VERM-) VERMICON AG.

PI Beinfuhr C, Snaidr J;

DR WPI; 2003-175243/17.

XX New oligonucleotides, useful for rapid detection of beer-spoilage
 PT bacteria by in situ hybridization, are specific for type, genus or
 PT species.

PS Claim 1; SEQ ID NO 331; 88bp; German.

XX This invention describes novel oligonucleotides used in a method for
 CC detecting beer-spoilage bacteria in a sample. The bacteria detected
 CC include lactic acid bacteria of the genera *Lactobacillus* or *Pediococcus*,
 CC especially the species *L. coryniformis*, *L. perolens*, *L. buchneri*, *L.*
 CC *plantarum*, *L. fructivorans*, *L. lindneri*, *L. casei*, *L. brevis* or *P.*
 CC *damosus* or Gram-negative bacteria of the genera *Pectinatus* and
 CC *Megasphaera*, specifically *P. irisingensis*, *P. cerevisiophilus* and *M.*
 CC *cerevisiae*. The oligonucleotides of the invention provide rapid detection

CC of spoilage bacteria (typically within 48 hours, compared with 7-12 days
 CC for conventional culture methods), can detect all relevant bacteria in
 CC parallel, can differentiate between species of the same genus, and are
 CC easy to use. ADE14806-ADE15247 represent the oligonucleotides used in the
 CC method of the invention.

XX Sequence 18 BP; 7 A; 7 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.8; DB 1; Length 18;
 Best Local Similarity 88.2%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1357 TCAGTGTCCGTGGGC 1373
 Db 18 TCAGTGTCCGTGGTC 2

RESULT 1382

AAD32456

ID AAD32456 standard; DNA; 15 BP.

AC AAD32456;

DT 18-JUN-2002 (first entry)

DE Human ORIG1 gene polymorphism detecting ASO probe #13.

XX Human; olfactory receptor family 1 subfamily G member 1; ORIG1; therapy;

KW polymorphism; drug screening; olfactory sensory deficit; gene therapy;

OS Homo sapiens.

PN WO200212561-A2.

PD 14-FEB-2002.

PP 03-AUG-2001; 2001WO-US024478.

PR 03-AUG-2000; 2000US-0222755P.

PA (GENA-) GENAISSANCE PHARM INC.

PI Kazemi A, Messer C, Tanguay DA;

PN WPI; 2002-269097/31.

XX Novel isolated human olfactory receptor, family 1, subfamily G, member 1
 PT polynucleotide, for therapeutic purposes, for studying expression and
 PT function of the polynucleotide and for expressing receptor protein.

PS Claim 16; Page 13; 96pp; English.

XX The present invention relates to an isolated human olfactory receptor,
 CC family 1, subfamily G, member 1, (ORIG1) polynucleotide comprising a
 CC sequence which is a polymorphic variant for a reference sequence for the
 CC ORIG1 gene or its fragment, or a polymorphic variant of a reference
 CC sequence for a ORIG1 cDNA or its fragment. ORIG1 is useful in studying
 CC the expression and function of ORIG1 and in expressing ORIG1 protein for
 CC use in screening for candidate drugs to treat diseases related to ORIG1
 CC activity. ORIG1 is useful for therapeutic purposes. The invention is
 CC useful for studying expression of the ORIG1 isogenes in vivo, for in vivo
 CC screening and testing of drugs targeted against ORIG1 protein, and for
 CC testing the efficacy of therapeutic agents and compounds for olfactory
 CC sensory deficits, in a biological system. The invention is useful in gene
 CC therapy and is located on the . The present sequence is human ORIG1 gene
 CC polymorphism detecting ASO (allele specific oligonucleotide) probe

XX Sequence 15 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 1 Other;

Query Match 0.8%; Score 13.6; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 8.4e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY 1149 CTGCTACGTGGCCA 1162
Db 2 CTGCTAYGTGGCCA 15

RESULT 1383
ABN87920/C
ID ABN87920 standard; DNA; 15 BP.
XX
AC ABN87920;
DT 12-AUG-2002 (first entry)
XX
DE Human GSR allele specific oligonucleotide primer SEQ ID NO:39.
XX
KW Human; glutathione reductase; GSR; enzyme; haemolytic anaemia; SNP;
KW gene therapy; antianaemic; polymorphic; single nucleotide polymorphism;
KW primer; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 14 /*tag= a
FT /note= "polymorphic base"
XX
PN WO200242320-A2.
XX
PD 30-MAY-2002.
XX
PF 13-NOV-2001; 2001WO-US046473.
XX
PR 10-NOV-2000; 2000US-0247202P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Bieglecki KM, Sanchis A, Sausker EA, Sun X;
XX
WPI; 2002-471719/50.
XX
DR
XX
PT New genetic variants of Glutathione reductase isogenes, useful for
PT improving efficiency and reliability in drug development for treating
PT hemolytic anemia.
XX
PS Claim 14; Page 14; 137pp; English.
XX
CC The present invention describes genetic variants of the human glutathione
CC reductase (GSR) gene (I). (I) has antianaemic activity and can be used in
CC gene therapy. (I) can be used in screening for drugs targeting (I) that
CC are useful for treating haemolytic anaemia. Methods from the present
CC invention can be used; for improving the efficiency and reliability of
CC several steps in the discovery and development of drugs for treating
CC diseases associated with GSR activity; for haplotyping, which is also
CC used by the pharmaceutical research scientist to validate GSR as a
CC candidate target for treating a specific condition or disease predicted
CC to be associated with GSR activity, e.g. haemolytic anaemia, and in the
CC design of clinical trials for treating a specific condition of disease
CC associated with GSR activity; and for screening compounds targeting GSR.
CC (I) is useful in studying the expression and function of GSR, and in
CC expressing GSR protein for use in screening for candidate drugs to treat
CC diseases related to GSR activity. (I) is also useful in studying the
CC effect of the variation on the biological activity of GSR as well as on
CC the binding affinity of candidate drugs targeting GSR for the treatment
CC of haemolytic anaemia. The present sequence represents an allele specific
CC oligonucleotide (ASO) primer for the human GSR gene, which is given in
CC the exemplification of the present invention. N.B. The polymorphic base
CC (showing a single nucleotide polymorphism) in the ASO primer is shown
CC using an IUPAC ambiguity code (as given in the present invention)
XX
SQ Sequence 15 BP; 1 A; 0 C; 0 G; 13 T; 0 U; 1 Other;

Query Match 0.8%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.4e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1020 TGGGGATGGGGCTG 1033
Db 14 YGGGGATGGGGCTG 1

RESULT 1385
AAD25688/C
ID AAD25688 standard; DNA; 15 BP.
XX
AC AAD25688;

Best Local Similarity 92.9%; Pred. No. 8.4e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1749
Db 14 WAAAAAAAAAAAAA 1

RESULT 1384
ABK92606/C
ID ABK92606 standard; DNA; 15 BP.
XX
AC ABK92606;
DT 20-AUG-2002 (first entry)
XX
DE ASO primer #4 to detect human ADORA3 gene polymorphisms.
XX
KW Human; single nucleotide polymorphism; SNP; ADORA3; haplotyping;
KW chromosome 1p21-p13; adenosine A3 receptor; genotyping;
KW pathophysiological heart condition; myocardial ischaemia;
KW chronic heart failure; allele-specific oligonucleotide; ASO; primer; ss.
XX
OS Homo sapiens.
XX
PN WO200236610-A2.
XX
PD 10-MAY-2002.
XX
PF 31-OCT-2001; 2001WO-US045718.
XX
PR 31-OCT-2000; 2000US-0244626P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Gilson CR, Kazemi A, Koshy B, Monroe G;
XX
WPI; 2002-489998/52.
XX
DR
XX
PT Novel genetic variants of the adenosine A3 receptor, useful
PT therapeutically and in screening for drugs to treat diseases related to
PT ADORA3 activity e.g., myocardial ischemia and chronic heart failure.
XX
PS Claim 15; Page 14; 82pp; English.
XX
CC The present invention relates to novel single nucleotide polymorphisms
CC (SNPs) in the human adenosine A3 receptor (ADORA3) gene located on
CC chromosome 1p21-p13, and methods for haplotyping and/or genotyping the
CC ADORA3 gene. The methods of the invention make use of allele-specific
CC oligonucleotides (ASOs) as probes and primers and/or primer-extension
CC oligonucleotides for detecting the ADORA3 gene polymorphisms. The
CC polynucleotides and screened compounds are useful for the treatment of
CC diseases associated with ADORA3 activity, such as pathophysiological
CC conditions of the heart e.g. myocardial ischaemia and chronic heart
CC failure. ABK92603-ABK92628 represent ASO primers for detecting human
CC ADORA3 gene polymorphisms
XX
SQ Sequence 15 BP; 2 A; 10 C; 1 G; 1 T; 0 U; 1 Other;

Query Match 0.8%; Score 13.6; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 8.4e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

XX 26-MAR-2002 (first entry)
 XX Human CDK4 gene polymorphism detecting ASO primer #12.
 DE
 XX
 XX Human; cyclin-dependent kinase 4; CDK4; chromosome 12q13; therapy;
 KW cancer; melanoma; protein synthesis disorder; drug screening; primer;
 KW ASO; allele-specific oligonucleotide; ss.
 XX
 XX Homo sapiens.
 XX
 XX WO200190115-A2.
 PN
 XX
 XX 29-NOV-2001.
 PD
 XX
 XX 18-MAY-2001; 2001WO-US016350.
 PF
 XX
 XX 19-MAY-2000; 2000US-0205867P.
 PR
 XX
 XX (GENA-) GENAISANCE PHARM INC.
 PA
 XX
 XX Duda AE, Kazemi A, Koshiy B, Sausker EA;
 PI
 XX
 XX WPI; 2002-083072/11.
 DR
 XX
 XX New genetic variants comprising haplotypes of the cyclin-dependent kinase
 PT 4 (CDK4) gene, useful in improving the efficiency drug screening
 PT protocols for compounds targeting CDK4.
 PT
 XX
 XX Claim 16; Page 13; 58pp; English.
 PS
 XX
 XX The invention relates to an isolated polynucleotide comprising fragments
 CC and haplotypes of the cyclin-dependent kinase 4 (CDK4) gene. Human CDK4
 CC gene is located on chromosome 12q13 and contains 8 exons. The haplotypes
 CC and polymorphisms of CDK4 gene are useful for validating whether CDK4 is
 CC a suitable target for drugs to treat cancer, melanoma and disorders
 CC associated with impaired protein synthesis in cells, screening for such
 CC drugs and reducing bias in clinical trials of such drugs. Haplotype
 CC information would be useful in improving the efficiency and output of
 CC several steps in the drug discovery and development process, including
 CC target validation, identifying lead compounds, early phase clinical
 CC trials. The methods are useful in screening for compounds targeting CDK4
 CC to treat a specific condition or disease predicted to be associated with
 CC CDK4 activity. The present sequence is a ASO primer used for detecting
 CC human CDK4 gene polymorphism
 XX
 XX Sequence 15 BP; 3 A; 4 C; 4 G; 3 T; 0 U; 1 Other;
 SQ
 Query Match 0.8%; Score 13.6; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 8.4e+02;
 Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 909 GCCTCCAGGATG 922
 Db :|||||
 14 RCCTCCAGGATG 1
 RESULT 1386
 AAX56927
 ID AAX56927 standard; DNA; 15 BP.
 XX
 XX AAX56927;
 AC
 XX
 XX 16-OCT-2003 (revised)
 DT
 XX 15-JUL-1999 (first entry)
 DT
 XX HIV-1 proviral DNA fragment 10.
 DE
 XX DNA-targeting conjugate; anticancer drug; viral DNA-cleaving agent;
 KW viral DNA-binding agent; solid support; primer; ss.
 KW
 XX Human immunodeficiency virus 1.
 OS
 XX

PN WO9531434-A1.
 XX
 XX 23-NOV-1995.
 PD
 XX
 XX 12-MAY-1995; 95WO-US006379.
 PF
 XX
 XX 13-MAY-1994; 94US-00242664.
 PR
 XX
 XX (SLOK) SLOAN KETTERING INST CANCER RES.
 PA (ZWBI-) ZW BIOMEDICAL RES AG.
 XX
 XX Watanabe KA, Ren W, Weil R;
 PI
 XX
 XX WPI; 1996-010846/01.
 DR
 XX
 XX Derivatised solid supports and reagents for oligonucleotide synthesis -
 PT and new oligo-nucleotide phosphoramidate conjugates.
 PT
 XX
 XX Disclosure; Page 44; 68pp; English.
 PS
 XX
 XX This invention describes novel derivatised solid supports of formula S'-L
 CC -Z-CH₂CH₂-R, where: S' = a solid support; L = a bond or an (in)organic
 CC linker; Z = SO₂ or S-S; R = OH, an H-phosphonate, alkanephosphonate,
 CC phosphotriester, phosphite triester, phosphite diester, phosphorothioate,
 CC phosphorodithioate, phosphoramidate or phosphoramidite group, OR1, SR1,
 CC an optionally substituted or modified nucleotide (N'), or an
 CC oligonucleotide of formula (N')GR₂; G = 1-200; R₁ = a protecting group;
 CC R₂ = an H-phosphonate, alkanephosphonate, phosphotriester, phosphite
 CC triester, phosphite diester, phosphorothioate, phosphorodithioate,
 CC phosphoramidate or phosphoramidite group, OH, OR1, SR1 or
 CC OP(OCH₂CH₂CN)OCH₂CH₂CH₂OR1. Also mentioned are compounds of formula
 CC R₃CH₂CH₂CH₂CH₂OR1, where: R₃ = a protecting group; and R₄ = OH or an H-
 CC phosphonate, alkanephosphonate, phosphotriester, phosphite triester,
 CC phosphite diester, phosphorothioate, phosphorodithioate, phosphoramidate
 CC or phosphoramidite group. Also claimed are new phosphoramidates, a
 CC process for preparing an oligonucleotide 5'-phosphate, a process for
 CC preparing a solid support useful for preparation of an oligonucleotide 3'-
 CC phosphate, a process for preparing an oligonucleotide 3'-phosphate and a
 CC process for preparing an oligonucleotide 3',5'-diphosphate. The
 CC oligonucleotide 3'- and/or 5'-phosphates may be used to prepare DNA-
 CC targeting conjugates, e.g. with anticancer drugs or viral (e.g. HIV) DNA-
 CC cleaving or -binding agents. The process for preparing oligonucleotide
 CC 3',5'-diphosphates is simple and suitable for use in automatic DNA
 CC synthesizers. This sequence represents a fragment of the HIV-1 provirus
 CC genome, used to describe the method of the invention. (Updated on 16-OCT-
 CC 2003 to standardise OS field)
 XX
 XX Sequence 15 BP; 6 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
 SQ
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 864 AAGAGGAGGAGGAGG 878
 Db :|||||
 1 AAGAGGAGGAGGAGG 15
 RESULT 1387
 AAT86603
 ID AAT86603 standard; DNA; 15 BP.
 XX
 XX AAT86603;
 AC
 XX
 XX 04-JUN-1998 (first entry)
 DT
 XX
 XX Oligonucleotide separated by capillary affinity gel electrophoresis.
 DE
 XX Capillary affinity gel electrophoresis; separation; polymer-gel;
 KW polyacrylamide; ss.
 KW
 XX Synthetic.
 OS
 XX

XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX Example 7; Page 45; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 XX antisenesc oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 XX inhibiting or reducing growth factor mediated cell proliferation,
 XX inflammation and/or other disorders. The present sequence is an
 XX oligonucleotide which can be used to design the antisenesc
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
 XX F45161). The method is useful for ameliorating the effects of psoriasis,
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 XX hyperneovascular condition such as a neovascular condition of the retina,
 XX brain or skin, growth factor-mediated malignancies, other sclerotic
 XX disease, kidney disease, hyperproliferation of the inside of blood
 XX vessels or any other hyperplasia
 XX Sequence 15 BP; 0 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
 XX Query Match 0.8%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 255 GCGCCGCGGAGCAGC 269
 Db 15 GCGCCGCGGAGCAGC 1
 RESULT 1390
 AAF49276
 ID AAF49276 standard; DNA; 15 BP.
 XX AAF49276;
 XX 30-MAR-2001 (first entry)
 XX IGF-1 oligonucleotide #236.
 XX Antisenesc therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 XX hyperneovascular condition; hyperplasia; kidney disease;
 XX neovascular condition of the retina; ss.
 XX Homo sapiens.
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.

XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or
 XX inflammation.
 XX Example 8; Page 62; 201pp; English.
 XX The present invention relates to a method for ameliorating the effects of
 XX skin disorders. The method comprises contacting the skin with an
 XX antisenesc oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 XX receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 XX inhibiting or reducing growth factor mediated cell proliferation,
 XX inflammation and/or other disorders. The present sequence is an
 XX oligonucleotide which can be used to design the antisenesc
 XX oligonucleotides of the present invention (see AAF45151 and AAF45153-
 XX F45161). The method is useful for ameliorating the effects of psoriasis,
 XX ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 XX neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 XX hyperneovascular condition such as a neovascular condition of the retina,
 XX brain or skin, growth factor-mediated malignancies, other sclerotic
 XX disease, kidney disease, hyperproliferation of the inside of blood
 XX vessels or any other hyperplasia
 XX Sequence 15 BP; 3 A; 5 C; 5 G; 2 T; 0 U; 0 Other;
 XX Query Match 0.8%; Score 13.4; DB 1; Length 15;
 XX Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 762 TCTCCAGCGCGAGG 776
 Db 1 TCTCCAGCGCGAGG 15
 RESULT 1391
 AAF45532/C
 ID AAF45532 standard; DNA; 15 BP.
 XX AAF45532;
 XX 30-MAR-2001 (first entry)
 XX IGFBP2 oligonucleotide #371.
 XX Antisenesc therapy; antiproliferative; antiinflammatory; antipsoriatic;
 XX cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 XX skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 XX IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 XX growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 XX keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 XX hyperneovascular condition; hyperplasia; kidney disease;
 XX neovascular condition of the retina; ss.
 XX Homo sapiens.
 XX WO200078341-A1.
 XX 28-DEC-2000.
 XX 21-JUN-2000; 2000WO-AU000693.
 XX 21-JUN-1999; 99US-0140345P.
 XX (MURD-) MURDOCH CHILDRENS RES INST.
 XX Wraight CJ, Werther GA, Edmondson SR;
 XX WPI; 2001-041421/05.
 XX Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 XX UV (ultra-violet) treatment (optional) and an antisenesc nucleic acid that
 XX inhibits or reduces growth factor mediated cell proliferation and/or

```

PT inflammation.
XX
PS Example 6; Page 36; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
SQ Sequence 15 BP; 0 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 188 AGCAGCGCGAGCCCG 202
Db 15 AGCAGCGCGAGCCCG 1

RESULT 1392
AAF46883/c
ID AAF46883 standard; DNA; 15 BP.
XX
AC AAF46883;
XX
DT 30-MAR-2001 (first entry)
DE IGFBP3 oligonucleotide #303.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 46; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation,
CC inflammation and/or other disorders. The present sequence is an
CC oligonucleotide which can be used to design the antisense
CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
CC F45161). The method is useful for ameliorating the effects of psoriasis,
CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
CC hyperneovascular condition such as a neovascular condition of the retina,
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
XX vessels or any other hyperplasia
SQ Sequence 15 BP; 0 A; 5 C; 7 G; 3 T; 0 U; 0 Other;

Query Match      0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 188 AGCAGCGCGAGCCCG 202
Db 15 AGCAGCGCGAGCCCG 1

RESULT 1392
AAF46883/c
ID AAF46883 standard; DNA; 15 BP.
XX
AC AAF46883;
XX
DT 30-MAR-2001 (first entry)
DE IGFBP3 oligonucleotide #303.
XX
KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
KW skin disorder; Insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
KW hyperneovascular condition; hyperplasia; kidney disease;
KW neovascular condition of the retina; ss.
XX
OS Homo sapiens.
XX
PN WO200078341-A1.
XX
PD 28-DEC-2000.
XX
PF 21-JUN-2000; 2000WO-AU000693.
XX
PR 21-JUN-1999; 99US-0140345P.
XX
PA (MURD-) MURDOCH CHILDRENS RES INST.
XX
PI Wright CJ, Werther GA, Edmondson SR;
XX
DR WPI; 2001-041421/05.
XX
PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
PT inhibits or reduces growth factor mediated cell proliferation and/or
PT inflammation.
XX
PS Example 7; Page 46; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
CC inhibiting or reducing growth factor mediated cell proliferation and/or
CC inflammation.
XX
PS Example 7; Page 45; 201pp; English.
XX
CC The present invention relates to a method for ameliorating the effects of
CC skin disorders. The method comprises contacting the skin with an
CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of

```

CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 0 A; 7 C; 6 G; 2 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 254 CGCCCGGAGCAG 268
 DB 15 CGCCCGGAGCAG 1

RESULT 1394
 AAF46738/C
 ID AAF46738 standard; DNA; 15 BP.
 XX
 AC AAF46738;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP3 oligonucleotide #158.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 7; Page 45; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX

CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX
 SQ Sequence 15 BP; 0 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 257 CCCGCGGAGCAGC 271
 DB 15 CCCGCGGAGCAGC 1

RESULT 1395
 AAF46739/C
 ID AAF46739 standard; DNA; 15 BP.
 XX
 AC AAF46739;
 XX
 DT 30-MAR-2001 (first entry)
 XX
 DE IGFBP3 oligonucleotide #159.
 XX
 KW Antisense therapy; antiproliferative; antiinflammatory; antipsoriatic;
 KW cytostatic; dermatological; cardiant; virucide; ophthalmological; keloid;
 KW skin disorder; insulin-like Growth Factor 1 receptor; IGF-1; pityriasis;
 KW IGF binding protein; IGFBP-2; IGFBP3; inflammation; psoriasis; pilaris;
 KW growth factor mediated cell proliferation; ichthyosis; serborrhea; ruba;
 KW keratosis; neoplasia; scleroderma; wart; skin cancer; sclerotic disease;
 KW hyperneovascular condition; hyperplasia; kidney disease;
 KW neovascular condition of the retina; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200078341-A1.
 XX
 PD 28-DEC-2000.
 XX
 PF 21-JUN-2000; 2000WO-AU000693.
 XX
 PR 21-JUN-1999; 99US-0140345P.
 XX
 PA (MURD-) MURDOCH CHILDRENS RES INST.
 XX
 PI Wright CJ, Werther GA, Edmondson SR;
 XX
 DR WPI; 2001-041421/05.
 XX
 PT Ameliorating the effects of a disorder, e.g. psoriasis, by administering
 PT UV (ultra-violet) treatment (optional) and an antisense nucleic acid that
 PT inhibits or reduces growth factor mediated cell proliferation and/or
 PT inflammation.
 XX
 PS Example 7; Page 45; 201pp; English.
 XX
 CC The present invention relates to a method for ameliorating the effects of
 CC skin disorders. The method comprises contacting the skin with an
 CC antisense oligonucleotide, (for Insulin-like Growth Factor [IGF]-1
 CC receptor, IGF binding protein [IGFBP]-2 or IGFBP3), which is capable of
 CC inhibiting or reducing growth factor mediated cell proliferation,
 CC inflammation and/or other disorders. The present sequence is an
 CC oligonucleotide which can be used to design the antisense
 CC oligonucleotides of the present invention (see AAF45151 and AAF45153-
 CC F45161). The method is useful for ameliorating the effects of psoriasis,
 CC ichthyosis, pityriasis, ruba, pilaris, serborrhea, keloids, keratosis,
 CC neoplasias, scleroderma, warts, benign growths, cancers of the skin, a
 CC hyperneovascular condition such as a neovascular condition of the retina,
 CC brain or skin, growth factor-mediated malignancies, other sclerotic
 CC disease, kidney disease, hyperproliferation of the inside of blood
 CC vessels or any other hyperplasia
 XX

```
CC brain or skin, growth factor-mediated malignancies, other sclerotic
CC disease, kidney disease, hyperproliferation of the inside of blood
CC vessels or any other hyperplasia
XX
SQ Sequence 15 BP; 0 A; 6 C; 6 G; 3 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 256 GCCCAGGAGCAGCA 270
DB 15 GCCCGGAGCAGCA 1
RESULT 1396
AAF80919/C
ID AAF80919 standard; DNA; 15 BP.
XX
AC AAF80919;
XX
DT 02-MAY-2001 (first entry)
XX
DE PTGS2 allele specific oligonucleotide probe SEQ ID 25.
XX
KW Human; prostaglandin-endoperoxide synthase 2; PTGS2; cyclooxygenase 2;
KW single nucleotide polymorphism; SNP; immune-related disorder; arthritis;
KW inflammation; probe; ss.
XX
OS Homo sapiens.
XX
PN WO200107662-A1.
XX
PD 01-FEB-2001.
XX
PF 24-JUL-2000; 2000WO-US020114.
XX
PR 22-JUL-1999; 99US-0145170P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Denton RR, Nandabalan K, Sanchis A, Stephens JC, Tanguay DA;
XX
DR WPI; 2001-182805/18.
XX
PT New nucleic acid containing polymorphisms in the cyclooxygenase-2 gene,
PT for gene therapy of inflammation and for establishing a genotype or
PT haplotype.
XX
PS Disclosure; Page 21; 118pp; English.
XX
CC This invention relates to a polynucleotide sequence that is a polymorphic
CC variant of the human prostaglandin-endoperoxide synthase 2 (PTGS2) gene
CC also referred to as cyclooxygenase 2. The human PTGS2 gene sequence
CC AAF80896 contains 27 single nucleotide polymorphisms (SNPs). AAF80896 and
CC AAF80897 represent human PTGS2 gene and coding sequence, and the PTGS2
CC protein is represented by AAB72199. The invention includes PCR and
CC sequencing primers, and probes represented in AAF80898 - AAF81151 which
CC are used to isolate and characterise the PTGS2 gene sequence, and to
CC locate the positions of the SNPs. PTGS2 proteins and polynucleotide
CC sequences are used to express variant PTGS2 proteins, for structural
CC analysis or drug-binding studies and also in gene therapy (either
CC expressing PTGS2 or inhibitory RNA). Antibodies raised against PTGS2 are
CC useful for diagnosis, prognosis and therapy and analysis of the new, and
CC known, polymorphisms and used to determine PTGS2 haplotype and genotype,
CC especially for determining association between a particular trait, e.g. a
CC clinical response to drugs that target PTGS2 but also disease
CC susceptibility, severity or stage. Anti-PTGS2 antibodies are particularly
CC used for developing diagnostic tests and treatments for immune-related
CC disorders such as arthritis and inflammation. The polymorphisms may also
CC be used to study expression and biological function of PTGS2. Transgenic
CC animals that express PTGS2 are used to study expression of PTGS2
CC isogenes, for in vivo drug screening and testing, and for assessing
```

```
CC effects of therapeutic agents
XX
SQ Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
DB 15 AAAAAAAAAAATATA 1
RESULT 1397
ABA97405/C
ID ABA97405 standard; DNA; 15 BP.
XX
AC ABA97405;
XX
DT 18-JUN-2002 (first entry)
XX
DE Nucleotide sequence of oligomer # 12 used to compare mismatches.
XX
KW Protein nucleic acid molecule; PNA; ds.
XX
OS Synthetic.
XX
PN WO200168673-A1.
XX
PD 20-SEP-2001.
XX
PF 13-MAR-2001; 2001WO-US008111.
XX
PR 14-MAR-2000; 2000US-0189190P.
PR 30-NOV-2000; 2000US-0250334P.
XX
PA (ACTI-) ACTIVE MOTIF.
XX
PI Efimov V, Fernandez J, Archdeacon D, Archdeacon J;
PI Chakhmakhechev O, Buryakova A, Choob M, Hondorp K;
XX
DR WPI; 2002-041177/05.
XX
PT Oligonucleotides analogs useful in detection, separation and purification
PT of nucleic acid molecules, comprise monomers, dimers and oligomers.
XX
PS Example 20; Page 123; 197pp; English.
XX
CC This invention relates to oligonucleotide analogues comprising a protein
CC nucleic acid molecule (PNA) monomer. They are used in the detection and
CC separation of nucleic acid molecules and as probes, primers, linkers,
CC adaptors and antisense agents on solid supports. Modifications enhance
CC their use as capture and detection probes e.g. by the incorporation of
CC biotin, digoxigenin, radioisotopes, fluorescent labels such as
CC fluorescein and reporter molecules such as alkaline phosphatase. They are
CC also used for enhancing or inhibiting the activity of an enzyme or
CC cellular activity. The compounds are stable to nucleases and proteases,
CC have high affinity, binding specificity and solubility. The polyamide
CC backbone of PNAs is resistant to both nucleases and proteases. PNAs bind
CC nucleic acid molecules with greater affinity than DNA or RNA
CC concentration. The compounds are relatively simple to synthesize and are
CC used in a wide variety of applications. This sequence represents a DNA
CC oligomer which is used to represent the effect of single base mismatches
CC on oligonucleotides
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1736 AAAAAAAAAAAAAA 1750
||||||| |||||
```



```

Db      15 AAAAAAAAAAAAAA 1
RESULT 1398
ABK98166/c
ID ABK98166 standard; DNA; 15 BP.
XX
AC ABK98166;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #36.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 6; Fig 20A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1736 AAAAAAAAAAAAAA 1750

```

```

Db      15 AAAAAAAAAAAAAA 1
RESULT 1399
ABK98185/c
ID ABK98185 standard; DNA; 15 BP.
XX
AC ABK98185;
XX
DT 07-OCT-2002 (first entry)
XX
DE Triple helix forming associated oligonucleotide #49.
XX
KW Triple-helix formation; purine-rich target sequence; double-helix DNA;
KW gene expression; regulatory sequence; pathogenic double-stranded DNA;
KW pathogenic bacteria; virus; replication; virulence; cancer;
KW oncogene suppression; cancerous cell; cytostatic; antimicrobial; ss.
XX
OS Synthetic.
XX
PN US6403302-B1.
XX
PD 11-JUN-2002.
XX
PF 16-DEC-1993; 93US-00168920.
XX
PR 17-SEP-1992; 92US-00946976.
XX
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
XX
PI Dervan PB, Beal PA;
XX
DR WPI; 2002-536030/57.
XX
PT A triple-helix comprising a double helical nucleic acid (DHNA) and an
PT oligonucleotide which binds in parallel and antiparallel orientation,
PT respectively, for targeting sequences on alternate strands of DHNA to
PT control gene expression.
XX
PS Example 7; Fig 24A; 108pp; English.
XX
CC The present invention relates to methods and oligonucleotides for forming
CC a triple-helix comprising a double helical nucleic acid comprising first
CC and second substantially complementary strands, and an oligonucleotide
CC bound to a purine-rich target sequence within the double helical nucleic
CC acid, where the oligonucleotide binds in a parallel and antiparallel
CC orientation, respectively, to target sequences on alternate strands of
CC the double helical nucleic acid. The method has therapeutic applications,
CC where gene expression is controlled by selective triple-helix formation
CC within expression regulatory sequences of a target gene. The
CC oligonucleotides can be used to form triple-helices, and are useful to
CC detect the presence or absence of specific sequences within genomic DNA
CC for diagnostic and therapeutic purposes. The oligonucleotides can be
CC selected to specifically bind to pathogenic double-stranded DNA including
CC specific sequences required by pathogenic bacteria or viruses for
CC replication or virulence, reducing their pathogenicity. Alternatively,
CC the oligonucleotide can be chosen to target a unique sequence of the
CC pathogen which is not found in the genome of pathogen's host. The
CC oligonucleotides can be used in cancer treatment by way of triple-helix
CC suppression of specific oncogenes including those of endogenous or viral
CC origin. Such therapeutic oligonucleotides are capable of forming triple-
CC helices with such sequences in cancerous cells containing the activated
CC oncogene, so preferentially killing or repressing the cancer causing
CC cell. The present sequence represents an oligonucleotide used in the
CC methods of the present invention
XX
SQ Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```
OY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1400
ABX79839/c
ID ABX79839 standard; cDNA; 15 BP.
XX
XX ABX79839;
AC
XX
XX
DT 17-APR-2003 (first entry)
DE
DE EST polymorphic DNA repeat polynucleotide #164.
XX
XX EST; expressed sequence tag; ss; polymorphic repeat; tandem repeat;
XX polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;
KW Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;
KW Haw River syndrome; Huntington's disease; fragile-X syndrome;
KW Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;
KW spinal atrophy; bulbar atrophy; spinocerebellar ataxia.
XX
XX Homo sapiens.
OS
XX
XX
XX US6472154-B1.
PN
XX
XX 29-OCT-2002.
PD
XX
XX 31-DEC-1999; 99US-00475947.
PF
XX
XX 31-DEC-1999; 99US-00475947.
PR
XX
XX (TEXA ) UNIV TEXAS SYSTEM.
PA
XX
XX Garner HR, Wren JD, Minna JD, Fondon JW;
PI
XX
XX WPI; 2003-208818/20.
DR
XX
XX Identifying a candidate polymorphic repeat within a coding sequence, for
PT understanding or treating genetic disease, comprises detecting tandem
PT repeats in a target coding sequence and scoring the repeats for
PT polymorphic probability.
XX
XX Example; Col 779; 589pp; English.
PS
XX
XX The invention discloses a method for identifying a candidate polymorphic
CC repeat within a coding sequence (expressed sequence tag, EST), which
CC comprises detecting tandem repeats in a target coding sequence, scoring
CC the repeats for polymorphic probability and generating a dataset
CC correlating the repeats with polymorphic probability to identify a
CC candidate polymorphic repeat. The computational methods (polymorphic
CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are
CC useful for identifying and detecting candidate polymorphic repeats in
CC human genes, which can be used to understand, treat or eliminate genetic
CC diseases, predispositions or adverse drug-treatment reactions. Examples
CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River
CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,
CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and
CC spinocerebellar ataxia. The sequences presented in ABX79676-ABX80022 are
CC the polymorphic repeats identified for a search of human ESTs
XX
XX Sequence 15 BP; 1 A; 0 C; 0 G; 14 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1736 AAAAAAAAAAAAAA 1750
Db 15 AAAAAAAAAAAAAA 1

RESULT 1401
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
ACD82442
ID ACD82442 standard; DNA; 15 BP.
XX
XX ACD82442;
AC
XX
XX 19-SEP-2003 (first entry)
DT
DE Nucleic acid cloning associated adaptor molecule #143.
XX
XX Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
XX Synthetic.
OS
XX
XX US2003044791-A1.
PN
XX
XX 06-MAR-2003.
PD
XX
XX 13-JUN-2001; 2001US-00880313.
PF
XX
XX 13-JUN-2001; 2001US-00880313.
PR
XX
XX (FLEM/) FLEMINGTON E K.
PA
XX
XX Flemington EK;
PI
XX
XX WPI; 2003-521745/49.
DR
XX
XX New adaptor molecules, useful for cloning nucleic acid molecules that
PT does not require the design and synthesis of oligonucleotides or PCR
PT primers.
XX
XX Claim 12; Fig 3; 100pp; English.
PS
XX
XX The invention describes adaptor molecules, where each end of the adaptor
CC is compatible with a nucleic acid digested with a restriction enzyme or a
CC nucleic acid comprising an end that is compatible with a nucleic acid
CC digested with a restriction enzyme. The adaptor molecules, compositions,
CC kits and arrays are useful for cloning nucleic acid molecules that does
CC not require the design and synthesis of oligonucleotides or PCR primers.
CC The adaptors, kits and arrays are also useful for ligating two ends of a
CC single nucleic acid molecule, or ligating two or more nucleic acid
CC molecules. The kits can also be used for performing internal deletion
CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
CC vehicle, making the cloning procedure more rapid and efficient, and less
CC error-prone. This sequence represents a nucleic acid cloning associated
CC adaptor molecule
XX
XX Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.9e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1530 CAAGGCCCTGCAGCGC 1544
Db 1 CATGGCCTGCAGCGC 15

RESULT 1402
ACD82604
ID ACD82604 standard; DNA; 15 BP.
XX
XX ACD82604;
AC
XX
XX 19-SEP-2003 (first entry)
DT
DE Nucleic acid cloning associated adaptor molecule #305.
XX
XX Adaptor molecule; nucleic acid cloning; nucleic acid ligating;
KW internal deletion mutagenesis analysis; cloning vehicle; ss.
XX
XX Synthetic.
OS
```

XX US2003044791-A1.
 PN 06-MAR-2003.
 PD 13-JUN-2001; 2001US-00880313.
 PF 13-JUN-2001; 2001US-00880313.
 PR (FLEM/) FLEMINGTON E K.
 XX Flemington EK;
 PI WPI; 2003-521745/49.
 DR New adaptor molecules, useful for cloning nucleic acid molecules that
 XX does not require the design and synthesis of oligonucleotides or PCR
 PT primers.
 PT Example 9; Page 37; 100pp; English.
 PS The invention describes adaptor molecules, where each end of the adaptor
 XX is compatible with a nucleic acid digested with a restriction enzyme or a
 CC nucleic acid comprising an end that is compatible with a nucleic acid
 CC digested with a restriction enzyme. The adaptor molecules, compositions,
 CC kits and arrays are useful for cloning nucleic acid molecules that does
 CC not require the design and synthesis of oligonucleotides or PCR primers.
 CC The adaptors, kits and arrays are also useful for ligating two ends of a
 CC single nucleic acid molecule, or ligating two or more nucleic acid
 CC molecules. The kits can also be used for performing internal deletion
 CC mutagenesis analysis. The adaptor molecules are ligated to a cloning
 CC vehicle, making the cloning procedure more rapid and efficient, and less
 CC error-prone. This sequence represents a nucleic acid cloning associated
 CC adaptor molecule
 XX Sequence 15 BP; 2 A; 6 C; 5 G; 2 T; 0 U; 0 Other;
 SQ

Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1530 CAAGGCGTCGACGC 1544
 Db |||||||||
 1 CATGGCGTCGACGC 15

RESULT 1403
 ADB68522/c
 ID ADB68522 standard; DNA; 15 BP.
 XX ADB68522;
 AC 04-DEC-2003 (first entry)
 DT Single-base mismatch oligonucleotide SEQ ID 12 DNA.
 XX hydroxyproline nucleic acid; HypNA; PNA; peptide nucleic acid;
 KW gene expression; respiration; secretion; signalling;
 KW ion-channel activity; cell motility; developmental phenotype;
 KW tumour regression; single-base mismatch; ss;
 KW phosphono-peptide nucleic acid; pPNA.
 XX Synthetic.
 OS WO2003068798-A2.
 PN 21-AUG-2003.
 XX 07-FEB-2003; 2003WO-US003904.
 PF 09-FEB-2002; 2002US-00072975.
 PR (ACTI-) ACTIVE MOTIF.
 PA

XX Efimov V, Fernandez J, Archdeacon D, Archdeacon J, Choob M;
 XX WPI; 2003-689653/65.
 DR Method of inhibiting expression of genes or RNA transcripts, useful for
 PT therapy and determining effects of genes, by administering oligomers
 PT containing hydroxyproline nucleic acid.
 XX Disclosure; Page 234; 240pp; English.
 PS The invention relates to a novel method of inhibiting the expression of
 CC one or more genes or RNA transcripts by administering at least one
 CC oligonucleotide analogue that includes at least one hydroxyproline
 CC nucleic acid (HypNA) monomer to a cell or organism or their extracts. The
 CC oligonucleotides of the invention may be used to monitor properties
 CC including gene expression, respiration, secretion, signalling, ion-
 CC channel activity, cell motility, developmental phenotype and tumour
 CC regression. Furthermore, they may be utilised to determine the effects of
 CC particular genes, as antisense or homologous recombination constructs
 CC e.g. for creating animal models of disease and finally, for increasing
 CC the activity of some enzymes, such as polymerases. The current sequence
 CC is that of the single-base mismatch oligonucleotide SEQ ID 12 DNA of the
 CC invention. This sequence may also comprise a peptide nucleic acid (PNA),
 CC a phosphono-PNA (pPNA) or a HypNA.
 XX Sequence 15 BP; 0 A; 1 C; 0 G; 14 T; 0 U; 0 Other;
 SQ

Query Match 0.8%; Score 13.4; DB 1; Length 15;
 Best Local Similarity 93.3%; Pred. No. 8.9e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
 Db |||||||||
 15 AAAAAAAAAAAAAA 1

RESULT 1404
 AAQ25457
 ID AAQ25457 standard; DNA; 16 BP.
 XX AAQ25457;
 AC 25-MAR-2003 (revised)
 DT 07-DEC-1992 (first entry)
 DE Purine rich HIV target duplex sequence.
 XX Target; Human Immunodeficiency Virus; AIDS; triplex; hepatitis; herpes;
 KW malignancy; ds.
 KW Synthetic.
 OS WO9209705-A1.
 PN 11-JUN-1992.
 XX 25-NOV-1991; 91WO-US008811.
 PF 23-NOV-1990; 90US-00617907.
 PR 18-JAN-1991; 91US-00643382.
 PR 08-APR-1991; 91US-00683420.
 PR 17-APR-1991; 91US-00686544.
 PR 17-APR-1991; 91US-00686546.
 PR 17-APR-1991; 91US-00686547.
 PR 27-SEP-1991; 91US-00766733.
 XX (GILE-) GILEAD SCI INC.
 PA Froehler B, Krawczyk S, Matteucci MD, Milligan J;
 PI WPI; 1992-217083/26.
 XX

PT New oligomers contg. modified bases - which form a triplex with G-C
PT doublet in a DNA duplex, for treating and diagnosing HIV, hepatitis,
PT herpes malignancy and inflammation.
PS Claim 11; Page 63; 77pp; English.
XX
CC The sequence depicts a HIV viral duplex sequence which contains a purine-
CC rich region concentrated on one chain of the duplex. The sequence may be
CC prep'd. by standard DNA synthesis. The HIV duplex sequence is used as a
CC target for novel oligomers which are capable of forming a triplex at
CC physiological pH by coupling into the major groove of the DNA duplex.
CC Three such oligomers HIV141 - HIV143 are capable of forming a triplex with
CC this sequence. The oligomers are used in the diagnosis and therapy of HIV
CC infection. Similar oligomers may be used to target viral DNA duplexes
CC specific for hepatitis, herpes and malignancy. The triple helices form
CC under mild conditions thus assays may be carried out without subjecting
CC the test specimen to harsh conditions. The oligomer is able to inhibit
CC gene expression, as verified by in vitro systems See also AAQ25452-25501
CC and AAQ30226-448. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 16 BP; 7 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAAGAGGAGG 878
Db ||||| ||||| |||||
2 AAGAGGAGGAGGAGG 16

RESULT 1405
AAT44591/c
ID AAT44591 standard; DNA; 16 BP.
XX
AC AAT44591;
XX
DT 03-JUL-1997 (first entry)
XX
DE Cryptosporidium parvum 18S rRNA gene primer/probe.
XX
KW Cryptosporidium parvum; 18S rRNA; ribosomal RNA; detection; diagnosis;
KW polymerase chain reaction; hybridisation probe; ss.
XX
OS Synthetic.
XX
PN WO9634978-A1.
XX
PD 07-NOV-1996.
XX
PF 06-MAY-1996; 96WO-AU000274.
XX
PR 05-MAY-1995; 95AU-00002831.
XX
PA (MACQ-) MACQUARIE RES LTD.
PA (SYDN-) SYDNEY WATER CORP LTD.
XX
PI Vesey G, Veal D, Williams KL, Ashbolt NJ, Dorsch M;
XX WPI; 1996-506178/50.
DR
XX Oligonucleotide for detection of viable Cryptosporidium parvum cells -
PT hybridises with unique sequences in 18S rRNA, useful as probe or primer
PT for PCR amplification.
XX
PS Claim 4; Page 15; 22pp; English.
XX
CC The present sequence is for detecting viable Cryptosporidium parvum cells
CC by hybridising specifically to unique 18S rRNA sequences of C. parvum. It
CC can be used when labelled as a probe or as a primer for PCR amplification
CC of 18S rRNA. It can detect live C. parvum oocysts, or other cells,
CC particularly in water but also in other environmental or clinical samples
CC such as animal or human body fluids or excretions. It does not detect

CC dead cells, because RNA degrades too quickly in such cells, or cells of
CC other Cryptosporidium species that are not pathogenic to humans
XX
SQ Sequence 16 BP; 2 A; 0 C; 1 G; 13 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1733 TACAAAAA 1747
Db ||||| ||||| |||||
15 TACTAAAAA 1

RESULT 1406
AAC73333/c
ID AAC73333 standard; DNA; 16 BP.
XX
AC AAC73333;
XX
DT 02-FEB-2001 (first entry)
XX
DE Forward primer #66 used in multiplexing PCR/SBE assay.
XX
KW Oligonucleotide array; genotyping; single base extension reaction; SBE;
KW PCR primer; polymorphic locus; single nucleotide polymorphism; ss.
XX
OS Unidentified.
XX
PN WO200058516-A2.
XX
PD 05-OCT-2000.
XX
PF 27-MAR-2000; 2000WO-US008069.
XX
PR 26-MAR-1999; 99US-0126473P.
PR 23-JUN-1999; 99US-0140359P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFY-) AFFYMETRIX INC.
XX
PI Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
PI Ryder T, Sklar P;
XX
DR WPI; 2000-656171/63.
XX
PT Universal array of oligonucleotides tags attached to a solid substrate
PT along with locus-specific tagged oligonucleotides useful in genotyping
PT using single base extension reactions.
XX
PS Example 7; Page 55; 70pp; English.
XX
CC The present invention relates to an oligonucleotide array comprising
CC oligonucleotide tags fixed to a solid substrate. The oligonucleotide
CC array is useful for genotyping a nucleic acid sample at one or more loci
CC via single base extension (SBE) reactions. A pair of primers is used to
CC amplify a polymorphic locus in a sample e.g. a single nucleotide
CC polymorphism (SNP). The present sequence is one of the primers used in
CC the method of the present invention to amplify a polymorphic sample. The
CC amplified nucleic acid product is then used as a template in a SBE
CC reaction with an extension primer. The SBE reaction products are used to
CC form the oligonucleotide array
XX
SQ Sequence 16 BP; 5 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 16;
Best Local Similarity 93.3%; Pred. No. 9.2e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 984 CTTTCGCCAGTGTGG 998
Db ||||| ||||| |||||
15 CCTTCGCCAGTGTGG 1

RESULT 1407
 ABL57076
 ID ABL57076 standard; DNA; 16 BP.
 XX
 AC ABL57076;
 XX
 DT 22-JUL-2002 (first entry)
 XX
 DE Molecular beacon target sequence (single mismatch).
 XX
 DE Molecular beacon; fluorophore; nanoparticle; nucleic acid detection; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT misc_feature 9
 FT /*tag= a
 FT /note= "mismatch site"
 XX
 PN WO200218951-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 29-AUG-2001; 2001WO-US041941.
 XX
 PR 29-AUG-2000; 2000US-0228728P.
 PR 30-MAR-2001; 2001US-0280350P.
 XX
 PA (UVRQ) UNIV. ROCKEFELLER.
 XX
 PI Dubertret B, Calame M, Libchaber A;
 XX
 DR WPI; 2002-404569/43.
 XX
 PT Sensitive detecting proximity changes in a system that utilizes an
 PT interacting fluorophore and quencher, for high sensitivity applications,
 PT involves utilizing a metal surface as quencher.
 XX
 PS Example 3; Page 30; 62pp; English.
 XX
 CC The present sequence is that of a single mismatch target sequence for a
 CC molecular beacon comprising an oligonucleotide probe (see ABL57069)
 CC covalently attached at the 3' end to fluorescent dye and at the 5' end to
 CC a nanoparticle. In the native state, the probe forms a hairpin
 CC conformation with hybridised termini. The proximity of the fluorophore
 CC and quencher (gold nanoparticle) in the molecular beacon results in
 CC little or no detectable fluorescence. Upon hybridisation of the central
 CC complementary stretch of the probe to a target sequence, such as the
 CC present sequence, the hairpin undergoes a conformational change resulting
 CC in an increase in fluorescence, the extent of which is proportional to
 CC the amount of target sequence present. Experiments with the present
 CC sequence and a perfectly-matched target (see ABL57071) showed that
 CC hybridisation was very specific to the matched target. The invention
 CC relates generally to the use of metal surface quenchers such as particles
 CC or films for high sensitivity applications in, for example, detection and
 CC diagnostic systems
 XX
 SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 16;
 Best Local Similarity 93.3%; Pred. No. 9.2e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 |||||
 DB 2 AAAAAAAAACAAAAAA 16
 |||||
 RESULT 1408
 ACF63316/c
 ID ACF63316 standard; DNA; 16 BP.
 XX

AC ACF63316;
 XX
 DT 09-OCT-2003 (first entry)
 XX
 DE Human Ghrelin antisense oligonucleotide SEQ ID NO:38.
 XX
 KW Human; pharmacological; hypotensive; antilipaeamic; vasotropic; laxative;
 KW dermatological; antidepressant; tranquiliser; antiinflammatory; eczema;
 KW antitumor; antimigraine; neuroprotective; antiparkinsonian; analgesic;
 KW gynaecological; virucide; vulnery; antiarthritic; antipsoriatic; cold;
 KW antimicrobial; cytostatic; litholytic; pathological disorder; depression;
 KW abnormal appetite; hypertension; hypercholesterolaemia; hyperlipidaemia;
 KW erectile dysfunction; anxiety; stress; inflammatory bowel syndrome;
 KW ulcerative colitis; Crohn's disease; renal stone; gall stone; migraine;
 KW constipation; headache; seizure; multiple sclerosis; polymyositis;
 KW fibromyalgia; Parkinson's disease; amyotrophic lateral sclerosis; trauma;
 KW chronic pain; pre-menstrual syndrome; sinusitis; carpal tunnel syndrome;
 KW chronic fatigue syndrome; rosacea; arthritis; psoriasis; prostatitis;
 KW inflammation; heart burn; infection; colon cancer; malignant melanoma;
 KW skin disorder; antisense oligonucleotide; ss.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003006478-A1.
 XX
 PD 23-JAN-2003.
 XX
 PF 10-JUL-2002; 2002WO-US021664.
 XX
 PR 10-JUL-2001; 2001US-0303820P.
 XX
 PA (OLIG-) OLIGOS ETC INC.
 XX
 PI Dale RMK, Arrow A, Thompson T;
 XX
 DR WPI; 2003-221709/21.
 XX
 PT Composition with a modified oligonucleotide useful for treating a patient
 PT with a pathological disorder such as abnormal appetite, hypertension,
 PT eczema, anxiety, stress, and cancer.
 XX
 PS Claim 17; Page 8; 173pp; English.
 XX
 CC The present invention describes a composition (I) suitable for
 CC administration in a mammal, which comprises a modified oligonucleotide
 CC (II) of 7-75 nucleotides containing 7 or more contiguous ribose groups
 CC linked by achiral 5'-3' internucleoside phosphate linkages, where the
 CC modified oligonucleotide is complementary to a region of a gene
 CC associated with a pathological disorder. Also described: (1) a
 CC nutritional supplement comprising (II); and (2) a cosmetic composition
 CC comprising (II), where the modified oligonucleotide is complementary to a
 CC region of a gene associated with a skin disorder. (I) and (II) can have
 CC hypotensive, antilipaeamic, vasotropic, dermatological, antidepressant,
 CC tranquiliser, antiinflammatory, antitumor, laxative, antimigraine,
 CC neuroprotective, antiparkinsonian, analgesic, gynaecological, virucide,
 CC vulnery, antiarthritic, antipsoriatic, antimicrobial, cytostatic and
 CC litholytic activities. (I) can be used for treating a patient with a
 CC pathological disorder selected from abnormal appetite, hypertension,
 CC hypercholesterolaemia, hyperlipidaemia, erectile dysfunction, eczema,
 CC depression, anxiety, stress, inflammatory bowel syndrome, ulcerative
 CC colitis, Crohn's disease, renal stones, gall stones, constipation, colds,
 CC migraine headache, seizure, multiple sclerosis, polymyositis, sinusitis,
 CC fibromyalgia, Parkinson's disease, amyotrophic lateral sclerosis (ALS),
 CC chronic pain, pre-menstrual syndrome, trauma, carpal tunnel syndrome,
 CC chronic fatigue syndrome, rosacea, arthritis, psoriasis, prostatitis,
 CC inflammation, heart burn, infection, poison ivy, colon cancer, malignant
 CC melanoma, and malignant nasal polyps. The nutritional supplement is
 CC useful for supplementing the diet of an individual, and the cosmetic
 CC composition is useful for improving the appearance of the skin in an
 CC individual with a skin disorder. ACF63279 to ACF63410 represent
 CC nucleotide sequence given in the exemplification of the present invention
 XX

```

SQ Sequence 16 BP; 3 A; 4 C; 7 G; 2 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 16;
  Best Local Similarity 93.3%; Pred. No. 9.2e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 167 GGCCACCTGGCTGC 181
Db 16 GGCCACCTGGCTGC 2

RESULT 1409
AAD57846
ID RAD57846 standard; DNA; 16 BP.
XX
AC RAD57846;
XX
DT 20-NOV-2003 (first entry)
XX
DE Target oligonucleotide #3 used in nonlinear optical technique.
XX
KW Nonlinear optical technique; screening; ss.
XX
OS Unidentified.
XX
PN WO2003064991-A2.
XX
PD 07-AUG-2003.
XX
PF 17-JUL-2002; 2002WO-US022681.
XX
PR 17-JUL-2001; 2001US-0306040P.
XX
PR 23-OCT-2001; 2001US-0347821P.
XX
PR 06-FEB-2002; 2002US-0354668P.
XX
PA (SALA/) SALAFSKY J S.
XX
PI Salafsky JS;
XX
WPI; 2003-646172/61.
XX
  Screening candidate binding partner(s) for binding to test molecule by
  PT applying external force field to sample in homogeneous phase,
  PT illuminating sample with light beam(s) at fundamental frequencies, and
  PT measuring physical properties.
XX
PS Disclosure; Fig 20-B; 146pp; English.
XX
  The present invention relates to a method for detecting interactions
  CC between biological components using a nonlinear optical technique. The
  CC invention is used for screening candidate binding partner(s) for binding
  CC to test molecule. It can also be used to detect changes in orientation or
  CC conformation of the probe and/or target. The present sequence is a target
  CC oligonucleotide used in nonlinear optical technique
  XX
SQ Sequence 16 BP; 14 A; 1 C; 1 G; 0 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 16;
  Best Local Similarity 93.3%; Pred. No. 9.2e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1736 AAAAAAAAAAAAAA 1750
Db 2 AAAAAAAAAAAAAA 16

RESULT 1410
AAQ94364/C
ID AAQ94364 standard; DNA; 17 BP.
XX
AC AAQ94364;
XX
DT 04-JUN-1996 (first entry)
XX

SQ Sequence 17 BP; 2 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 17;
  Best Local Similarity 93.3%; Pred. No. 9.6e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 CCCCACTCCAGCCTC 626
Db 16 CACCACTCCAGCCTC 2

RESULT 1411
AAQ81619/C
ID AAQ81619 standard; DNA; 17 BP.
XX
AC AAQ81619;
XX
DT 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
DE Plasmodium falciparum MSA-1 gene PCR primer C008.
XX
KW Plasmodium falciparum; MSA-1 gene; recombinant poxvirus;
KW multicomponent multistage malarial vaccines; immunogens;
KW malaria diagnosis; PCR primer C008; ss.
XX
OS Synthetic.
XX
PN WO9428930-A1.
XX
PD 22-DEC-1994.

```

```

XX Septoria tritici ITS primer JB446.
DE Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;
XX Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;
KW Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;
KW internal transcribed region; strain; capture; colourimetric assay;
KW isolate; development; population; ss.
XX
OS Synthetic.
XX
PN WO9529260-A2.
XX
PD 02-NOV-1995.
XX
PF 19-APR-1995; 95WO-US004712.
XX
PR 25-APR-1994; 94US-00233608.
XX
PA (CIBA ) CIBA GEIGY AG.
XX
PI Ligon JM, Beck JJ;
XX
WPI; 1995-383005/49.
XX
  DNA encoding intervening transcribed sequence - used for detection of
  PT plant fungal pathogens.
XX
PS Claim 3; Page 15; 65pp; English.
XX
  A novel method for the detection of plant pathogenic strains of fungi
  CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides,
  CC Mycosphaerella fijiensis, M. musicola or Fusarium spp, involves the PCR
  CC amplification of sequences found in the internal transcribed region (ITS)
  CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93
  CC and AAQ05357-72. These primers are derived from the ITS sequences of
  CC these fungi (AAQ05394-T05404 and AAQ94398) and are strain specific. The
  CC amplification products of the reactions using these primers can be used
  CC with the capture primers AAT05378-93 in colourimetric assays. The primers
  CC and ITS DNAs can be used for the detection of specific fungal pathogen
  CC isolates and in monitoring disease development in plant populations
  XX
SQ Sequence 17 BP; 2 A; 2 C; 9 G; 4 T; 0 U; 0 Other;
  Query Match      0.8%; Score 13.4; DB 1; Length 17;
  Best Local Similarity 93.3%; Pred. No. 9.6e+02;
  Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 612 CCCCACTCCAGCCTC 626
Db 16 CACCACTCCAGCCTC 2

RESULT 1411
AAQ81619/C
ID AAQ81619 standard; DNA; 17 BP.
XX
AC AAQ81619;
XX
DT 25-MAR-2003 (revised)
DT 30-AUG-1995 (first entry)
XX
DE Plasmodium falciparum MSA-1 gene PCR primer C008.
XX
KW Plasmodium falciparum; MSA-1 gene; recombinant poxvirus;
KW multicomponent multistage malarial vaccines; immunogens;
KW malaria diagnosis; PCR primer C008; ss.
XX
OS Synthetic.
XX
PN WO9428930-A1.
XX
PD 22-DEC-1994.

```


CC made double stranded by synthesising complementary strands. Making the
CC products double stranded causes "nicks" to be created (via the RE
CC recognition sites). Further extension occurs from the nicks, thereby
CC displacing a copy of the target sequence from the double stranded
CC amplification primer extension products. The nicking, extending and
CC displacing steps are repeated, and the target sequence amplified in situ.
CC The method can be used for the amplification of DNA in situ in cells in
CC suspension, on slides or in tissues, with speed, sensitivity and
CC specificity. In situ TSDA also remains compatible with immunohistochemical
CC techniques in spite of the increased reaction temperature so both
CC amplification of DNA and immunological staining (see AAT88934 for an
CC example of a detector probe) can be performed on the same specimen
XX
SQ Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 828 CAAAGAGGAGCTGC 842
||| ||||| |||||
DB 15 CATTGAGGAGCTGC 1

RESULT 1414
AAAX70026/c
ID AAX70026 standard; RNA; 17 BP.
XX
AC AAX70026;
XX
XX Homo sapiens.
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1321.
XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

OS Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.
XX
XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 86; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples

CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 0 T; 10 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAGC 47
||||| ||||| |||||
DB 17 AGGAAAAAAAAGC 3

RESULT 1415
AAAX70027/c
ID AAX70027 standard; RNA; 17 BP.
XX
AC AAX70027;
XX
XX 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1322.

XX
XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.

OS Homo sapiens.
XX
XX WO9715662-A2.
XX
XX 01-MAY-1997.
XX
XX 25-OCT-1996; 96WO-US017480.

XX 26-OCT-1995; 95US-0005974P.
XX 11-JAN-1996; 96US-00584040.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (CHIR) CHIRON CORP.
XX
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX
XX WPI; 1997-259017/23.

XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 86; 218pp; English.

XX The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention

XX Sequence 17 BP; 2 A; 4 C; 1 G; 0 T; 10 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 AGGAAAAAAAAGC 47
||||| ||||| |||||
DB 16 AGGAAAAAAAAGC 2


```

RESULT 1416
AAAX70028/C
ID AAX70028 standard; RNA; 17 BP.
XX
AC AAX70028;
XX
DT 28-JUL-1999 (first entry)
XX
DE Human flt1 VEGF receptor hammerhead ribozyme substrate #1323.
XX
KW Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
KW foetal liver kinase 1; ss.
XX
OS Homo sapiens.
XX
PN WO9715662-A2.
XX
PD 01-MAY-1997.
XX
PF 25-OCT-1996; 96WO-US017480.
XX
PR 26-OCT-1995; 95US-0005974P.
XX
PR 11-JAN-1996; 96US-00584040.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (CHIR ) CHIRON CORP.
XX
PI Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
PT Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
PT stability - useful for treating e.g. tumour angiogenesis, psoriasis,
PT rheumatoid arthritis, etc., in a human patient.
XX
PS Claim 4; Page 86; 218pp; English.
XX
CC The present invention describes nucleic acid molecules which modulate the
CC synthesis, expression and/or stability of a mRNA encoding 1 or more
CC receptors of vascular endothelial growth factor (VEGF). A patient
CC (preferably human) having a condition associated with the level of the
CC fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
CC receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
CC angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
CC treated by administering the nucleic acid molecule or the expression
CC vector to the patient. AAX67275 to AAX75752 represent specific examples
CC of nucleic acid molecules from the present invention
XX
SQ Sequence 17 BP; 2 A; 4 C; 1 G; 0 T; 10 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 33 AGGAAAAAAGC 47
Db 15 AGGAAAAAAGC 1

RESULT 1417
AAV62512/C
ID AAV62512 standard; DNA; 17 BP.
XX
AC AAV62512;
XX
DT 17-DEC-1998 (first entry)
XX
DE Septoria tritici species specific primer JB446.

```

```

XX Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum;
KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KW Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen;
XX PCR; nucleic acid detection; PCR primer; ss.
XX
OS Synthetic.
OS Mycosphaerella graminicola.
XX
PN US5814453-A.
XX
PD 29-SEP-1998.
XX
XX 02-JUL-1997; 97US-00887480.
XX
XX 19-APR-1995; 95WO-US004712.
XX
XX 15-OCT-1996; 96US-00722187.
XX
XX (NOVS ) NOVARTIS FINANCE CORP.
XX
XX Beck JJ;
XX
XX WPI; 1998-541745/46.
XX
XX DNA isolated from fungal RNA, and its internal transcribed spacer
XX sequence - used for detecting fungal pathogens in plant tissue.
XX
XX Example 6; Col 16; 56pp; English.
XX
XX Sequences AAV62507 to AAV62566 represent species specific PCR primers for
XX various fungal isolates used for fungal detection in the course of the
XX invention. The primers are designed based on the internal transcribed
XX spacer (ITS) sequences of the various fungal species. The invention
XX provides a DNA molecule isolated from the ribosomal RNA gene region of a
XX fungal pathogen, where the DNA molecule consists of an ITS sequence
XX selected from ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum,
XX Fusarium moniliforme, Septoria avenae or Microdochium nivale. A method
XX for detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
XX avenaceum and M. nivale isolates is also provided which comprises
XX isolating DNA from a plant leaf infected with at least one of the above
XX pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
XX PCR using specific primers from within these sequences. The pathogen(s)
XX are detected by visualising the amplified part of the ITS sequence
XX
XX Sequence 17 BP; 2 A; 2 C; 9 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 612 CCCACCTCCAGCCTC 626
Db 16 CACCACCTCCAGCCTC 2

RESULT 1418
AAA23089
ID AAA23089 standard; RNA; 17 BP.
XX
AC AAA23089;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin subunit beta 3 substrate sequence SEQ ID NO:6315.
XX
KW Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
KW hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
KW dermatologic; RNA cleavage; cancer; diabetic retinopathy; arthritis;
KW age related macular degeneration; inflammation; neovascular glaucoma;
KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
KW tuberosus sclerosis; pot-wine stain; Sturge Weber syndrome;

```

KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX Homo sapiens.
 OS
 XX 24-MAR-1999; 99WO-US006507.
 PF
 XX 27-MAR-1998; 98US-0079678P.
 PR
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 PI WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 PS Claim 54; Page 261; 305pp; English.
 XX The present invention describes enzymatic cleave RNA molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 1 A; 3 C; 3 G; 0 T; 10 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 40.0%; Pred. No. 9.6e+02;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
 QY 58 TTTCTTTTCTGGAGT 72
 Db 1 UUUCUUCUGGAGU 15
 RESULT 1419
 ID AAA23088
 XX AAA23088 standard; RNA; 17 BP.
 AC AAA23088;
 XX
 XX 19-JUN-2000 (first entry)
 DT Integrin subunit beta 3 substrate sequence SEQ ID NO:6314.
 DE
 XX Human; aryl hydrocarbon nuclear transporter; ARNT; Tie-2; angiogenesis;
 KW integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
 KW hammerhead ribozyme; angiogenic factor; cytostatic; antidiabetic;

KW ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
 KW dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
 KW age related macular degeneration; inflammation; neovascular glaucoma;
 KW myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
 KW tuberos scleriosis; pot-wine stain; Sturge Weber syndrome;
 KW Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9950403-A2.
 XX
 PD 07-OCT-1999.
 PF
 XX 24-MAR-1999; 99WO-US006507.
 PR
 XX 27-MAR-1998; 98US-0079678P.
 XX (RIBO-) RIBOZYME PHARM INC.
 PA
 XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
 PI WPI; 1999-591315/50.
 DR
 XX Novel ribozymes for modulating the synthesis, expression and/or stability
 PT of an mRNA encoding an angiogenic factors.
 PS Claim 54; Page 261; 305pp; English.
 XX The present invention describes enzymatic cleave RNA molecules with RNA
 CC cleaving activity, which specifically cleave RNA encoded by an aryl
 CC hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
 CC gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
 CC AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
 CC and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
 CC corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
 CC AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
 CC and AAA19155 to AAA19222 represent their corresponding target sequences;
 CC AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
 CC sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
 CC AAA21596 to AAA21688 represent their corresponding target sequences;
 CC AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
 CC for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
 CC AAA23422 represent their corresponding target sequences. The ribozymes of
 CC the invention are used for modulating the synthesis, expression and/or
 CC stability of an mRNA encoding angiogenic factor, especially ARNT,
 CC integrin subunit beta-3, integrin subunit alpha-6, or Tie-2. They are
 CC especially used to treat cancer, diabetic retinopathy, age related
 CC macular degeneration (ARMD), inflammation, and arthritis, as well as
 CC neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
 CC angiofibroma of tuberous sclerosis, pot-wine stains, Sturge Weber
 CC syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
 CC and other syndromes and diseases related to the levels of ARNT, Tie-2,
 CC integrin subunit alpha-6, or integrin subunit beta-3
 XX
 SQ Sequence 17 BP; 2 A; 3 C; 3 G; 0 T; 9 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 40.0%; Pred. No. 9.6e+02;
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;
 QY 58 TTTCTTTTCTGGAGT 72
 Db 2 UUUCUUCUGGAGU 16
 RESULT 1420
 ID AAX30261/c
 XX AAX30261 standard; DNA; 17 BP.
 AC AAX30261;
 XX
 XX 21-JUN-1999 (first entry)
 DT
 XX

```

DE HIV gag bumper primer B2.
XX HIV; gag; bumper primer; amplification primer; probe; detection;
KW fluorescence quenching; Chlamydia trachomatis; Neisseria gonorrhoeae;
KW human; placental DNA; pathogen; ss.
XX Synthetic.
XX EP915173-A2.
XX 12-MAY-1999.
XX 03-NOV-1998; 98EP-00120832.
XX 04-NOV-1997; 97US-00964020.
XX (BECT ) BECTON DICKINSON & CO.
XX Little MC, Vonk GP;
XX WPI; 1999-265943/23.
XX New method for real-time fluorescence-detection assays useful for
PT detecting nucleic acids from pathogens in samples from patients.
XX Example 1; Page 8; 16pp; English.
XX The present invention describes a kit for conducting a fluorescence
CC detection assay to determine the presence, absence or amount of a target
CC analyte in a sample. The method and kit may be used to detect
CC amplification of nucleic acid molecules in real time using fluorescence
CC quenching for example. The assays may be used to detect the presence of
CC nucleic acids from pathogens in samples of body fluid from patients. The
CC kit allows a homogeneous nucleic acid amplification and real time nucleic
CC acid probe detection assay to be carried out with minimal complexity
CC which yields a consistent reliable fluorescent detection signal. The
CC present sequence represents a primer used in the exemplification of the
CC present invention
XX Sequence 17 BP; 3 A; 5 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 828 CAAGAGGAGAGCTGC 842
DB 15 CAATGAGGAGAGCTGC 1

RESULT 1421
AAC72533/c
ID AAC72533 standard; DNA; 17 BP.
XX AAC72533;
XX 09-FEB-2001 (first entry)
XX Single nucleotide polymorphism PCR primer #1575.
XX Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX Homo sapiens.
XX WO200058519-A2.
XX 05-OCT-2000.
XX 30-MAR-2000; 2000WO-US008440.
XX 31-MAR-1999; 99US-0127248P.
XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.

```

```

XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX WPI; 2000-611722/58.
XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX Claim 8; Fig 5; 214pp; English.
XX The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1461 GTGTGGGCTGCTGCT 1475
DB 16 GTGTGGGCTGCTGCT 2

RESULT 1422
AAC72524/c
ID AAC72524 standard; DNA; 17 BP.
XX AAC72524;
XX 09-FEB-2001 (first entry)
XX Single nucleotide polymorphism PCR primer #1569.
XX Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX Homo sapiens.
XX WO200058519-A2.
XX 05-OCT-2000.
XX 30-MAR-2000; 2000WO-US008440.
XX 31-MAR-1999; 99US-0127248P.
XX (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX WPI; 2000-611722/58.
XX Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.

```

```
XX
PS Claim 8; Fig 5; 214pp; English.
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
    Query Match          0.8%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 9.6e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY 1461 GTGTGGGCTGCTGCT 1475
    Db 16 GTGTGGGCTGCTCCT 2
    RESULT 1423
    AAC72521/c
    ID AAC72521 standard; DNA; 17 BP.
    XX
    AC AAC72521;
    XX
    DT 09-FEB-2001 (first entry)
    XX
    DE Single nucleotide polymorphism PCR primer #1567.
    XX
    KW Single nucleotide polymorphism; SNP; human; genetic disease;
    KW disease susceptibility; cardiovascular system; endocrine system;
    KW neurological system; forensic testing; paternity testing; PCR primer; ss.
    OS Homo sapiens.
    XX
    PN WO200058519-A2.
    XX
    PD 05-OCT-2000.
    XX
    PF 30-MAR-2000; 2000WO-US008440.
    XX
    PR 31-MAR-1999; 99US-0127248P.
    XX
    PA (WHED ) WHITEHEAD INST BIOMEDICAL RES.
    PA (AFFY-) AFFYMETRIX INC.
    PI Altschuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
    PI Lipshutz RJ, Patil N, Sklar P;
    XX
    DR WPI; 2000-611722/58.
    XX
    PT Nucleic acid selected from one of 106 genes comprising single nucleotide
    PT polymorphisms, allele-specific oligonucleotides to the genes are useful
    PT for phenotypic correlations, forensics, paternity testing, medicine and
    PT genetic analysis.
    XX
    PS Claim 8; Fig 5; 214pp; English.
    XX
    CC The present invention is concerned with a number of human single
    CC nucleotide polymorphisms (SNPs) which the inventors identified in human
    CC genes. These SNPs can be used in disease diagnosis and prediction of an
    CC individual's susceptibility to disease, in forensic and paternity testing
    CC and in genetic mapping. In particular, the SNPs of the invention can be
    CC used to diagnose susceptibility to diseases of the cardiovascular,
    CC endocrine and neurological systems, such as coronary artery disease,
    CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
    CC diseases
    XX
```

```
SQ Sequence 17 BP; 6 A; 6 C; 4 G; 1 T; 0 U; 0 Other;
    Query Match          0.8%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 9.6e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY 1461 GTGTGGGCTGCTGCT 1475
    Db 16 GTGTGGGCTGCTCCT 2
    RESULT 1424
    AAA70335
    ID AAA70335 standard; DNA; 17 BP.
    XX
    AC AAA70335;
    XX
    DT 19-DEC-2000 (first entry)
    XX
    DE DNA synthesis adaptor sequence NR17.
    XX
    KW DNA synthesis; nucleic acid identification; primer; adaptor; ss.
    XX
    OS Synthetic.
    XX
    PN WO200040757-A2.
    XX
    PD 13-JUL-2000.
    XX
    PF 07-JAN-2000; 2000WO-US000402.
    XX
    PR 08-JAN-1999; 99US-0115109P.
    PR 13-OCT-1999; 99US-00417386.
    XX
    PA (CURA-) CURAGEN CORP.
    XX
    PI Rothberg JM, McKenna M, Predki P, Windemuth A, Shinkets RA;
    XX
    DR WPI; 2000-466001/40.
    XX
    PT Identification of novel nucleic acid sequences used to identify
    PT variations within the human genome including in diseased tissues.
    XX
    PS Disclosure; Page 18; 45pp; English.
    XX
    CC The present sequence is an adaptor sequence used in the method of the
    CC invention. It was used to normalise the cDNA sequences in a sample for
    CC study, which then enabled the PCR amplification of 'rare' sequences i.e.
    CC those which are not found most often in the sample. This is useful in
    CC procedures such as gene identification, particularly those genes
    CC transcribed at low levels, therapeutic protein identification,
    CC identification of variations within the human genome such as single
    CC nucleotide polymorphisms, identification of differences between normal
    CC and diseased tissue and analysis of differential gene expression between
    CC different tissues or species
    XX
    SQ Sequence 17 BP; 4 A; 8 C; 2 G; 3 T; 0 U; 0 Other;
    Query Match          0.8%; Score 13.4; DB 1; Length 17;
    Best Local Similarity 93.3%; Pred. No. 9.6e+02;
    Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
    QY 613 CCCACTCCAGCCTCT 627
    Db 3 CACACTCCAGCCTCT 17
    RESULT 1425
    AAF81949/c
    ID AAF81949 standard; DNA; 17 BP.
    XX
    AC AAF81949;
    XX
```

DT 15-JUN-2001 (first entry)
 XX MSAL N-terminal fragment PCR primer C008 SEQ ID NO:16.
 DE
 XX
 KW Vaccinia virus; merocytite surface antigen 1; MSAL; plasmodium;
 KW recombinant poxvirus; vaccine; immunological response; mutagenesis;
 KW antimalarial; malaria; PCR primer; ss.
 XX
 OS Vaccinia virus.
 OS Synthetic.
 XX
 XX US6214353-B1.
 XX
 PD 10-APR-2001.
 XX
 XX 21-MAY-1998; 98US-00083366.
 PF
 XX
 PR 01-JUL-1991; 91US-00724109.
 PR 07-JAN-1994; 94US-00178476.
 XX
 XX (INMR) PASTEUR MERIEUX SERUMS & VACCINS SA.
 PA (UYHA-) UNIV HAWAII.
 XX
 PI Paoletti E, De Taisne C, Chang S, Hui G, Siddiqui WA;
 XX
 DR WPI; 2001-280989/29.
 XX
 XX Novel recombinant vaccinia or avipox virus containing DNA encoding
 PT plasmodium falciparum merocytite surface antigen 1 or its subfragment,
 PT useful for inducing immunological response in host against Plasmodium.
 XX
 PS Example 5; Col 11; 15pp; English.
 XX
 CC The present invention describes a recombinant vaccinia or avipox virus
 CC (RV1) containing DNA coding for Plasmodium falciparum (Pf) merocytite
 CC surface antigen 1 (MSAL) or its subfragment, operably linked to a
 CC promoter for controlling expression of the DNA. The subfragment of Pf (I)
 CC consists of an N-terminal 83 kDa fragment or the N-terminal 83 kDa
 CC fragment and the C-terminal gp42 fragment of Pf MSAL. Also described are:
 CC (1) a recombinant vaccinia or avipox virus (RV2) containing a DNA coding
 CC for a subfragment of Plasmodium MSAL of the Uganda Palo-Alto isolate of
 CC Pf, operably linked to promoter for controlling expression of DNA, the
 CC subfragment of Plasmodium MSAL consists of amino acids 1-752 or amino
 CC acids 1-752 and 1333-1726 of Plasmodium MSAL; (2) an immunological
 CC composition for inducing an immunological response in a host animal
 CC inoculated with the composition, comprising RV1 or RV2 in an admixture
 CC with a carrier; and (3) producing Plasmodium MSAL or its subfragment
 CC involves infecting a host cell with RV1 or RV2. The RV from the present
 CC invention can have antimalarial activity, and can be used in vaccine
 CC production. RV1 or RV2 is useful for inducing an immunological response
 CC in a host against Plasmodium infections such as malaria. The present
 CC sequence represents a PCR primer for the MSAL N-terminal, which is used
 CC in an example from the present invention for the expression of vaccinia
 CC recombinants of N-terminal fragments of MSAL
 XX
 SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e-02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1096 CAGCTTCGCGGCCAG 1110
 Db 17 CAGCTTCGAGGCCAG 3
 RESULT 1426
 ABK03736
 ID ABK03736 standard; RNA; 17 BP.
 XX
 AC ABK03736;
 XX
 DT 12-MAR-2002 (first entry)

XX Human CD20 Amberzyme #85.
 DE
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 PF
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 XX Blatt L, Mcswiggen J, Chowrira BM;
 PI WPI; 2001-607195/69.
 XX
 DR
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 30; Page 168; 200pp; English.
 CC
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob

CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an amberzyme molecule of the invention

XX
 SQ Sequence 17 BP; 4 A; 1 C; 8 G; 0 T; 4 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 73.3%; Pred. No. 9.6e+02;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1009 GAAGATGTGGTGGG 1023
 ||||| |:|:|:|
 Db 1 GAAGAAGUGGUGGG 15

RESULT 1427
 ABK02365
 ID ABK02365 standard; RNA; 17 BP.
 AC ABK02365;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Human NOGO Amberzyme #37.
 XX
 KW Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KW cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
 KW muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KW DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
 KW B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KW human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KW MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
 KW inflammatory arthropathy; central nervous system injury;
 KW cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KW chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KW Parkinson's disease; ataxia; Huntington's disease;
 KW Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 PN WO200159103-A2.
 XX
 PD 16-AUG-2001.
 XX
 PF 09-FEB-2001; 2001WO-US004273.
 XX
 PR 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 XX
 DR WPI; 2001-607195/69.
 XX
 PT Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 PS Claim 88; Page 131; 200pp; English.
 XX
 CC The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving a an RNA motif) pr
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NVN motif) pr

CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
 CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is an amberzyme molecule of the invention

XX
 SQ Sequence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAGAGGAGG 878
 ||||| |||||
 Db 1 AGGAGGAGAGGAGG 15

RESULT 1428
 ABA80561
 ID ABA80561 standard; DNA; 17 BP.
 XX
 AC ABA80561;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE APOE mutation correcting oligonucleotide SEQ ID NO: 3407.
 XX
 KW Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin;
 KW retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 KW cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 KW adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis;
 KW haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE;
 KW mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR;
 KW familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense;
 KW UDP-glucuronosyltransferase; amyloid precursor protein; presenilin-1;
 KW Alzheimer's disease; cytostatic; antisickling; antianaemic; haemostatic;
 KW antilipemic; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200173002-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-US009761.
 XX
 PR 27-MAR-2000; 2000US-0192176P.
 PR 27-MAR-2000; 2000US-0192179P.
 PR 01-JUN-2000; 2000US-0208538P.
 PR 30-OCT-2000; 2000US-0244989P.
 XX
 PA (UYDE) UNIV DELAWARE.

PT toxicological analysis, involves determining or comparing the expression
PT levels of at least one endogenous gene.

PS Example 3; Page 27; 77pp; English.

XX The sequence represents a downstream PCR primer used in a DDRT-PCR
CC experiment (and in cDNA synthesis), demonstrating the method of the
CC invention. The method relates to evaluating a cellular response to an
CC environmental compound, comprising determining or comparing the
CC expression levels of at least one endogenous gene e.g by differential
CC display of reverse transcribed mRNAs by PCR (DDRT-PCR). The method can be
CC adapted to identify compounds that act on the level of endogenous gene
CC expression through activating nuclear receptors. The method is useful in
CC toxicological analysis, diagnostics, for diagnosing cancer (e.g.
CC testicular, breast, prostate and endometrium), asthma, hypospadias,
CC cryptorchidism and/or allergy, and for evaluating the efficiency of a
CC treatment for hormonal deficiency or hormonal replacement therapy, in a
CC human such as a post-menopausal female. The method is also useful for
CC identifying environmental chemicals or pharmaceutical compositions that
CC interact with endocrine systems, and for detecting chemicals that pose a
CC health threat. Expression levels of endogenous genes are determined
CC rapidly using a sensitive technique, and the expression of any gene can
CC be monitored. The assays are far more informative than the currently used
CC assays, and significantly reduces the number of animals required for the
CC testing, as it is expected that essentially all the animals in a test
CC group will respond to the compound

SQ Sequence 17 BP; 2 A; 2 C; 1 G; 12 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 33 ACGAAAAAAGC 47

DB 17 ACGAAAAAAGC 3

RESULT 1431

AA171138
ID AA171138 standard; DNA; 17 BP.

XX AC AA171138;

XX DT 18-DEC-2001 (first entry)

XX DE Detection probe SEQ ID NO:38.

XX KW Shigella; Salmonella; differentiation; determination; primer; probe;
XX KW detection; microorganism; bacterium; ss.

XX OS Salmonella sp.

XX PN JP2001245677-A.

XX PD 11-SEP-2001.

XX PF 27-DEC-2000; 2000JP-00398087.

XX PR 27-DEC-1999; 99JP-00368920.

XX (SRLS-) SRL KK.
PA (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
PA (NIGE-) NIPPON GENE KK.

XX WPI; 2001-610077/70.

XX Determination of Shigella or Salmonella spp. bacteria comprises using
PT nucleic acid probes with different base sequences.

XX Claim 16; Page 10; 40pp; Japanese.

XX The present invention describes a method for differentiating bacteria by

CC using primers or probes having different base sequences. The method can
CC be used for the differentiation or detection of Shigella flexneri,
CC Shigella boydii, Shigella sonnei or Salmonella typhi, Salmonella
CC paratyphi, Salmonella typhimurium, Salmonella chester, Salmonella
CC enteritidis, and Salmonella oranienburg spp. bacteria. The method can be
CC used for rapid differentiation of 9 lines of bacteria for prevention,
CC diagnosis and treatment of diseases caused by these bacteria. The present
CC sequence represents a detection probe which is used in an example from
CC the present invention

SQ Sequence 17 BP; 3 A; 6 C; 0 G; 8 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1692 TCTTCTTTCTTCTCA 1706

DB 2 TCTTCTTTCTTCTCA 16

RESULT 1432

ABN10029
ID ABN10029 standard; DNA; 17 BP.

XX AC ABN10029;

XX DT 29-MAY-2002 (first entry)

XX DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10021.

XX KW Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
XX KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX KW skeletal muscle disorder; amplicon; screening; ss.

XX OS Homo sapiens.

XX PN WO200192524-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US016981.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024283.

XX PR 30-JAN-2001; 2001WO-US000661.

XX PR 30-JAN-2001; 2001WO-US000662.

XX PR 30-JAN-2001; 2001WO-US000663.

XX PR 30-JAN-2001; 2001WO-US000664.

XX PR 30-JAN-2001; 2001WO-US000665.

XX PR 30-JAN-2001; 2001WO-US000666.

XX PR 30-JAN-2001; 2001WO-US000667.

XX PR 30-JAN-2001; 2001WO-US000668.

XX PR 30-JAN-2001; 2001WO-US000669.

XX PR 30-JAN-2001; 2001WO-US000670.

XX PR 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.

XX Disclosure; SEQ ID NO 10021; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-

CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 CC
 CC Sequence 17 BP; 1 A; 4 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 132 CGCTGCTGGAGTCC 146
 DB 2 CGCTGCTGGAGTCC 16
 |||||

RESULT 1433
 ABN10511
 ID ABN10511 standard; DNA; 17 BP.
 XX
 AC ABN10511;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10503.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX
 PA (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 PI

XX WPI; 2002-179446/23.
 DR
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 XX or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption/ionization, comprises human myosin-like protein hGDMPLP-1.
 PT
 XX Disclosure; SEQ ID NO 10503; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
 CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 CC
 CC Sequence 17 BP; 5 A; 3 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 807 GAGAGAGCCAGGCC 821
 DB 2 GAGAGAGCCAGGCAC 16
 |||||

RESULT 1434
 ABN06400
 ID ABN06400 standard; DNA; 17 BP.
 XX
 AC ABN06400;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6392.
 XX
 KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 OS Homo sapiens.
 XX
 PN WO200192524-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 25-MAY-2001; 2001WO-US016981.
 XX
 PR 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.

```
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 6392; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 2 A; 8 C; 4 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 9.6e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 1177 GCACGTGCTCCAG 1191
DB 1 GCCCGTGCTCCAG 15
XX
RESULT 1435
ABN07888
ID ABN07888 standard; DNA; 17 BP.
XX
AC ABN07888;
XX
XX 29-MAY-2002 (first entry)
XX
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7880.
XX
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
XX muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
XX skeletal muscle disorder; amplicon; screening; ss.
XX
XX Homo sapiens.
XX
XX WO200192524-A2.
XX
XX 06-DEC-2001.
XX
```

```
XX 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 7880; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
XX The present sequence represents an oligomer used in the screening of the
XX hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 17;
XX Best Local Similarity 93.3%; Pred. No. 9.6e+02;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 837 AGCTGCTGGGCTCTC 851
DB 2 AGCTGCTGGGCTCAC 16
XX
RESULT 1436
ABN10289/c
ID ABN10289 standard; DNA; 17 BP.
XX
XX ABN10289;
XX
XX 29-MAY-2002 (first entry)
XX
```

DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10281.
XX Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX Disclosure; SEQ ID NO 10281; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1288 TTCACAGTGGATGCT 1302
||||| |||||||

Db 17 TTCACAGTGGATGCT 3
RESULT 1437
ABN10291/c
ID ABN10291 standard; DNA; 17 BP.
XX AC ABN10291;
XX DT 29-MAY-2002 (first entry)
XX DE Human GDMLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10283.
XX KW Human; genome-derived myosin-like protein 1; GDMLP-1; hGDMLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX OS Homo sapiens.
XX PN WO200192524-A2.
XX PD 06-DEC-2001.
XX PF 25-MAY-2001; 2001WO-US016981.
XX PR 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMLP-1.
XX Disclosure; SEQ ID NO 10283; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMLP-1). The protein and polynucleotide sequences of hGDMLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMLP-1, in particular heart
CC and skeletal muscle disorders. hGDMLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;
 SQ Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1288 TTCACAGTGGATGCT 1302
 Db |||||
 15 TTCAAAGTGGATGCT 1

RESULT 1438
 ABN10508
 ID ABN10508 standard; DNA; 17 BP.
 XX
 AC ABN10508;
 XX
 DT 29-MAY-2002 (first entry)
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10500.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 XX WO200192524-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 25-MAY-2001; 2001WO-US016981.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 PT Disclosure; SEQ ID NO 10500; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

CC -1 proteins, as standards in assays used to determine the concentration
 CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
 CC capture probes for surface-enhanced laser desorption/ionisation, as
 CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
 CC production, and in vaccines or for replacement therapy. The
 CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
 CC disorder associated with the expression of hGDMPLP-1, in particular heart
 CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
 CC The present sequence represents an oligomer used in the screening of the
 CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequence
 XX
 SQ Sequence 17 BP; 5 A; 3 C; 9 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 805 CAGAGAGAGCCAGGG 819
 Db |||||
 3 CGGAGAGAGCCAGGG 17

RESULT 1439
 ABN06399
 ID ABN06399 standard; DNA; 17 BP.
 XX
 AC ABN06399;
 XX
 DT 29-MAY-2002 (first entry)
 XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6391.
 DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
 KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
 KW skeletal muscle disorder; amplicon; screening; ss.
 XX Homo sapiens.
 OS
 XX WO200192524-A2.
 PN
 XX 06-DEC-2001.
 PD
 XX 25-MAY-2001; 2001WO-US016981.
 PF
 XX 26-MAY-2000; 2000US-0207456P.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 PR 30-JAN-2001; 2001WO-US000661.
 PR 30-JAN-2001; 2001WO-US000662.
 PR 30-JAN-2001; 2001WO-US000663.
 PR 30-JAN-2001; 2001WO-US000664.
 PR 30-JAN-2001; 2001WO-US000665.
 PR 30-JAN-2001; 2001WO-US000666.
 PR 30-JAN-2001; 2001WO-US000667.
 PR 30-JAN-2001; 2001WO-US000668.
 PR 30-JAN-2001; 2001WO-US000669.
 PR 05-FEB-2001; 2001US-0266860P.
 XX (AEOM-) AEOMICA INC.
 PA
 XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
 XX WPI; 2002-179446/23.
 XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
 PT or as specific biomolecule capture probes for surface-enhanced laser
 PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
 PT Disclosure; SEQ ID NO 10500; 214pp; English.
 PS
 XX The present invention describes a human genome-derived myosin-like
 CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
 CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
 CC nucleic acids can be used as probes to detect, characterise and quantify
 CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
 CC provide initial substrates for the recombinant engineering of hGDMPLP-1
 CC protein variants having desired phenotypic improvements, and for
 CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
 CC used as immunogens to raise antibodies that specifically recognise hGDMPLP

PS Disclosure; SEQ ID NO 6391; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1177 GCCACGTCGCTCCAG 1191
Db 2 GCCCGCTGCTCCAG 16
|||||

RESULT 1440

ID ABN07889

XX ABN07889 standard; DNA; 17 BP.

AC ABN07889;

XX 29-MAY-2002 (first entry)

DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7881.

DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

XX WO200192524-A2.

PN 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

PF 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

PR 04-OCT-2000; 2000US-0236359P.

PR 30-JAN-2001; 2001WO-US000661.

PR 30-JAN-2001; 2001WO-US000662.

PR 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000666.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 30-JAN-2001; 2001WO-US000670.

PR 05-FEB-2001; 2001US-0266860P.

XX (AEOM-) AEOMICA INC.

XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;

XX WPI; 2002-179446/23.

DR New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption/ionization, comprises human myosin-like protein hGDMPLP-1.

PT Disclosure; SEQ ID NO 7881; 214pp; English.

XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence

XX SQ Sequence 17 BP; 2 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 837 AGCTGCTGGGGTCTC 851
Db 1 AGCTGCTGGGGTCTC 15
|||||

RESULT 1441

ABN06398

ID ABN06398 standard; DNA; 17 BP.

XX ABN06398;

XX 29-MAY-2002 (first entry)

DT Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:6390.

DE Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.

OS Homo sapiens.

XX WO200192524-A2.

PN 06-DEC-2001.

XX 25-MAY-2001; 2001WO-US016981.

PF 26-MAY-2000; 2000US-0207456P.

XX 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000US-0266860P.

PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 6390; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 3 A; 8 C; 4 G; 2 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1177 GCACGCTGCTCCAG 1191
Db |||||
3 GCCCGTGTCTCCAG 17
RESULT 1442
ID ABN07884
XX ABN07884 standard; DNA; 17 BP.
XX
XX AC ABN07884;
XX
XX DT 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:7876.
XX Human; genome-derived myosin-like protein 1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX
XX OS Homo sapiens.

XX WO200192524-A2.
XX
XX PD 06-DEC-2001.
XX
XX PF 25-MAY-2001; 2001WO-US016981.
XX
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 21-SEP-2000; 2000US-0234687P.
XX PR 27-SEP-2000; 2000US-0236359P.
XX PR 04-OCT-2000; 2000GB-00024263.
XX PR 30-JAN-2001; 2001WO-US000661.
XX PR 30-JAN-2001; 2001WO-US000662.
XX PR 30-JAN-2001; 2001WO-US000663.
XX PR 30-JAN-2001; 2001WO-US000664.
XX PR 30-JAN-2001; 2001WO-US000665.
XX PR 30-JAN-2001; 2001WO-US000666.
XX PR 30-JAN-2001; 2001WO-US000667.
XX PR 30-JAN-2001; 2001WO-US000668.
XX PR 30-JAN-2001; 2001WO-US000669.
XX PR 30-JAN-2001; 2001WO-US000670.
XX PR 05-FEB-2001; 2001US-0266860P.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
XX Disclosure; SEQ ID NO 7876; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterize and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
XX Sequence 17 BP; 2 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
SQ
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 834 GGAGCTCTCGGGT 848
Db |||||
3 GGAGCTCTCGGGT 17
RESULT 1443
ABN10509
ID ABN10509 standard; DNA; 17 BP.
XX

AC ABN10509;
XX 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10501.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX (ABOM-) ABOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 10501; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart
XX disorder associated with the expression of hGDMPLP-1, in particular heart

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 805 CAGAGAGAGCCAGGG 819
Db 2 CGGAGAGAGCCAGGG 16
RESULT 1444
ABN10028
ID ABN10028 standard; DNA; 17 BP.
XX AC ABN10028;
XX 29-MAY-2002 (first entry)
XX Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10020.
XX Human; genome-derived myosin-like protein 1; GDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
XX Homo sapiens.
XX WO200192524-A2.
XX 06-DEC-2001.
XX 25-MAY-2001; 2001WO-US016981.
XX 26-MAY-2000; 2000US-0207456P.
XX 21-SEP-2000; 2000US-0234687P.
XX 27-SEP-2000; 2000US-0236359P.
XX 04-OCT-2000; 2000GB-00024263.
XX 30-JAN-2001; 2001WO-US000661.
XX 30-JAN-2001; 2001WO-US000662.
XX 30-JAN-2001; 2001WO-US000663.
XX 30-JAN-2001; 2001WO-US000664.
XX 30-JAN-2001; 2001WO-US000665.
XX 30-JAN-2001; 2001WO-US000666.
XX 30-JAN-2001; 2001WO-US000667.
XX 30-JAN-2001; 2001WO-US000668.
XX 30-JAN-2001; 2001WO-US000669.
XX 30-JAN-2001; 2001WO-US000670.
XX 05-FEB-2001; 2001US-0266860P.
XX (ABOM-) ABOMICA INC.
XX Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
XX or as specific biomolecule capture probes for surface-enhanced laser
XX desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX Disclosure; SEQ ID NO 10020; 214pp; English.
XX The present invention describes a human genome-derived myosin-like
XX protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
XX 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
XX nucleic acids can be used as probes to detect, characterise and quantify
XX hGDMPLP-1 nucleic acids in samples, as amplification substrates, to
XX provide initial substrates for the recombinant engineering of hGDMPLP-1
XX protein variants having desired phenotypic improvements, and for
XX expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
XX used as immunogens to raise antibodies that specifically recognise hGDMPLP
XX -1 proteins, as standards in assays used to determine the concentration
XX and/or amount specifically of hGDMPLP proteins, as specific biomolecule
XX capture probes for surface-enhanced laser desorption ionisation, as
XX therapeutic supplement in patients having specific deficiency in hGDMPLP-1
XX production, and in vaccines or for replacement therapy. The
XX polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
XX disorder associated with the expression of hGDMPLP-1, in particular heart

CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 1 A; 4 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 132 CGCTGCTCGAGTCC 146
DB 3 CGGTGCTCGAGTCC 17

RESULT 1445
ABN10290/c
ID ABN10290 standard; DNA; 17 BP.
XX ABN10290;
AC ABN10290;
DT 29-MAY-2002 (first entry)
DE Human GDMPLP-1 17-mer scanning SEQ ID NO:5 sequence SEQ ID NO:10282.
XX
KW Human; genome-derived myosin-like protein 1; GDMPLP-1; hGDMPLP-1; heart;
KW muscle; myosin; chromosome 22; gene therapy; vaccine; heart disease;
KW skeletal muscle disorder; amplicon; screening; ss.
OS Homo sapiens.
XX
PN WO200192524-A2.
XX
PD 06-DEC-2001.
XX
PF 25-MAY-2001; 2001WO-US016981.
XX
XX 26-MAY-2000; 2000US-0207456P.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
PR 30-JAN-2001; 2001WO-US000661.
PR 30-JAN-2001; 2001WO-US000662.
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000666.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 30-JAN-2001; 2001WO-US000670.
PR 05-FEB-2001; 2001US-0266860P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Gu Y, Ji Y, Penn SG, Hanzel DK, Rank DR, Chen W, Shannon ME;
XX WPI; 2002-179446/23.
XX
XX New polypeptide, for raising antibodies that recognize hGDMPLP-1 proteins,
PT or as specific biomolecule capture probes for surface-enhanced laser
PT desorption ionization, comprises human myosin-like protein hGDMPLP-1.
XX
PS Disclosure; SEQ ID NO 10282; 214pp; English.
XX
XX The present invention describes a human genome-derived myosin-like
CC protein 1 (hGDMPLP-1). The protein and polynucleotide sequences of hGDMPLP-
CC 1 can be used in gene therapy and vaccine production. The hGDMPLP-1
CC nucleic acids can be used as probes to detect, characterise and quantify
CC hGDMPLP-1 nucleic acids in samples, as amplification substrates, to

CC provide initial substrates for the recombinant engineering of hGDMPLP-1
CC protein variants having desired phenotypic improvements, and for
CC expressing the proteins. The hGDMPLP-1 proteins or polypeptides may be
CC used as immunogens to raise antibodies that specifically recognise hGDMPLP
CC -1 proteins, as standards in assays used to determine the concentration
CC and/or amount specifically of hGDMPLP proteins, as specific biomolecule
CC capture probes for surface-enhanced laser desorption/ionisation, as
CC therapeutic supplement in patients having specific deficiency in hGDMPLP-1
CC production, and in vaccines or for replacement therapy. The
CC polynucleotide sequences encoding hGDMPLP-1 may be used for diagnosing a
CC disorder associated with the expression of hGDMPLP-1, in particular heart
CC and skeletal muscle disorders. hGDMPLP-1 is localised to chromosome 22.
CC The present sequence represents an oligomer used in the screening of the
CC hGDMPLP-1 sequence in the exemplification of the present invention. N.B.
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequence
XX
SQ Sequence 17 BP; 7 A; 4 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1288 TTCACAGTGGATGCT 1302
DB 16 TTCAGAGTGGATGCT 2

RESULT 1446
ABV79402/c
ID ABV79402 standard; DNA; 17 BP.
XX ABV79402;
AC ABV79402;
XX
DT 03-JAN-2003 (first entry)
XX
DE Human HTPL scanning oligonucleotide SEQ ID 648.
XX
KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
KW human testis expressed Patched like protein; testis; adrenal; liver;
KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
KW prostate; skeletal muscle; colon; male infertility; cancer; ss.
OS Homo sapiens.
XX
PN EP1229046-A2.
XX
PD 07-AUG-2002.
XX
PF 28-JAN-2002; 2002EP-00001167.
XX
PR 30-JAN-2001; 2001WO-US000663.
PR 30-JAN-2001; 2001WO-US000664.
PR 30-JAN-2001; 2001WO-US000665.
PR 30-JAN-2001; 2001WO-US000667.
PR 30-JAN-2001; 2001WO-US000668.
PR 30-JAN-2001; 2001WO-US000669.
PR 23-MAY-2001; 2001US-00864761.
PR 09-OCT-2001; 2001US-0327899P.
XX
PA (AEOM-) AEOMICA INC.
XX
PI Zhan J;
XX
DR WPI; 2002-676582/73.
XX
XX Novel isolated human testis expressed Patched like protein (HTPL), useful
PT for identifying agonist and antagonist and specific binding partners, and
PT for treating subjects having defects in HTPL.
XX
PS Example 2; Page 148; 718pp; English.
XX

CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX
 SQ Sequence 17 BP; 2 A; 5 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 852 TGGCCCTGCAGGAG 866
 |||||
 Db 16 TGGCCCTGCAGGAG 2

RESULT 1447
 ABV79403/C
 ID ABV79403 standard; DNA; 17 BP.

AC ABV79403;

DT 03-JAN-2003 (first entry)

DE Human HTPL scanning oligonucleotide SEQ ID 649.

KW Human; gene therapy; tumour suppressor; HTPL; chromosome 10p12.1;
 KW human testis expressed Patched like protein; testis; adrenal; liver;
 KW male germ cell development; bone marrow; brain; kidney; lung; placenta;
 KW prostate; skeletal muscle; colon; male infertility; cancer; ss.

OS Homo sapiens.

FN EPI229046-A2.

XX 07-AUG-2002.

XX 28-JAN-2002; 2002EP-00001167.

XX 30-JAN-2001; 2001WO-US000663.

PR 30-JAN-2001; 2001WO-US000664.

PR 30-JAN-2001; 2001WO-US000665.

PR 30-JAN-2001; 2001WO-US000667.

PR 30-JAN-2001; 2001WO-US000668.

PR 30-JAN-2001; 2001WO-US000669.

PR 23-MAY-2001; 2001US-00864761.

PR 09-OCT-2001; 2001US-0327898P.

PA (AEOM-) AEOMICA INC.

PI Zhan J;

XX WPI; 2002-676582/73.

PT Novel isolated human testis expressed Patched like protein (HTPL), useful
 PT for identifying agonist and antagonist and specific binding partners, and
 PT for treating subjects having defects in HTPL.

XX

BS Example 2; Page 148; 718pp; English.

CC The present invention relates to human testis expressed Patched like
 CC protein (HTPL, see ABV78759 to ABV78762 and AB98519 to AB98520). HTPL
 CC has two isoforms, with a few single base pair differences between the
 CC two. One of the single base pair changes introduces a premature stop
 CC codon in HTPL-S (S for short) compared to HTPL-L (L for long). HTPL
 CC shares an overall structure organisation with the Patched protein. The
 CC shared structural features strongly imply that HTPL plays a role similar
 CC to that of Patched, and is a potential tumour suppressor. HTPL is
 CC important in regulating male germ cell development, and the HTPL gene was
 CC mapped to human chromosome 10p12.1. HTPL and its coding sequence are
 CC useful for diagnosing a disorder caused by mutation in HTPL, and in
 CC therapy and manufacture of a medicament for treatment or prevention of
 CC such disorder associated with decreased expression or activity of human
 CC HTPL. Such disorders include disorders of testis, or adrenal, adult and
 CC foetal liver, bone marrow, brain, kidney, lung, placenta, prostate,
 CC skeletal muscle or colon function. HTPL proteins and nucleic acids are
 CC clinically useful diagnostic markers and potential therapeutic agents for
 CC male infertility and cancer. The present oligonucleotide was used in an
 CC example from the invention
 XX

SQ Sequence 17 BP; 2 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 852 TGGCCCTGCAGGAG 866

|||||
 Db 15 TGGCCCTGCAGGAG 1

RESULT 1448

ABK19204/C

ID ABK19204 standard; RNA; 17 BP.

AC ABK19204;

DT 09-APR-2002 (first entry)

DE Human ERG Amberzyme target sequence Seq ID No 1851.

KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antarthritic; antipsoriatic; virucide; osteopathic;
 KW vulvular; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.

OS Homo sapiens.

XX WO200188124-A2.

XX 22-NOV-2001.

XX 16-MAY-2001; 2001WO-US015866.

XX 16-MAY-2000; 2000US-00572021.

PR (RIBO-) RIBOZYME PHARM INC.

PA (GLAX) GLAXO GROUP LTD.

XX Järvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin P, Randi AM;
 PI WPI; 2002-082995/11.

DR Novel polynucleotide which down regulates expression of Ets-related gene,

PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX PS Claim 4; Page 122; 149pp; English.

XX CC The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK17354-ABK22719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

XX SQ Sequence 17 BP; 2 A; 3 C; 9 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 613 CCCACTCCAGCCTCT 627
|||||

DB 16 CCACCTCCAGCCACT 2

RESULT 1449

ABK18235

ID ABK18235 standard; RNA; 17 BP.

XX AC ABK18235;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 882.

XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;

KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

amberzyme.

OS Homo sapiens.

XX WO200188124-A2.

XX PD 22-NOV-2001.

XX PF 16-MAY-2001; 2001WO-US015866.

XX PR 16-MAY-2000; 2000US-00572021.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PA (GLAX) GLAXO GROUP LTD.

PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;

XX WPI; 2002-082995/11.

XX PT Novel polynucleotide which down regulates expression of Ets-related gene,

PT useful for treating cancer, diabetic retinopathy, macular degeneration,

PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.

XX PS Claim 4; Page 75; 149pp; English.

XX CC The invention relates to a nucleic acid molecule (I) which down regulates

CC expression of an Ets-related gene (ERG). (I) is useful for treating

CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,

CC tumour angiogenesis, diabetic retinopathy, macular degeneration,

CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca

CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge

CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu

CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for

CC treating a patient having a condition associated with the level of ERG,

CC by contacting cells of the patient with (I) under conditions suitable for

CC the treatment. The method comprises the use of one or more therapies

CC under conditions suitable for the treatment. Leukaemia or tumour

CC angiogenesis is treated by administering (I) to the patient in

CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a

CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of

CC ERG gene, by contacting (I) with RNA, in the presence of a divalent

CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and

CC diseases related to the expression of ERG, and as diagnostic tool to

CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.

CC ABK17354-ABK22719 represent nucleic acids, including antisense and

CC enzymatic nucleic acid molecules which regulate expression of ERG, and

CC related PCR primers of the invention

XX SQ Sequence 17 BP; 2 A; 9 C; 3 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;

Best Local Similarity 80.0%; Pred. No. 9.6e+02;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 655 CCAGCCTTCCCGTG 669
|||||

DB 2 CCAGCCUCCCGUG 16

RESULT 1450

ABK17536

ID ABK17536 standard; RNA; 17 BP.

XX AC ABK17536;

XX DT 09-APR-2002 (first entry)

XX DE Human ERG hammerhead ribozyme target sequence, Seq ID No 183.

XX KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;

KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;

KW vulnary; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;

KW tumour angiogenesis; diabetic retinopathy; macular degeneration;

KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;

KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;

KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;

KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;

amberzyme.

OS Homo sapiens.

XX WO200188124-A2.

XX PD 22-NOV-2001.

PF 16-MAY-2001; 2001WO-US015866.
 PR XX
 XX OS Homo sapiens.
 XX EN WO200188124-A2.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PD 22-NOV-2001.
 XX PF 16-MAY-2001; 2001WO-US015866.
 XX PR 16-MAY-2000; 2000US-00572021.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX DR WPI; 2002-082995/11.
 XX PT Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX PS Claim 4; Page 62; 149pp; English.
 XX CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX SQ Sequence 17 BP; 2 A; 10 C; 3 G; 0 T; 2 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 655 CCAGCTTTCCTCCCGTG 669
 ||||| :|||:
 Db 1 CCAGCCUCCUCCCGUG 15
 RESULT 1451
 ABK19388
 ID ABK19388 standard; RNA; 17 BP.
 AC ABK19388;
 XX 09-APR-2002 (first entry)
 DT Human ERG Amberzyme target sequence Seq ID No 2035.
 DE Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 XX opthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.

XX OS Homo sapiens.
 XX EN WO200188124-A2.
 XX XX PD 22-NOV-2001.
 XX PF 16-MAY-2001; 2001WO-US015866.
 XX PR 16-MAY-2000; 2000US-00572021.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PA (GLAX) GLAXO GROUP LTD.
 XX PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 XX DR WPI; 2002-082995/11.
 XX PT Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX PS Claim 4; Page 127; 149pp; English.
 XX CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX SQ Sequence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 861 AGGAGGAGGAGAGG 875
 ||||| :|||:
 Db 2 AGGAGGAGGAGAGG 16
 RESULT 1452
 ABK19205/c
 ID ABK19205 standard; RNA; 17 BP.
 XX AC ABK19205;
 XX 09-APR-2002 (first entry)
 DT Human ERG Amberzyme target sequence Seq ID No 1852.
 DE Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW opthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW amberzyme.

KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
 KW amberzyme.
 XX Homo sapiens.
 OS
 XX WO200188124-A2.
 PN
 XX 22-NOV-2001.
 PD
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAXO) GLAXO GROUP LTD.
 PA
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 XX
 DR Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 PT
 PS Claim 4; Page 122; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 2 A; 2 C; 10 G; 0 T; 3 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 613 CCCACTCCAGCTCT 627
 DB 15 CCCACTCCAGCCACT 1
 RESULT 1453
 ABK19389
 ID ABK19389 standard; RNA; 17 BP.
 XX
 AC ABK19389;

XX 09-APR-2002 (first entry)
 DE Human ERG Amberzyme target sequence Seq ID No 2036.
 XX
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulnery; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberous sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
 KW Osler-Weber-rendu syndrome, leukaemia; osteoporosis; DNAzyme; inozyme;
 KW amberzyme.
 XX Homo sapiens.
 OS
 XX WO200188124-A2.
 PN
 XX 22-NOV-2001.
 PD
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (GLAXO) GLAXO GROUP LTD.
 PA
 XX Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 PI WPI; 2002-082995/11.
 XX
 DR Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 PT
 PS Claim 4; Page 127; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberous sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or
 CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 7 A; 1 C; 9 G; 0 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 861 AGGAGAGGAGAGG 875
 DB 1 AGGAGAGGAGAGG 15

RESULT 1454
ABK17999/c
ID ABK17999 standard; RNA; 17 BP.
XX
AC ABK17999;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 646.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulvular; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
KW amberyze.
OS Homo sapiens.
XX
FN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 70; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically
CC targeting genes that share homology with ERG gene or ERG fusion genes.
CC ABK17354-ABK22719 represent nucleic acids, including antisense and
CC enzymatic nucleic acid molecules which regulate expression of ERG, and
CC related PCR primers of the invention
XX
SQ Sequence 17 BP; 2 A; 2 C; 10 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 613 CCCACTCCAGCCTCT 627
|||||||
Db 17 CCCACTCCAGCCTCT 3

RESULT 1455
ABK18187
ID ABK18187 standard; RNA; 17 BP.
XX
AC ABK18187;
XX
DT 09-APR-2002 (first entry)
XX
DE Human ERG hammerhead ribozyme target sequence, Seq ID No 834.
XX
KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
KW vulvular; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; ss;
KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
KW amberyze.
OS Homo sapiens.
XX
FN WO200188124-A2.
XX
PD 22-NOV-2001.
XX
PF 16-MAY-2001; 2001WO-US015866.
XX
PR 16-MAY-2000; 2000US-00572021.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
XX
DR WPI; 2002-082995/11.
XX
PT Novel polynucleotide which down regulates expression of Ets-related gene,
PT useful for treating cancer, diabetic retinopathy, macular degeneration,
PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
XX
PS Claim 4; Page 74; 149pp; English.
XX
CC The invention relates to a nucleic acid molecule (I) which down regulates
CC expression of an Ets-related gene (ERG). (I) is useful for treating
CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
CC treating a patient having a condition associated with the level of ERG,
CC by contacting cells of the patient with (I) under conditions suitable for
CC the treatment. The method comprises the use of one or more therapies
CC under conditions suitable for the treatment. Leukaemia or tumour
CC angiogenesis is treated by administering (I) to the patient in
CC conjunction with one or more of other therapies such as radiation or
CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
CC cation such as Mg2+. (I) is useful for diagnosis of conditions and
CC diseases related to the expression of ERG, and as diagnostic tool to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ERG RNA in a cell. (I) is useful for specifically

CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 3 A; 10 C; 3 G; 0 T; 1 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 86.7%; Pred. No. 9.6e+02;
 Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 268 GCATCCAGCCGAC 282
 |||:|||||||
 Db 3 GCCCUCAGCCGAC 17
 RESULT 1456
 ABK18234
 ID ABK18234 standard; RNA; 17 BP.
 XX
 AC ABK18234;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Human ERG hammerhead ribozyme target sequence, Seq ID No 881.
 KW Human; hammerhead ribozyme; cytostatic; antitumour; antidiabetic;
 KW ophthalmological; antiarthritic; antipsoriatic; virucide; osteopathic;
 KW vulvar; cancer; lymphoma; Ewing's sarcoma; melanoma; psoriasis;
 KW tumour angiogenesis; diabetic retinopathy; macular degeneration;
 KW neovascular glaucoma; myopic degeneration; arthritis; verruca vulgaris;
 KW angiofibroma of tuberosus sclerosis; port-wine stain; wound healing;
 KW Sturge Weber syndrome; Kippel-Trenaunay-Weber syndrome; leukaemia; as;
 KW Osler-Weber-rendu syndrome; leukaemia; osteoporosis; DNazyme; inozyme;
 KW amberzyme.
 XX
 OS Homo sapiens.
 XX
 PN WO200188124-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015866.
 XX
 PR 16-MAY-2000; 2000US-00572021.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Jarvis T, Von Carlowitz I, Mcswiggen JA, McLaughlin F, Randi AM;
 DR WPI; 2002-082995/11.
 XX
 PT Novel polynucleotide which down regulates expression of Ets-related gene,
 PT useful for treating cancer, diabetic retinopathy, macular degeneration,
 PT arthritis, psoriasis, verruca vulgaris and Sturge Weber syndrome.
 XX
 PS Claim 4; Page 75; 149pp; English.
 XX
 CC The invention relates to a nucleic acid molecule (I) which down regulates
 CC expression of an Ets-related gene (ERG). (I) is useful for treating
 CC conditions selected from cancer, lymphoma, Ewing's sarcoma, melanoma,
 CC tumour angiogenesis, diabetic retinopathy, macular degeneration,
 CC neovascular glaucoma, myopic degeneration, arthritis, psoriasis, verruca
 CC vulgaris, angiofibroma of tuberosus sclerosis, port-wine stains, Sturge
 CC Weber syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-rendu
 CC syndrome, leukaemia, osteoporosis and wound healing. (I) is useful for
 CC treating a patient having a condition associated with the level of ERG,
 CC by contacting cells of the patient with (I) under conditions suitable for
 CC the treatment. The method comprises the use of one or more therapies
 CC under conditions suitable for the treatment. Leukaemia or tumour
 CC angiogenesis is treated by administering (I) to the patient in
 CC conjunction with one or more of other therapies such as radiation or

CC chemotherapy treatment. (I) is useful for reducing ERG activity in a
 CC cell, by contacting the cell with (I). (I) is useful for cleaving RNA of
 CC ERG gene, by contacting (I) with RNA, in the presence of a divalent
 CC cation such as Mg²⁺. (I) is useful for diagnosis of conditions and
 CC diseases related to the expression of ERG, and as diagnostic tool to
 CC examine genetic drift and mutations within diseased cells or to detect
 CC the presence of ERG RNA in a cell. (I) is useful for specifically
 CC targeting genes that share homology with ERG gene or ERG fusion genes.
 CC ABK17354-ABK22719 represent nucleic acids, including antisense and
 CC enzymatic nucleic acid molecules which regulate expression of ERG, and
 CC related PCR primers of the invention
 XX
 SQ Sequence 17 BP; 1 A; 10 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 655 CCAGCCTTCCCGTG 669
 |||||:|||||
 Db 3 CCAGCCUCCCGUG 17
 RESULT 1457
 ABK57766/c
 ID ABK57766 standard; RNA; 17 BP.
 XX
 AC ABK57766;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE Human CLCA1 gene enzymatic nucleic acid #2137.
 KW Human; chloride channel calcium activated 1; CLCA1; as; antiasthmatic;
 KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
 KW acetylcysteine.
 XX
 OS Homo sapiens.
 XX
 PN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US024970.
 XX
 PR 09-AUG-2000; 2000US-0224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNTE) SYNTE USA LLC.
 PA (THOM/) THOMPSON J.
 XX
 PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Grupe A;
 XX
 DR WPI; 2002-217145/27.
 XX
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.
 XX
 PS Claim 4; Page 135; 152pp; English.
 XX
 CC The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition

CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 908 AGCTCTCCGAGGATG 922
Db 15 AGCTCTCCGAGGATG 1
RESULT 1458
ABK56032/c
ID ABK56032 standard; RNA; 17 BP.
XX
AC ABK56032;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #403.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 60; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect

CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 0 T; 3 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 908 AGCTCTCCGAGGATG 922
Db 17 AGCTCTCCGAGGATG 3
RESULT 1459
ABK57765/c
ID ABK57765 standard; RNA; 17 BP.
XX
AC ABK57765;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #2136.
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
OS Homo sapiens.
XX
PN WO200211674-A2.
XX
PD 14-FEB-2002.
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grupe A;
XX
DR WPI; 2002-217145/27.
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 4; Page 135; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect

CC the presence of C1CA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
SQ Sequence 17 BP; 3 A; 6 C; 5 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 908 AGCTCCAGAGGATG 922
|||
Db 16 AGCTCCAGAGGATG 2

RESULT 1460
ACC53048/c
ID ACC53048 standard; DNA; 17 BP.

XX
AC ACC53048;

XX
DT 27-JUN-2003 (first entry)

XX
DE Human tumour suppressor sequence #1815.

XX ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
KW tumour regression; apoptosis; virus resistance; diagnosis;
KW cellular degeneration.

XX
OS Homo sapiens.

XX
PN FR2826373-A1.

XX
PD 27-DEC-2002.

XX
PF 20-JUN-2001; 2001FR-00008139.

XX
PR 20-JUN-2001; 2001FR-00008139.

XX
PA (MOLE-) MOLECULAR ENGINES LAB SA.

XX
PI Tuijnder M, Telerman A, Amson R;

XX
DR WPI; 2003-250498/25.

XX New nucleic acid sequences associated with tumor suppression, regression,
PT apoptosis or virus resistance are useful to diagnose and treat viral
PT disease, development of tumor cells and cell degeneration.

XX
PS Claim 1; Page 459; 798pp; French.

XX This sequence represents an isolated nucleic acid sequence associated
CC with tumour suppression or regression, apoptosis or virus resistance. The
CC invention relates to these sequences or sequences having at least 80%
CC identity to them, and polypeptides encoded by the sequences or
CC polypeptides having 80% identity to the polypeptide sequences. The
CC invention is used to diagnose or treat viral disease or disease
CC characterized by development of tumour cells or cellular degeneration

XX
SQ Sequence 17 BP; 3 A; 4 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 907 CAGCTCCAGAGGAT 921
|||
Db 16 CAGCTCCAGAGGAT 2

RESULT 1461

ACC52311/c

ID ACC52311 standard; DNA; 17 BP.

XX

AC
XX
DT
XX
DE
XX
KW
KW
KW
OS
XX
PN
PD
XX
PF
XX
PR
XX
PA
XX
PI
XX
DR
XX
PT
PT
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
SQ

ACC52311;
27-JUN-2003 (first entry)
Human tumour suppressor sequence #1078.
ss; tumour suppressor; antitumour; cytostatic; tumour suppression;
tumour regression; apoptosis; virus resistance; diagnosis;
cellular degeneration.

Homo sapiens.

FR2826373-A1.

27-DEC-2002.

20-JUN-2001; 2001FR-00008139.

20-JUN-2001; 2001FR-00008139.

(MOLE-) MOLECULAR ENGINES LAB SA.

Tuijnder M, Telerman A, Amson R;

WPI; 2003-250498/25.

New nucleic acid sequences associated with tumor suppression, regression,
apoptosis or virus resistance are useful to diagnose and treat viral
disease, development of tumor cells and cell degeneration.

Claim 1; Page 289; 798pp; French.

This sequence represents an isolated nucleic acid sequence associated
with tumour suppression or regression, apoptosis or virus resistance. The
invention relates to these sequences or sequences having at least 80%
identity to them, and polypeptides encoded by the sequences or
polypeptides having 80% identity to the polypeptide sequences. The
invention is used to diagnose or treat viral disease or disease
characterized by development of tumour cells or cellular degeneration

Sequence 17 BP; 3 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1386 GCCAGGTCAGGAGGA 1400
|||
Db 17 GCCAGGTCAGGAGGA 3

RESULT 1462

ACA06577

ID ACA06577 standard; RNA; 17 BP.

XX
AC ACA06577;

XX
DT 03-JUN-2003 (first entry)

XX
DE NFkB sub-unit modulating inozyme substrate #396.

XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW G-cleaver; amberyze; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;

KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
OS Homo sapiens.
XX US2002177568-A1.
XX 28-NOV-2002.
XX 23-MAY-2001; 2001US-00864785.
XX 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-00777916.
XX (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX WPI; 2003-340953/32.
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX Claim 3; Page 33; 72pp; English.
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, docetaxel, cisplatin, methotrexate,
CC chemotherapy including paclitaxel, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX Sequence 17 BP; 4 A; 7 C; 5 G; 0 T; 1 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 704 GCCCACCAGCGGG 718
|||||||
Db 3 GCCCACCAGCGUGG 17
RESULT 1463
ACA07733/C
ID ACA07733 standard; RNA; 17 BP.
XX ACA07733;
AC ACA07733;
XX
XX 03-JUN-2003 (first entry)
XX

DE NFkB sub-unit modulating zinzyme substrate #132.
XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX Homo sapiens.
OS
XX US2002177568-A1.
PN
XX 28-NOV-2002.
PD
XX 23-MAY-2001; 2001US-00864785.
PF
XX 07-DEC-1992; 92US-00987132.
PR
XX 18-MAY-1994; 94US-00245466.
PR
XX 15-AUG-1994; 94US-00291932.
PR
XX 23-DEC-1996; 96US-00777916.
XX (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX Stinchcomb DT, Mcswiggen J, Draper KG;
XX WPI; 2003-340953/32.
XX Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX Claim 3; Page 39; 72pp; English.
XX The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX Sequence 17 BP; 3 A; 10 C; 2 G; 0 T; 2 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1023 GGATGGGCTGGGGT 1037
 DB 17 GGATAGGGCTGGGGT 3

RESULT 1464
 ID ACA06470 standard; RNA; 17 BP.
 XX ACA06470;
 AC ACA06470;
 XX 03-JUN-2003 (first entry)
 DT 03-JUN-2003 (first entry)
 XX NFkB sub-unit modulating inozyme substrate #289.
 DE NFkB sub-unit modulating inozyme substrate #289.
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberyze; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherap; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US2002177568-A1.
 PN US2002177568-A1.
 XX 28-NOV-2002.
 PD 28-NOV-2002.
 XX 23-MAY-2001; 2001US-00864785.
 PF 23-MAY-2001; 2001US-00864785.
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX (STIN/) STINCHOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX Claim 3; Page 31; 72pp; English.
 XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberyze
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic

acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX Sequence 17 BP; 2 A; 10 C; 1 G; 0 T; 4 U; 0 Other;
 SQ Sequence 17 BP; 2 A; 10 C; 1 G; 0 T; 4 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1022 GGGATGGGCTGGGG 1036
 DB 15 GGGATAGGGCTGGGG 1

RESULT 1465
 ID ACA09009 standard; RNA; 17 BP.
 XX ACA09009;
 AC ACA09009;
 XX 03-JUN-2003 (first entry)
 DT 03-JUN-2003 (first entry)
 XX NFkB sub-unit modulating amberyze substrate #172.
 DE NFkB sub-unit modulating amberyze substrate #172.
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberyze; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherap; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX US2002177568-A1.
 PN US2002177568-A1.
 XX 28-NOV-2002.
 PD 28-NOV-2002.
 XX 23-MAY-2001; 2001US-00864785.
 PF 23-MAY-2001; 2001US-00864785.
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX (STIN/) STINCHOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX Claim 3; Page 54; 72pp; English.
 XX The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor

CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapies including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 SQ Sequence 17 BP; 3 A; 7 C; 6 G; 0 T; 1 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 705 CCCACCCCGCGGG 719
 DB 1 CCCACCCCGCGGG 15
 RESULT 1466
 ACA06875/c
 ID ACA06875 standard; RNA; 17 BP.
 AC ACA06875;
 AC
 DT 03-JUN-2003 (first entry)
 XX
 DE NFkB sub-unit modulating inozyme substrate #694.
 XX
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapies; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2002177568-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 23-MAY-2001; 2001US-00864785.
 XX
 PR 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX
 PA (STIN)/ STINCHOMB D T.
 PA (MCSW)/ MCSWIGGEN J.

PA (DRAP)/ DRAPER K G.
 XX
 PI Stinchcomb DT, Mcswiggen J, Draper KG;
 XX
 DR WPI; 2003-340953/32.
 XX
 PT Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 PS Claim 3; Page 37; 72pp; English.
 XX
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFkB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
 CC chemotherapies including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubicin, fluorouracil carboplatin, edatrexate,
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 SQ Sequence 17 BP; 8 A; 3 C; 3 G; 0 T; 3 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1636 CTTTGATTGTCAC 1650
 DB 16 CTTTGATTGTCAC 2
 RESULT 1467
 ACA07620
 ID ACA07620 standard; RNA; 17 BP.
 XX
 AC ACA07620;
 XX
 DT 03-JUN-2003 (first entry)
 XX
 DE NFkB sub-unit modulating zinzyme substrate #19.
 XX
 KW Enzymatic nucleic acid; nuclear factor kappa B; NFkB; inozyme; zinzyme;
 KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapies; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubicin; fluorouracil carboplatin; edatrexate;
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX
 OS Homo sapiens.

XX US2002177568-A1.
 PN 28-NOV-2002.
 PD
 XX
 XX 23-MAY-2001; 2001US-00864785.
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX
 XX (STIN/) STINCHCOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 DR
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 XX Claim 3; Page 38; 72pp; English.
 XX
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, docetaxel, cisplatin, methotrexate,
 CC chemotherapeutic including paclitaxel, fluorouracil carboplatin, edatrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 XX Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;
 SQ
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1445 GTTACAGTGCAGG 1459
 DB 2 GCUACAAGGCGAGG 16
 RESULT 1468
 ACA07621
 ID ACA07621 standard; RNA; 17 BP.
 XX
 XX ACA07621;
 AC
 XX
 XX 03-JUN-2003 (first entry)
 DT
 XX NFKB sub-unit modulating zinzyme substrate #20.
 DE
 XX Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
 KW

KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
 KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
 KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
 KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
 KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
 KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
 KW gencitabine; radiation therapy; inflammatory disease; asthma; diabetes;
 KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
 KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
 KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
 KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
 XX
 OS Homo sapiens.
 XX
 XX US2002177568-A1.
 PN
 XX 28-NOV-2002.
 PD
 XX
 XX 23-MAY-2001; 2001US-00864785.
 XX 07-DEC-1992; 92US-00987132.
 PR 18-MAY-1994; 94US-00245466.
 PR 15-AUG-1994; 94US-00291932.
 PR 23-DEC-1996; 96US-00777916.
 XX
 XX (STIN/) STINCHCOMB D T.
 PA (MCSW/) MCSWIGGEN J.
 PA (DRAP/) DRAPER K G.
 XX
 XX Stinchcomb DT, Mcswiggen J, Draper KG;
 PI WPI; 2003-340953/32.
 DR
 XX Novel enzymatic nucleic acid molecules which down regulates expression of
 PT a sequence encoding a subunit of nuclear factor kappa B useful for
 PT treating cancer, inflammatory disorders and autoimmune diseases.
 XX
 XX Claim 3; Page 38; 72pp; English.
 XX
 CC The invention describes an enzymatic nucleic acid molecule (I) which down
 CC regulates expression of a sequence encoding a subunit of nuclear factor
 CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
 CC configuration. The enzymatic nucleic acid molecule is adapted to treat
 CC cancer and is useful for down-regulating REL-A activity in a cell, for
 CC treating a patient having a condition associated with the level of REL-A.
 CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
 CC the presence of a divalent cation, especially Mg²⁺. The enzymatic and
 CC antisense nucleic acid molecules are useful for treating breast, lung,
 CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
 CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
 CC multidrug resistant cancer. The method involves use of other drug
 CC therapies such as monoclonal antibodies, docetaxel, cisplatin, methotrexate,
 CC chemotherapeutic including paclitaxel, docetaxel, cisplatin, methotrexate,
 CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
 CC gencitabine or radiation therapy. The enzymatic and antisense nucleic
 CC acid molecules are also useful for treating inflammatory disease such as
 CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
 CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
 CC rejection, gene therapy applications, ischaemia/reperfusion injury
 CC (central nervous system (CNS) and myocardial), glomerulonephritis,
 CC sepsis, allergic airway inflammation, inflammatory bowel disease or
 CC infection. This sequence represents the substrate of a novel enzymatic
 CC nucleic acid molecule
 XX
 XX Sequence 17 BP; 4 A; 4 C; 7 G; 0 T; 2 U; 0 Other;
 SQ
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1447 TACAAGTGCAGGAG 1461
 :|||||:|||||

Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 80.0%; Pred. No. 9.6e+02;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


```
KW developmental disorder; ss.
XX
OS Homo sapiens.
XX
PN EP1281758-A2.
XX
XX 05-FEB-2003.
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 3186; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 864 AAGAGGAGGAGGAGG 878
DB | ||||| ||||| |||||
3 AGGAGGAGGAGGAGG 17

RESULT 1472
ADB00092
ID ADB00092 standard; DNA; 17 BP.
XX
XX ADB00092;
AC | ||||| ||||| |||||
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD23 scanning oligonucleotide SEQ ID 1078.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
```

```
PF 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
XX WPI; 2003-423107/40.
XX
XX New zinc finger-containing proteins and nucleic acids, useful in
PT manufacturing a medicament for treating or preventing a disorder
PT associated with decreased or increased expression or activity of MD23,
PT MD24, MD27 or MD212, e.g. cancer.
XX
XX Example 8; SEQ ID NO 1078; 103pp; English.
XX
XX The present invention relates to novel human zinc finger-containing
CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is
CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,
CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome
CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,
CC or in manufacturing a medicament for treating or preventing a disorder
CC associated with decreased or increased expression or activity of MD23,
CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic
CC acids and proteins are also useful for diagnosing or monitoring a disease
CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic
CC acids can also be used as probes to detect and characterize gross
CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are
CC useful in constructing microarrays for measuring gene expression. The
CC proteins are useful as therapeutic agents for gene therapy or as
CC vaccines. The present sequence was used to illustrate the invention.
XX
XX Sequence 17 BP; 2 A; 5 C; 7 G; 3 T; 0 U; 0 Other;
SQ Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 852 TGGCCCTGCAGGAGG 866
DB | ||||| ||||| |||||
2 TGGCCCTGCAGGAGG 16

RESULT 1473
ADB04267/C
ID ADB04267 standard; DNA; 17 BP.
XX
XX ADB04267;
AC | ||||| ||||| |||||
XX 20-NOV-2003 (first entry)
DT
XX
XX Human MD27 scanning oligonucleotide SEQ ID 5253.
DE
XX
XX Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;
KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW developmental disorder; ss.
XX
XX Homo sapiens.
OS
XX
XX EP1281758-A2.
PN
XX
XX 05-FEB-2003.
PD
XX
XX 30-JUL-2002; 2002EP-00016874.
XX
XX 02-AUG-2001; 2001US-00922181.
XX
XX (AEOM-) AEOMICA INC.
XX
XX Shannon M, Gu Y, Nguyen C;
XX
```

DR WPI; 2003-423107/40.

XX New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

XX

PS Example 8; SEQ ID NO 5253; 103pp; English.

XX

CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX

SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1736 AAAAAAAAAAAAAA 1750

Db 17 AAAAAAAAAAAAAA 3

RESULT 1474

ADB02202

ID ADB02202 standard; DNA; 17 BP.

AC ADB02202;

XX

DT 20-NOV-2003 (first entry)

XX

DE Human MD24 scanning oligonucleotide SEQ ID 3188.

XX

KW Cytostatic; immunostimulant; gene therapy; vaccine; human;

KW zinc finger protein; MD23; MD24; MD27; MD212; chromosome 7q22.1;

KW chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;

KW developmental disorder; ss.

OS Homo sapiens.

XX

PN EP1281758-A2.

XX

PD 05-FEB-2003.

XX

PF 30-JUL-2002; 2002EP-00016874.

XX

PR 02-AUG-2001; 2001US-00922181.

XX

PA (AEOM-) AEOMICA INC.

XX

PI Shannon M, Gu Y, Nguyen C;

XX

DR WPI; 2003-423107/40.

XX

PT New zinc finger-containing proteins and nucleic acids, useful in

PT manufacturing a medicament for treating or preventing a disorder

PT associated with decreased or increased expression or activity of MD23,

PT MD24, MD27 or MD212, e.g. cancer.

XX

PS Example 8; SEQ ID NO 3188; 103pp; English.

XX

CC The present invention relates to novel human zinc finger-containing

CC proteins and their coding sequences: MD23, MD24, MD27, MD212. MD23 is

CC encoded at chromosome 7q22.1, MD24 is encoded at chromosome 6p21.3-22.2,

CC MD27 is encoded at chromosome 16p11.2 and MD212 is encoded at chromosome

CC 15q26.1. The MD23, MD24, MD27, and MD212 sequences are useful in therapy,

CC or in manufacturing a medicament for treating or preventing a disorder

CC associated with decreased or increased expression or activity of MD23,

CC MD24, MD27, or MD212, e.g. cancer or developmental disorders. The nucleic

CC acids and proteins are also useful for diagnosing or monitoring a disease

CC caused by altered expression of MD23, MD24, MD27, or MD212. The nucleic

CC acids can also be used as probes to detect and characterize gross

CC alterations in MD23, MD24, MD27, or MD212 genetic locus. The probes are

CC useful in constructing microarrays for measuring gene expression. The

CC proteins are useful as therapeutic agents for gene therapy or as

CC vaccines. The present sequence was used to illustrate the invention.

XX

SQ Sequence 17 BP; 8 A; 0 C; 9 G; 0 T; 0 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;

Best Local Similarity 93.3%; Pred. No. 9.6e+02;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 864 AAGAGGAAGAGGAGG 878

Db 1 AGGAGGAAGAGGAGG 15

RESULT 1475

ABZ59906/C

ID ABZ59906 standard; RNA; 17 BP.

XX

AC ABZ59906;

XX

DT 21-MAR-2003 (first entry)

XX

DE Human K-Ras DNzyme substrate #18.

XX

KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;

KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytosstatic; anti-HIV;

KW anti-rheumatic; cancer; AIDS; ss.

XX

OS Homo sapiens.

XX

PN WO200297114-A2.

XX

PD 05-DEC-2002.

XX

PF 29-MAY-2002; 2002WO-US016840.

XX

PR 29-MAY-2001; 2001US-0294140P.

PR 06-JUN-2001; 2001US-0296249P.

PR 10-SEP-2001; 2001US-0318471P.

XX

PA (RIBO-) RIBOZYME PHARM INC.

XX

PI Mcswiggen J;

XX

DR WPI; 2003-140484/13.

XX

PT Novel short interfering RNA and enzymatic nucleic acid useful for

PT treating cancer, modulates the expression of a nucleic acid encoding

PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX

PS Claim 58; Page 85; 185pp; English.

XX

CC The invention relates to a novel short interfering RNA (siRNA) nucleic

CC acid molecule or an enzymatic nucleic acid molecule, that modulates

CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,

CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic

CC acid molecule of the invention has cytosstatic, anti-HIV, and anti-

CC rheumatic activity. The nucleic acid molecules are useful for reducing

CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are

CC also useful for treating breast, ovarian, colorectal, lung, prostate, bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524, CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human CC ribozymes of the invention

XX SQ Sequence 17 BP; 1 A; 4 C; 10 G; 0 T; 2 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 529 GAGCCCGCCGACCT 543

DB 15 GAGCCCGCCGACCT 1

RESULT 1476

ID ABZ61980 standard; RNA; 17 BP.

XX AC ABZ61980;

XX DT 21-MAR-2003 (first entry)

XX DE Human H-Ras DNzyme target #771.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 58; Page 125; 185pp; English.

XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX CC ribozymes of the invention

XX SQ Sequence 17 BP; 0 A; 10 C; 4 G; 0 T; 3 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 9.6e+02;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 888 GCCCAGGTGCCCT 902

DB 2 GCCCCGUGGCCCU 16

RESULT 1477

ID ABZ61544 standard; RNA; 17 BP.

XX AC ABZ61544;

XX DT 21-MAR-2003 (first entry)

XX DE Human H-Ras DNzyme target #335.

XX KW Human; ribozyme; short interfering RNA; siRNA; HER2; K-Ras;
XX KW enzymatic nucleic acid; H-Ras; N-Ras; HIV; cytostatic; anti-HIV;
XX KW anti-rheumatic; cancer; AIDS; ss.

XX OS Homo sapiens.

XX PN WO200297114-A2.

XX PD 05-DEC-2002.

XX PF 29-MAY-2002; 2002WO-US016840.

XX PR 29-MAY-2001; 2001US-0294140P.

XX PR 06-JUN-2001; 2001US-0296249P.

XX PR 10-SEP-2001; 2001US-0318471P.

XX PA (RIBO-) RIBOZYME PHARM INC.

XX PI Mcswiggen J;

XX WPI; 2003-140484/13.

XX PT Novel short interfering RNA and enzymatic nucleic acid useful for
XX PT treating cancer, modulates the expression of a nucleic acid encoding
XX PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.

XX PS Claim 58; Page 117; 185pp; English.

XX CC The invention relates to a novel short interfering RNA (siRNA) nucleic
XX CC acid molecule or an enzymatic nucleic acid molecule, that modulates
XX CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
XX CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
XX CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
XX CC rheumatic activity. The nucleic acid molecules are useful for reducing
XX CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
XX CC also useful for treating breast, ovarian, colorectal, lung, prostate,
XX CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
XX CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ65531, ABZ66520 - ABZ66524,
XX CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
XX CC ribozymes of the invention

XX SQ Sequence 17 BP; 2 A; 6 C; 4 G; 0 T; 5 U; 0 Other;

Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1529 GCAGCCCTGCAGCG 1543

DB 16 GCAGGACTGCAGCG 2

RESULT 1478

ID ACD65653 standard; RNA; 17 BP.

XX AC ACD65653;

XX 30-SEP-2003 (first entry)
XX HCV minus strand DNazyme substrate sequence #2172.
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberyne; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer I region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX virucide; antiinflammatory; substrate; ss.
XX Hepatitis C virus.
XX WO200281494-A1.
XX 17-OCT-2002.
XX 26-MAR-2002; 2002WO-US009187.
XX 26-MAR-2001; 2001US-00817879.
XX 08-JUN-2001; 2001US-00877478.
XX 08-JUN-2001; 2001US-0296876P.
XX 24-OCT-2001; 2001US-0335059P.
XX 05-DEC-2001; 2001US-0337055P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MACE/) MACEJAK D.
XX (MCSW/) MCSWIGGEN J.
XX (MORR/) MORRISSEY D.
XX (PAVC/) PAVCO P.
XX (LEEP/) LEE P.
XX (DRAP/) DRAPER K.
XX (ROBE/) ROBERTS E.
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
XX Draper K, Roberts E;
XX WPI; 2003-229207/22.
XX Novel compound useful for treating cirrhosis, liver failure,
XX hepatocellular carcinoma, or condition associated with hepatitis C virus
XX infection.
XX Claim 1; Page 313; 387pp; English.
XX The present invention relates to nucleic acid molecules which modulate
XX the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
XX Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
XX and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
XX inozymes, zinzymes, amberyne, and G-cleaver ribozymes. Also disclosed
XX are nucleic acid decoy molecules and aptamers that bind to HBV reverse
XX transcriptase and/or HBV reverse transcriptase primer sequences, as well
XX as oligonucleotides that specifically bind the Enhancer I region of HBV
XX DNA. The nucleic acids may be used to modulate the expression of HBV
XX genes and HBV viral replication. Also disclosed is a method for screening
XX compounds and/or potential therapies directed against HBV, and compounds
XX that modulate the expression and/or replication of HCV. The compounds and
XX methods of the invention are useful for the treatment of degenerative and
XX disease states related to HBV and HCV infection, replication and gene
XX expression such as cirrhosis, liver failure, and hepatocellular
XX carcinoma. The present sequence represents a substrate for one of the HCV
XX DNazyme or minus strand DNazyme sequences disclosed in the present
XX invention
XX Sequence 17 BP; 2 A; 7 C; 6 G; 0 T; 2 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 882 GCACGGGCCCCAGGT 896
Db 16 GCAGGGGCCCCAGGT 2
RESULT 1479
ACC65252/C
ID ACC65252 standard; DNA; 17 BP.
XX ACC65252;
XX AC
XX 01-JUL-2003 (first entry)
XX Murine oligonucleotide associated with tumour suppression, SEQ ID 2499.
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
XX tumour suppression; tumour reversion; apoptosis; virus resistance;
XX viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
XX schizophrenia; ss.
XX Mus musculus.
XX WO2003025176-A2.
XX 27-MAR-2003.
XX 17-SEP-2002; 2002WO-IB004210.
XX 17-SEP-2001; 2001FR-00011979.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-333167/31.
XX New isolated nucleic acid, useful for treating viral diseases associated
XX with tumors and cell degeneration, also related polypeptides, antibodies
XX and transfected cells.
XX Disclosure; Page 323; 738pp; French.
XX The present invention relates to murine oligonucleotides (ACC62754-
XX ACC68806), which are associated with tumour suppression, tumour
XX reversion, apoptosis and virus resistance. The oligonucleotides are
XX useful as (1) as probes and primers for detecting, identifying,
XX quantifying and/or amplifying nucleic acid, e.g. as one component of a
XX gene chip; in vitro as (anti)sense reagents; and (2) for production of
XX recombinant polypeptides. The oligonucleotides are useful for preparation
XX of pharmaceuticals for prevention and/or treatment of viral diseases that
XX are characterised by development of tumours or cell degeneration,
XX specifically cancer but also Alzheimer's disease and schizophrenia
XX Sequence 17 BP; 1 A; 3 C; 3 G; 10 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 38 AAAAAAAGCCAGAA 52
Db 17 AAAAAAAGCCAGCA 3
RESULT 1480
ACC62770
ID ACC62770 standard; DNA; 17 BP.
XX ACC62770;
XX AC
XX 01-JUL-2003 (first entry)
XX

DE Murine oligonucleotide associated with tumour suppression, SEQ ID 17.
XX Cytostatic; virucide; neuroprotective; nootropic; neuroleptic; murine;
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW viral disease; tumour; cell degeneration; cancer; Alzheimer's disease;
KW schizophrenia; ss.
XX OS Mus musculus.
XX PN WO2003025176-A2.
XX PD 27-MAR-2003.
XX PF 17-SEP-2002; 2002WO-IB004210.
XX PR 17-SEP-2001; 2001FR-00011979.
XX PA (MOLE-) MOLECULAR ENGINES LAB.
XX PI Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-333167/31.
XX New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX PS Disclosure; Page 33; 738pp; French.
XX The present invention relates to murine oligonucleotides (ACC62754-
CC ACC68806), which are associated with tumour suppression, tumour
CC reversion, apoptosis and virus resistance. The oligonucleotides are
CC useful as (1) as probes and primers for detecting, identifying,
CC quantifying and/or amplifying nucleic acid, e.g. as one component of a
CC gene chip; in vitro as (anti)sense reagents; and (2) for production of
CC recombinant polypeptides. The oligonucleotides are useful for preparation
CC of pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia
XX
XX Sequence 17 BP; 12 A; 2 C; 1 G; 2 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1731 TTTACAAAAA 1745
DB 3 TCTACAAAAA 17
RESULT 1481
ADB42204/C
ID ADB42204 standard; DNA; 17 BP.
XX AC ADB42204;
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX Tumour suppression/reversion associated nucleotide #2527.
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX OS Homo sapiens.
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR 17-SEP-2001; 2001FR-00011981.

PF 17-SEP-2002; 2002WO-IB004219.
XX
XX 17-SEP-2001; 2001FR-00011981.
XX (MOLE-) MOLECULAR ENGINES LAB.
XX Telerman A, Amson R, Tuijnder M;
XX WPI; 2003-441574/41.
XX New nucleic acid encoding human prostate membrane-specific antigen,
PT useful e.g. for treatment of tumors and viral infection, also related
PT polypeptide and antibodies.
XX PS Disclosure; Page 327; 771pp; French.
XX The invention relates to the isolation of 6327 nucleotide sequences,
CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC sequence having at least 80% identity, after optimal alignment, with the
CC nucleotides, a sequence that hybridizes under stringent conditions with
CC the nucleotides, or the complement, or corresponding RNA, of the
CC nucleotides. The nucleotides are used as probes or primers for detecting,
CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC sense and antisense sequences, of nucleotides involved in tumour
CC suppression or reversion, apoptosis and or viral resistance, to produce
CC recombinant polypeptides, and to prepare transgenic animals, as
CC experimental models. The nucleotides (also vectors containing them and
CC cells containing the vectors), the encoded polypeptides and antibodies
CC (Ab) against the polypeptide are useful for prevention and/or treatment
CC of viral infections or diseases characterized by development of tumours
CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC Analysis of the expression of the nucleotides can be used for diagnosis
CC and/or prognosis of these diseases. The nucleotides and polypeptides can
CC also be used to screen for their specific interactive molecules,
CC potentially useful for treating diseases associated with abnormal
CC expression of the nucleotides.
XX
XX Sequence 17 BP; 1 A; 9 C; 1 G; 6 T; 0 U; 0 Other;
Query Match 0.8%; Score 13.4; DB 1; Length 17;
Best Local Similarity 93.3%; Pred. No. 9.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 862 GGAAGAGGAGAGGAGGA 876
DB 17 GGAGGAGGAGAGGAGGA 3
RESULT 1482
ADB40890/C
ID ADB40890 standard; DNA; 17 BP.
XX AC ADB40890;
XX 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX Tumour suppression/reversion associated nucleotide #1213.
XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX OS Homo sapiens.
XX PN WO2003040369-A2.
XX PD 15-MAY-2003.
XX PF 17-SEP-2002; 2002WO-IB004219.
XX PR 17-SEP-2001; 2001FR-00011981.

XX PA (MOLE-) MOLECULAR ENGINES LAB.
 XX PI Telerman A, Amson R, Tuijnder M;
 XX DR WPI; 2003-441574/41.
 XX PT New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX PS Disclosure; Page 173; 771pp; French.
 XX CC The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and/or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules,
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX SQ Sequence 17 BP; 1 A; 1 C; 1 G; 14 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1736 AAAAAAAAAAAAAA 1750
 DB |||||
 17 AAAAAAAAAAAAAA 3
 RESULT 1483
 ID ADD19872 standard; DNA; 17 BP.
 AC ADD19872;
 DT 15-JAN-2004 (first entry)
 XX Oreochromis niloticus microsatellite primer SEQ ID NO:507.
 DE single nucleotide polymorphism; SNP; fish; Salmo salar;
 KW Oreochromis niloticus; Atlantic halibut; microsatellite; cod;
 KW polymorphic site; seabass; salmonidae; Tilapia; rainbow trout; halibut;
 KW detection; primer; ss.
 XX Synthetic.
 OS Oreochromis niloticus.
 XX WO2003060160-A2.
 XX 24-JUL-2003.
 XX 17-JAN-2003; 2003WO-IB000112.
 XX 18-JAN-2002; 2002US-0349950P.
 XX 16-AUG-2002; 2002US-0404200P.
 XX (GENO-) GENOMAR ASA.

XX FI Lie O, Slettan A, Hoyum M, Lingaas F;
 XX DR WPI; 2003-627388/59.
 XX PT Novel isolated nucleic acid molecule comprising single nucleotide
 PT polymorphism associated with fish, useful for forming PCR primers which
 PT are used for detecting single nucleotide polymorphisms in fish nucleic
 PT acids.
 XX PS Claim 18; SEQ ID NO 507; 233pp; English.
 XX CC The present invention describes an isolated nucleic acid (I) comprising a
 CC single nucleotide polymorphism (SNP) chosen from: (i) a nucleic acid of
 CC Salmo salar SNPs, Oreochromis niloticus SNPs or Atlantic halibut SNPs;
 CC and (ii) a nucleic acid having nucleotide sequence that hybridises to
 CC (i), or its complement under highly stringent hybridisation conditions.
 CC Also described: (1) an isolated oligonucleotide (II) comprising at least
 CC 17 contiguous nucleotides of a nucleotide sequence of S. salar SNPs, O.
 CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
 CC polymorphic sites and seabass polymorphic sites, or their complement; (2)
 CC a primer pair (III) suitable for use in PCR, comprising two (ii) capable
 CC of amplifying a nucleotide sequence chosen from S. salar SNPs and, O.
 CC niloticus SNPs, O. niloticus microsatellites, Atlantic halibut SNPs, cod
 CC polymorphic sites and seabass polymorphic sites; and determining (M1) the
 CC origin of fish sample comprising providing a parentage genotype database
 CC comprising a collection of candidate parent genotypes, where each of the
 CC candidate parent genotype represents a distinct origin, and comparing a
 CC sample genotype to the parentage genotype database, where a match between
 CC the sample genotype and one of the candidate parent genotype identifies
 CC to the origin of the sample. (M1) is useful for determining the origin of
 CC a fish sample such as family salmonidae, S. salar, tilapia, O. niloticus,
 CC rainbow trout, halibut, seabass and Atlantic cod. (II) is useful for
 CC detecting nucleic acid molecule comprising SNP in a sample, which
 CC involves contacting the sample containing nucleic acids with one or more
 CC (II) derived from nucleotide sequence of S. salar SNPs and O. niloticus
 CC SNPs, and identifying nucleic acid that hybridises to (II). (II) is
 CC useful for detecting nucleic acid molecule comprising a polymorphic
 CC sequence in a sample, comprising contacting the sample containing nucleic
 CC acids with one or more (II) which is derived from O. niloticus
 CC microsatellite, O. niloticus SNPs, Atlantic halibut SNPs, cod polymorphic
 CC sites or seabass polymorphic sites, and identifying a nucleic acid that
 CC hybridises to (II). (III) is useful for detecting nucleic acid molecule
 CC comprising a microsatellite sequence in sample. The present sequence is
 CC used in the exemplification of the present invention.
 XX SQ Sequence 17 BP; 1 A; 3 C; 8 G; 5 T; 0 U; 0 Other;
 Query Match 0.8%; Score 13.4; DB 1; Length 17;
 Best Local Similarity 93.3%; Pred. No. 9.6e+02;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1024 GATGGGCTGGGGTT 1038
 DB |||||
 1 GATGGGCTGGGGTT 15
 RESULT 1484
 ACC82898
 ID ACC82898 standard; DNA; 20 BP.
 AC ACC82898;
 XX 27-AUG-2003 (first entry)
 DE Human TRIP6 antisense oligonucleotide ISIS #198770.
 XX Human; antisense; thyroid hormone receptor interactor 6; TRIP6; tumour;
 KW OPA-interacting protein-1; OIP-1; zyxin-related protein-1; prophylaxis;
 KW inflammation; therapy; hyperproliferative disorder; infection; cancer;
 KW chromosome 7q22; ZRP-1; phosphorothioate; ss.
 XX Homo sapiens.
 OS

```

OS Synthetic.
FH Key Location/Qualifiers
FT modified_base 1..20 /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone; All cytidine residues
FT are 5-methylcytidines"
FT modified_base 1..5 /*tag= b
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT modified_base 16..20 /*tag= c
FT /*mod_base= OTHER
FT /*note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX WO2003040328-A2.
PN 15-MAY-2003.
PD
XX
XX
XX 05-NOV-2002; 2002WO-US035479.
PF
XX
XX 08-NOV-2001; 2001US-00008789.
PR
XX (ISIS-) ISIS PHARM INC.
PA
XX Bennett CF, Dobie K;
PI
XX WPI; 2003-430662/40.
DR
XX New antisense oligonucleotides targeted to nucleic acids encoding thyroid
PT hormone receptor interactor 6, useful for diagnosing or treating
PT hyperproliferative disorders, such as cancer.
XX
XX Example 15; Page 76; 111pp; English.
XX
XX The invention relates to antisense compounds targetted to a nucleic acid
CC encoding thyroid hormone receptor interactor 6 (TRIP6) to inhibit its
CC expression. TRIP6 is also known as OPA-interacting protein-1 (OIP-1) and
CC zyxin-related protein-1 (ZRP-1). TRIP6 DNA is located on chromosome 7q22.
CC Antisense compounds of the invention are useful for modulating the
CC expression of TRIP6 and for treating diseases or conditions associated
CC with the expression of TRIP6 such as hyperproliferative disorders (e.g.
CC cancer). They are useful for diagnostics, therapeutics, prophylaxis e.g.
CC to prevent or delay infection, inflammation or tumour formation, as
CC research reagents and kits and in distinguishing between functions of
CC various members of a biological pathway. The are also useful in antisense
CC therapy. The present sequence is an antisense oligo targetted to human
CC TRIP6 DNA. This oligo is used in the exemplification of the invention
XX
XX Sequence 20 BP; 2 A; 5 C; 8 G; 5 T; 0 U; 0 Other;
XX
XX Query Match 0.8%; Score 13.4; DB 1; Length 20;
XX Best Local Similarity 93.3%; Pred. No. 1e+03;
XX Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 986 TTGGCCAGTGTGGTG 1000
XX ||||||| |||||
XX 1 TTGGCCAGCGTGGTG 15
XX
XX RESULT 1485
XX AAT18608/c
XX ID AAT18608 standard; DNA; 14 BP.
XX
XX AAT18608;
XX
XX 06-NOV-1996 (first entry)
XX
XX Degenerate 3' oligo dT DDRT-PCR primer T12VT.
XX
XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;

```

```

KW chondrocyte; gene specific; primer; probe; isolation; interleukin-beta;
KW IL-1beta; diagnosis; connective tissue disease; osteoarthritis;
KW rheumatoid arthritis; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
XX EP705842-A2.
XX
PD 10-APR-1996.
XX
XX 02-OCT-1995; 95EP-00115510.
XX
XX 06-OCT-1994; 94EP-00115751.
XX
XX (PARH.) HOECHST AG.
XX
XX Bartnik E, Margerie D;
XX
XX WPI; 1996-181045/19.
XX
XX Diagnosis and treatment of IL-1 mediated connective tissue diseases -
XX using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or
XX antibodies to them.
XX
XX Example; Page 15; 31pp; English.
XX
XX The present sequence is 1 of 4 degenerate 3' oligo dT primers, which were
XX used along with 25 arbitrary 5' oligodecamer primers for the differential
XX display of human chondrocyte mRNA by reverse transcription and PCR (DDRT-
XX PCR). Sequence analysis revealed the sequences of 52 cDNA clones, which
XX were then searched against DNA databases for homology to known human
XX genes. The cDNA mols. can be used for the prodn. of gene specific primers
XX and probes to isolate genes induced by the prodn. of gene specific primers
XX with interleukin-1beta (IL-1beta), and for the diagnosis of IL-1beta
XX related connective tissue diseases, in partic. osteoarthritis or
XX rheumatoid arthritis
XX
XX Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 1 Other;
XX
XX Query Match 0.8%; Score 13.2; DB 1; Length 14;
XX Best Local Similarity 92.9%; Pred. No. 8.9e+02;
XX Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1734 ACAAAAAAAAAAAAA 1747
XX ||||||| |||||
XX 14 AAAAAAAAAAAAAAA 1
XX
XX RESULT 1486
XX AAZ36741/c
XX ID AAZ36741 standard; DNA; 14 BP.
XX
XX AAZ36741;
XX
XX 13-MAR-2000 (first entry)
XX
XX Anchored oligo(dT) primer T13V used for modified differential display.
XX
XX Stimulus-regulated nucleic acid; sequence profile; nucleic acid level;
XX differentially expressed nucleic acid; disease state; cancer;
XX autoimmune disease; infectious disease; aging; developmental disorder;
XX proliferative disorder; neurological disorder; toxicity; primer;
XX treatment resistance; differential expression; drug discovery;
XX growth factor; epidermal growth factor; radiation; stress; pathogen; ss.
XX
XX Synthetic.
XX
XX WO9955913-A2.
XX
XX 04-NOV-1999.
XX
XX 27-APR-1999; 99WO-US009119.
XX
XX

```

```

PR 27-APR-1998; 98US-0083331P.
PR 27-AUG-1998; 98US-0098070P.
PR 04-FEB-1999; 99US-0118624P.
XX (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
XX McClelland M, Welsh J, Trenkle T;
XX WPI; 2000-086388/07.
DR
XX Measuring expression of low abundance reduced complexity target nucleic
XX acid molecules.
PT
XX Example 3; Page 91; 187pp; English.
PS
XX AA236739-41 represent oligo(dT) primers used for modified differential
XX display, in the method of the invention. The specification describes a
XX method for measuring the level of two or more nucleic acid molecules in a
XX target. The method comprises contacting a probe with an arbitrarily or
XX statistically sampled target and detecting the amount of specific binding
XX of the target to the probe. The methods can be used to identify
XX differentially expressed nucleic acid molecules associated with disease
XX states, such as cancer, autoimmune disease, infectious disease, aging,
XX developmental disorder, proliferative disorder or neurological disorder.
XX Alternatively the methods can be used to assess the efficacy or toxicity
XX of or a resistance to a treatment. Also the methods can be used to
XX determine differential expression of nucleic acid molecules in response
XX to a stimulus, e.g. a chemical, drug or growth factor (especially
XX epidermal growth factor), radiation, stress or a pathogen. The methods
XX can also be used to determine co-regulated genes that can be potential
XX targets for drug discovery
XX
XX Sequence 14 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 1 Other;
SQ
Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 8.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAIAAAAAAAAA 1748
Db :|||||
14 BAAAAAIAAAAAAAAA 1

RESULT 1487
AAD44146
ID AAD44146 standard; DNA; 14 BP.
XX
XX AAD44146;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Oligo-dT PCR primer #6 used to illustrate the method of the invention.
DE
XX
XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX
XX US6277571-B1.
PN
XX
XX 21-AUG-2001.
PD
XX
XX 30-SEP-1998; 98US-00163485.
PF
XX
XX 03-OCT-1997; 97US-00943162.
PR
XX 03-OCT-1997; 97US-0108152P.
PR
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
PA
XX
XX Fillmore H, Broadus W, Gillies G;
PI
XX WPI; 2002-412824/44.
DR

```

```

XX Sequential consensus region-directed amplification for sorting mixture of
XX DNAs into 2 or more subsets or distinguishing gene expression patterns in
XX 2 samples, useful for disease diagnosis and gene analysis.
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
XX amplification for sorting a mixture of DNAs into 2 or more subsets or
XX distinguishing gene expression patterns in 2 samples. The methods, kits
XX and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
XX more subsets or distinguishing gene expression patterns in 2 samples e.g.
XX for disease diagnosis and gene analysis. The present sequence is oligo dT
XX PCR primer used to illustrate the method of the invention
XX
XX Sequence 14 BP; 12 A; 1 C; 0 G; 0 T; 0 U; 1 Other;
SQ
Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 8.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1735 CAAAAAIAAAAAAAAA 1748
Db :|||||
1 CAAAAAIAAAAAAAAA 14

RESULT 1488
AAD44142
ID AAD44142 standard; DNA; 14 BP.
XX
XX AAD44142;
AC
XX
XX 13-DEC-2002 (first entry)
DT
XX
XX Oligo-dT PCR primer #2 used to illustrate the method of the invention.
DE
XX
XX Sequential consensus region-directed amplification; gene expression;
KW disease diagnosis; gene analysis; human; matrix metalloproteinase; PCR;
KW primer; ss.
XX
XX Unidentified.
OS
XX
XX US6277571-B1.
PN
XX
XX 21-AUG-2001.
PD
XX
XX 30-SEP-1998; 98US-00163485.
PF
XX
XX 03-OCT-1997; 97US-00943162.
PR
XX 03-OCT-1997; 97US-0108152P.
PR
XX
XX (UYVI-) UNIV VIRGINIA COMMONWEALTH INTELLECTUAL.
PA
XX
XX Fillmore H, Broadus W, Gillies G;
PI
XX WPI; 2002-412824/44.
DR
XX
XX Sequential consensus region-directed amplification for sorting mixture of
XX DNAs into 2 or more subsets or distinguishing gene expression patterns in
XX 2 samples, useful for disease diagnosis and gene analysis.
XX
XX Example; Fig 1C; 19pp; English.
XX
XX The invention relates to a method of sequential consensus region-directed
XX amplification for sorting a mixture of DNAs into 2 or more subsets or
XX distinguishing gene expression patterns in 2 samples. The methods, kits
XX and oligonucleotides are useful for sorting a mixture of DNAs into 2 or
XX more subsets or distinguishing gene expression patterns in 2 samples e.g.
XX for disease diagnosis and gene analysis. The present sequence is oligo dT
XX PCR primer used to illustrate the method of the invention
XX
XX Sequence 14 BP; 13 A; 0 C; 0 G; 0 T; 0 U; 1 Other;
SQ

```

Query Match 0.8%; Score 13.2; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 8.9e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1734 ACAAAAAAAAAA 1747
DB 1 AVAAAAAAAAAA 14

RESULT 1489
AA18386/c
ID AA18386 standard; DNA; 15 BP.
XX
XX AC AA18386;
XX
XX DT 11-MAY-1999 (first entry)
XX
XX DE RT-PCR primer of the invention SEQ ID 27.
XX
XX KW RT-PCR primer; DNA sequence determination; gene sequence analysis; ss.
XX
XX OS Synthetic.
XX
XX PN JP11032765-A.
XX
XX PD 09-FEB-1999.
XX
XX PF 18-JUL-1997; 97JP-00208312.
XX
XX PR 18-JUL-1997; 97JP-00208312.
XX
XX PA (TAKI) TAKARA SHUZO CO LTD.
XX
XX DR WPI; 1999-183822/16.
XX
XX PT Peptides having at least two new nucleotides - useful as primers in RT-PCR.
XX
XX PS Example 1; Page 12; 19pp; Japanese.

CC This sequence represents a primer of the invention. The invention relates to sequences of at least two nucleotides of formula: (X)m5'-(alpha)n-beta-N3'; or (X)m5'-(gamma)k-delta-N3'; where X = a labelled compound and/or a nucleotide with voluntary sequence; m = 0 or 1; alpha = thymine; n = natural number indicating the repetition of alpha; beta, delta = V or N; V = adenine, guanine or cytosine; N = adenine, guanine, cytosine or thymine; gamma = thymine; k = natural number of 3 or over indicating the repetition of gamma, in which thymine expressed by gamma is composed of 1/3 or less of adenine, guanine and/or cytosine. The new nucleotides are useful as primers for RT-PCR and determination of base sequences. The new sequences allow for reproductive and highly efficient analysis of gene sequences

Sequence 15 BP; 0 A; 0 C; 0 G; 13 T; 0 U; 2 Other;

Query Match 0.8%; Score 13.2; DB 1; Length 15;
Best Local Similarity 92.9%; Pred. No. 9.4e+02;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1735 CAAAAAAAAA 1748
DB 14 BAAAAAAAAA 1

Search completed: August 16, 2004, 15:23:58
Job time : 35 secs